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(21) International Application Number: PCT/IB98/01238 (22) International Filing Date: 31 July 1998 (31.07.98) (30) Priority Data: 08/905,134 1 August 1997 (01.08.97) US (71) Applicant (for all designated States except US): GENSET [FR/FR]; 24, rue Royale, F-75008 Paris (FR). (72) Inventors; and (75) Inventors/Applicants (for US only): DUMAS MILNE ED- WARDS, Jean-Baptiste [FR/FR]; 8, rue Grégoire de Tours, F-75006 Paris (FR). DUCLERT, Aymeric [FR/FR]; 6 ter, rue Victorine, F-94100 Saint-Maur (FR). LACROIX, Bruno [FR/FR]; 93, route de Vourles, F-69230 Saint-Genis Laval (FR). (74) Agents: MARTIN, Jean-Jacques et al.; Cabinet Regimbeau, 26, avenue Kléber, F-75116 Paris (FR).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: 5' ESTs FOR SECRETED PROTEINS EXPRESSED IN MUSCLE AND OTHER MESODERMAL TISSUES (57) Abstract The sequences of 5' ESTs derived from mRNAs encoding secreted proteins are disclosed. The 5' ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs. The 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5' ESTs. The 5' ESTs may also be used to design expression vectors and secretion vectors.		

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5' ESTs FOR SECRETED PROTEINS EXPRESSED IN MUSCLE AND OTHER MESODERMAL TISSUES

Background of the Invention

The estimated 50,000-100,000 genes scattered along the human chromosomes offer
5 tremendous promise for the understanding, diagnosis, and treatment of human diseases. In
addition, probes capable of specifically hybridizing to loci distributed throughout the human
genome find applications in the construction of high resolution chromosome maps and in the
identification of individuals.

In the past, the characterization of even a single human gene was a painstaking
10 process, requiring years of effort. Recent developments in the areas of cloning vectors, DNA
sequencing, and computer technology have merged to greatly accelerate the rate at which
human genes can be isolated, sequenced, mapped, and characterized. Cloning vectors such as
yeast artificial chromosomes (YACs) and bacterial artificial chromosomes (BACs) are able to
accept DNA inserts ranging from 300 to 1000 kilobases (kb) or 100-400 kb in length
15 respectively, thereby facilitating the manipulation and ordering of DNA sequences distributed
over great distances on the human chromosomes. Automated DNA sequencing machines
permit the rapid sequencing of human genes. Bioinformatics software enables the
comparison of nucleic acid and protein sequences, thereby assisting in the characterization of
human gene products.

20 Currently, two different approaches are being pursued for identifying and
characterizing the genes distributed along the human genome. In one approach, large
fragments of genomic DNA are isolated, cloned, and sequenced. Potential open reading
frames in these genomic sequences are identified using bioinformatics software. However,
this approach entails sequencing large stretches of human DNA which do not encode proteins
25 in order to find the protein encoding sequences scattered throughout the genome. In addition
to requiring extensive sequencing, the bioinformatics software may mischaracterize the
genomic sequences obtained. Thus, the software may produce false positives in which non-
coding DNA is mischaracterized as coding DNA or false negatives in which coding DNA is
misabeled as non-coding DNA.

30 An alternative approach takes a more direct route to identifying and characterizing
human genes. In this approach, complementary DNAs (cDNAs) are synthesized from

isolated messenger RNAs (mRNAs) which encode human proteins. Using this approach, sequencing is only performed on DNA which is derived from protein coding portions of the genome. Often, only short stretches of the cDNAs are sequenced to obtain sequences called expressed sequence tags (ESTs). The ESTs may then be used to isolate or purify extended
5 cDNAs which include sequences adjacent to the EST sequences. The extended cDNAs may contain all of the sequence of the EST which was used to obtain them or only a portion of the sequence of the EST which was used to obtain them. In addition, the extended cDNAs may contain the full coding sequence of the gene from which the EST was derived or, alternatively, the extended cDNAs may include portions of the coding sequence of the gene
10 from which the EST was derived. It will be appreciated that there may be several extended cDNAs which include the EST sequence as a result of alternate splicing or the activity of alternative promoters.

In the past, these short EST sequences were often obtained from oligo-dT primed cDNA libraries. Accordingly, they mainly corresponded to the 3' untranslated region of the
15 mRNA. In part, the prevalence of EST sequences derived from the 3' end of the mRNA is a result of the fact that typical techniques for obtaining cDNAs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs. (Adams *et al.*, *Nature* 377:3-174, 1996; Hillier *et al.*, *Genome Res.* 6:807-828, 1996).

In addition, in those reported instances where longer cDNA sequences have been
20 obtained, the reported sequences typically correspond to coding sequences and do not include the full 5' untranslated region of the mRNA from which the cDNA is derived. Such incomplete sequences may not include the first exon of the mRNA, particularly in situations where the first exon is short. Furthermore, they may not include some exons, often short ones, which are located upstream of splicing sites. Thus, there is a need to obtain sequences
25 derived from the 5' ends of mRNAs.

While many sequences derived from human chromosomes have practical applications, approaches based on the identification and characterization of those chromosomal sequences which encode a protein product are particularly relevant to diagnostic and therapeutic uses. Of the 50,000-100,000 protein coding genes, those genes encoding proteins which are
30 secreted from the cell in which they are synthesized, as well as the secreted proteins themselves, are particularly valuable as potential therapeutic agents. Such proteins are often

involved in cell to cell communication and may be responsible for producing a clinically relevant response in their target cells.

In fact, several secretory proteins, including tissue plasminogen activator, G-CSF, GM-CSF, erythropoietin, human growth hormone, insulin, interferon- α , interferon- β , interferon- γ , and interleukin-2, are currently in clinical use. These proteins are used to treat a wide range of conditions, including acute myocardial infarction, acute ischemic stroke, anemia, diabetes, growth hormone deficiency, hepatitis, kidney carcinoma, chemotherapy induced neutropenia and multiple sclerosis. For these reasons, extended cDNAs encoding secreted proteins or portions thereof represent a particularly valuable source of therapeutic agents. Thus, there is a need for the identification and characterization of secreted proteins and the nucleic acids encoding them.

In addition to being therapeutically useful themselves, secretory proteins include short peptides, called signal peptides, at their amino termini which direct their secretion. These signal peptides are encoded by the signal sequences located at the 5' ends of the coding sequences of genes encoding secreted proteins. Because these signal peptides will direct the extracellular secretion of any protein to which they are operably linked, the signal sequences may be exploited to direct the efficient secretion of any protein by operably linking the signal sequences to a gene encoding the protein for which secretion is desired. In addition, portions of signal sequences may also be used to direct the intracellular import of a peptide or protein of interest. This may prove beneficial in gene therapy strategies in which it is desired to deliver a particular gene product to cells other than the cell in which it is produced. Signal sequences encoding signal peptides also find application in simplifying protein purification techniques. In such applications, the extracellular secretion of the desired protein greatly facilitates purification by reducing the number of undesired proteins from which the desired protein must be selected. Thus, there exists a need to identify and characterize the 5' portions of the genes for secretory proteins which encode signal peptides.

Public information on the number of human genes for which the promoters and upstream regulatory regions have been identified and characterized is quite limited. In part, this may be due to the difficulty of isolating such regulatory sequences. Upstream regulatory sequences such as transcription factor binding sites are typically too short to be utilized as probes for isolating promoters from human genomic libraries. Recently, some approaches

have been developed to isolate human promoters. One of them consists of making a CpG island library (Cross, *et al.*, *Nature Genetics* 6: 236-244, 1994). The second consists of isolating human genomic DNA sequences containing SpeI binding sites by the use of SpeI binding protein. (Mortlock *et al.*, *Genome Res.* 6:327-335, 1996). Both of these approaches
5 have their limits due to a lack of specificity or of comprehensiveness.

The present 5' ESTs may be used to efficiently identify and isolate upstream regulatory regions which control the location, developmental stage, rate, and quantity of protein synthesis, as well as the stability of the mRNA. (Theil, *BioFactors* 4:87-93, 1993). Once identified and characterized, these regulatory regions may be utilized in gene therapy or
10 protein purification schemes to obtain the desired amount and locations of protein synthesis or to inhibit, reduce, or prevent the synthesis of undesirable gene products.

In addition, ESTs containing the 5' ends of secretory protein genes may include sequences useful as probes for chromosome mapping and the identification of individuals. Thus, there is a need to identify and characterize the sequences upstream of the 5' coding
15 sequences of genes encoding secretory proteins.

Summary of the Invention

The present invention relates to purified, isolated, or recombinant ESTs which include sequences derived from the authentic 5' ends of their corresponding mRNAs. The term
20 "corresponding mRNA" refers to the mRNA which was the template for the cDNA synthesis which produced the 5' EST. These sequences will be referred to hereinafter as "5' ESTs." As used herein, the term "purified" does not require absolute purity; rather, it is intended as a relative definition. Individual 5' EST clones isolated from a cDNA library have been conventionally purified to electrophoretic homogeneity. The sequences obtained from these
25 clones could not be obtained directly either from the library or from total human DNA. The cDNA clones are not naturally occurring as such, but rather are obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The conversion of mRNA into a cDNA library involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection. Thus,
30 creating a cDNA library from messenger RNA and subsequently isolating individual clones from that library results in an approximately 10^4 - 10^6 fold purification of the native message.

Purification of starting material or natural material to at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

As used herein, the term "isolated" requires that the material be removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide present in a living animal is not isolated, but the same polynucleotide, separated from some or all of the coexisting materials in the natural system, is isolated.

As used herein, the term "recombinant" means that the 5' EST is adjacent to "backbone" nucleic acid to which it is not adjacent in its natural environment. Additionally, to be "enriched" the 5' ESTs will represent 5% or more of the number of nucleic acid inserts in a population of nucleic acid backbone molecules. Backbone molecules according to the present invention include nucleic acids such as expression vectors, self-replicating nucleic acids, viruses, integrating nucleic acids, and other vectors or nucleic acids used to maintain or manipulate a nucleic acid insert of interest. Preferably, the enriched 5' ESTs represent 15% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. More preferably, the enriched 5' ESTs represent 50% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. In a highly preferred embodiment, the enriched 5' ESTs represent 90% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules.

"Stringent", moderate, and "low" hybridization conditions are as defined in Example 29.

Unless otherwise indicated, a "complementary" sequence is fully complementary.

Thus, 5' ESTs in cDNA libraries in which one or more 5' ESTs make up 5% or more of the number of nucleic acid inserts in the backbone molecules are "enriched recombinant 5' ESTs" as defined herein. Likewise, 5' ESTs in a population of plasmids in which one or more 5' EST of the present invention have been inserted such that they represent 5% or more of the number of inserts in the plasmid backbone are "enriched recombinant 5' ESTs" as defined herein. However, 5' ESTs in cDNA libraries in which 5' ESTs constitute less than 5% of the number of nucleic acid inserts in the population of backbone molecules, such as libraries in

which backbone molecules having a 5' EST insert are extremely rare, are not "enriched recombinant 5' ESTs."

In particular, the present invention relates to 5' ESTs which are derived from genes encoding secreted proteins. As used herein, a "secreted" protein is one which, when
5 expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal peptides in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g. soluble proteins), or partially (e.g. receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

10 Such 5' ESTs include nucleic acid sequences, called signal sequences, which encode signal peptides which direct the extracellular secretion of the proteins encoded by the genes from which the 5' ESTs are derived. Generally, the signal peptides are located at the amino termini of secreted proteins.

Secreted proteins are translated by ribosomes associated with the "rough"
15 endoplasmic reticulum. Generally, secreted proteins are co-translationally transferred to the membrane of the endoplasmic reticulum. Association of the ribosome with the endoplasmic reticulum during translation of secreted proteins is mediated by the signal peptide. The signal peptide is typically cleaved following its co-translational entry into the endoplasmic reticulum. After delivery to the endoplasmic reticulum, secreted proteins may proceed through the
20 Golgi apparatus. In the Golgi apparatus, the proteins may undergo post-translational modification before entering secretory vesicles which transport them across the cell membrane.

The 5' ESTs of the present invention have several important applications. For example, they may be used to obtain and express cDNA clones which include the full protein
25 coding sequences of the corresponding gene products, including the authentic translation start sites derived from the 5' ends of the coding sequences of the mRNAs from which the 5' ESTs are derived. These cDNAs will be referred to hereinafter as "full length cDNAs." These cDNAs may also include DNA derived from mRNA sequences upstream of the translation start site. The full length cDNA sequences may be used to express the proteins
30 corresponding to the 5' ESTs. As discussed above, secreted proteins are therapeutically important. Thus, the proteins expressed from the cDNAs may be useful in treating or

controlling a variety of human conditions. The 5' ESTs may also be used to obtain the corresponding genomic DNA. The term "corresponding genomic DNA" refers to the genomic DNA which encodes the mRNA from which the 5' EST was derived.

Alternatively, the 5' ESTs may be used to obtain and express extended cDNAs
5 encoding portions of the secreted protein. The portions may comprise the signal peptides of the secreted proteins or the mature proteins generated when the signal peptide is cleaved off. The portions may also comprise polypeptides having at least 10 consecutive amino acids encoded by the extended cDNAs or full length cDNAs. Alternatively, the portions may comprise at least 15 consecutive amino acids encoded by the extended cDNAs or full length
10 cDNAs. In some embodiments, the portions may comprise at least 25 consecutive amino acids encoded by the extended cDNAs or full length cDNAs. In other embodiments, the portions may comprise at least 40 amino acids encoded by the extended cDNAs or full length cDNAs.

Antibodies which specifically recognize the entire secreted proteins encoded by the
15 extended cDNAs, full length cDNAs, or fragments thereof having at least 10 consecutive amino acids, at least 15 consecutive amino acids, at least 25 consecutive amino acids, or at least 40 consecutive amino acids may also be obtained as described below. Antibodies which specifically recognize the mature protein generated when the signal peptide is cleaved may also be obtained as described below. Similarly, antibodies which specifically recognize the
20 signal peptides encoded by the extended cDNAs or full length cDNAs may also be obtained.

In some embodiments, the extended cDNAs obtained using the 5' ESTs include the signal sequence. In other embodiments, the extended cDNAs obtained using the 5' ESTs may include the full coding sequence for the mature protein (*i.e.* the protein generated when the signal polypeptide is cleaved off). In addition, the extended cDNAs obtained using the 5'
25 ESTs may include regulatory regions upstream of the translation start site or downstream of the stop codon which control the amount, location, or developmental stage of gene expression.

As discussed above, secreted proteins are therapeutically important. Thus, the proteins expressed from the extended cDNAs or full length cDNAs obtained using the 5'
30 ESTs may be useful in treating or controlling a variety of human conditions.

The 5' ESTs (or cDNAs or genomic DNAs obtained therefrom) may be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal expression of the genes corresponding to the 5' ESTs. In addition, the present invention is useful for constructing a high resolution map of the human chromosomes.

The present invention also relates to secretion vectors capable of directing the secretion of a protein of interest. Such vectors may be used in gene therapy strategies in which it is desired to produce a gene product in one cell which is to be delivered to another location in the body. Secretion vectors may also facilitate the purification of desired proteins.

The present invention also relates to expression vectors capable of directing the expression of an inserted gene in a desired spatial or temporal manner or at a desired level. Such vectors may include sequences upstream of the 5' ESTs, such as promoters or upstream regulatory sequences.

Finally, the present invention may also be used for gene therapy to control or treat genetic diseases. Signal peptides may also be fused to heterologous proteins to direct their extracellular secretion.

Bacterial clones containing Bluescript plasmids having inserts containing the 5' ESTs of the present invention (SEQ ID NOs: 38-305 are presently stored at 80°C in 4% (v/v) glycerol in the inventor's laboratories under the designations listed next to the SEQ ID NOs in II). The inserts may be recovered from the deposited materials by growing the appropriate clones on a suitable medium. The Bluescript DNA can then be isolated using plasmid isolation procedures familiar to those skilled in the art such as alkaline lysis minipreps or large scale alkaline lysis plasmid isolation procedures. If desired the plasmid DNA may be further enriched by centrifugation on a cesium chloride gradient, size exclusion chromatography, or anion exchange chromatography. The plasmid DNA obtained using these procedures may then be manipulated using standard cloning techniques familiar to those skilled in the art. Alternatively, a PCR can be done with primers designed at both ends of the EST insertion. The PCR product which corresponds to the 5' EST can then be manipulated using standard cloning techniques familiar to those skilled in the art.

One aspect of the present invention is a purified or isolated nucleic acid having the sequence of one of SEQ ID NOs: 38-305 or having a sequence complementary thereto. In one embodiment, the nucleic acid is recombinant.

Another aspect of the present invention is a purified or isolated nucleic acid comprising at least 10 consecutive bases of the sequence of one of SEQ ID NOs: 38-305 or one of the sequences complementary thereto.

Yet another aspect of the present invention is a purified or isolated nucleic acid comprising at least 15 consecutive bases of one of the sequences of SEQ ID NOs: 38-305 or one of the sequences complementary thereto. In one embodiment, the nucleic acid is recombinant.

A further aspect of the present invention is a purified or isolated nucleic acid of at least 15 bases capable of hybridizing under stringent conditions to the sequence of one of SEQ ID NOs: 38-305 or one of the sequences complementary to the sequences of SEQ ID NOs: 38-305. In one embodiment, the nucleic acid is recombinant.

Another aspect of the present invention is a purified or isolated nucleic acid encoding a human gene product, said human gene product having a sequence partially encoded by one of the sequences of SEQ ID NO: 38-305.

Still another aspect of the present invention is a method of making a cDNA encoding a human secretory protein, said human secretory protein being partially encoded by one of SEQ ID NOs 38-305, comprising the steps of contacting a collection of mRNA molecules from human cells with a primer comprising at least 15 consecutive nucleotides of a sequence complementary to one of SEQ ID NOs: 38-305; hybridizing said primer to an mRNA in said collection that encodes said protein; reverse transcribing said hybridized primer to make a first cDNA strand from said mRNA; making a second cDNA strand complementary to said first cDNA strand; and isolating the resulting cDNA encoding said protein comprising said first cDNA strand and said second cDNA strand.

Another aspect of the invention is an isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-305 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method described in the preceding paragraph. In one embodiment, the

cDNA comprises the full protein coding sequence of said protein which sequence is partially included in one of the sequences of SEQ ID NOs: 38-305.

Another aspect of the present invention is a method of making a cDNA encoding a human secretory protein that is partially encoded by one of SEQ ID NOs 38-305, comprising the steps of obtaining a cDNA comprising one of the sequences of SEQ ID NOs: 38-305; contacting said cDNA with a detectable probe comprising at least 15 consecutive nucleotides of said sequence of SEQ ID NO: 38-305 or a sequence complementary thereto under conditions which permit said probe to hybridize to said cDNA; identifying a cDNA which hybridizes to said detectable probe; and isolating said cDNA which hybridizes to said probe.

Another aspect of the present invention is an isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-305 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method described in the preceding paragraph. In one embodiment, the cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-305.

Another aspect of the present invention is a method of making a cDNA comprising one of the sequence of SEQ ID NOs: 38-305, comprising the steps of contacting a collection of mRNA molecules from human cells with a first primer capable of hybridizing to the polyA tail of said mRNA; hybridizing said first primer to said polyA tail; reverse transcribing said mRNA to make a first cDNA strand; making a second cDNA strand complementary to said first cDNA strand using at least one primer comprising at least 15 nucleotides of one of the sequences of SEQ ID NOs 38-305; and isolating the resulting cDNA comprising said first cDNA strand and said second cDNA strand.

Another aspect of the present invention is an isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-305 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method described in the preceding paragraph. In one embodiment, the cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-305.

In one embodiment of the method described in the two paragraphs above, the second cDNA strand is made by contacting said first cDNA strand with a first pair of primers, said

first pair of primers comprising a second primer comprising at least 15 consecutive nucleotides of one of the sequences of SEQ ID NOs 38-305 and a third primer having a sequence therein which is included within the sequence of said first primer, performing a first polymerase chain reaction with said first pair of nested primers to generate a first PCR product; contacting said first PCR product with a second pair of primers, said second pair of primers comprising a fourth primer, said fourth primer comprising at least 15 consecutive nucleotides of said sequence of one of SEQ ID NOs: 38-305, and a fifth primer, said fourth and fifth primers being capable of hybridizing to sequences within said first PCR product; and performing a second polymerase chain reaction, thereby generating a second PCR product.

One aspect of the present invention is an isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-305, or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of the preceding paragraph. In one embodiment, the cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-305.

Another aspect of the present invention is the method described four paragraphs above in which the second cDNA strand is made by contacting said first cDNA strand with a second primer comprising at least 15 consecutive nucleotides of the sequences of SEQ ID NOs: 38-305; hybridizing said second primer to said first strand cDNA; and extending said hybridized second primer to generate said second cDNA strand.

Another aspect of the present invention is an isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein partially encoded by one of SEQ ID NOs 38-305 or comprising a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method described in the preceding paragraph. In one embodiment, the cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-305.

Another aspect of the present invention is a method of making a protein comprising one of the sequences of SEQ ID NOs: 306-573, comprising the steps of obtaining a cDNA encoding the full protein sequence partially included in one of the sequences of sequence of SEQ ID NOs: 38-305; inserting said cDNA in an expression vector such that said cDNA is

operably linked to a promoter; introducing said expression vector into a host cell whereby said host cell produces the protein encoded by said cDNA; and isolating said protein.

Another aspect of the present invention is an isolated protein obtainable by the method described in the preceding paragraph.

5 Another aspect of the present invention is a method of obtaining a promoter DNA comprising the steps of obtaining DNAs located upstream of the nucleic acids of SEQ ID NOs: 38-305 or the sequences complementary thereto; screening said upstream DNAs to identify a promoter capable of directing transcription initiation; and isolating said DNA comprising said identified promoter. In one embodiment, the obtaining step comprises
10 chromosome walking from said nucleic acids of SEQ ID NOs: 38-305 or sequences complementary thereto. In another embodiment, the screening step comprises inserting said upstream sequences into a promoter reporter vector. In another embodiment, the screening step comprises identifying motifs in said upstream DNAs which are transcription factor binding sites or transcription start sites.

15 Another aspect of the present invention is an isolated promoter obtainable by the method described above.

Another aspect of the present invention is an isolated or purified protein comprising one of the sequences of SEQ ID NOs: 306-573.

Another aspect of the present invention is the inclusion of at least one of the
20 sequences of SEQ ID NOs: 38-305, or one of the sequences complementary to the sequences of SEQ ID NOs: 38-305, or a fragment thereof of at least 15 consecutive nucleotides in an array of discrete ESTs or fragments thereof of at least 15 nucleotides in length. In one embodiment, the array includes at least two of the sequences of SEQ ID NOs: 38-305, the sequences complementary to the sequences of SEQ ID NOs: 38-305, or fragments thereof of
25 at least 15 consecutive nucleotides. In another embodiment, the array includes at least five of the sequences of SEQ ID NOs: 38-305, the sequences complementary to the sequences of SEQ ID NOs: 38-305, or fragments thereof of at least 15 consecutive nucleotides.

Another aspect of the present invention is a promoter having a sequence selected from the group consisting of SEQ ID NOs: 31, 34, and 37.

Brief Description of the Drawings

Figure 1 is a summary of a procedure for obtaining cDNAs which have been selected to include the 5' ends of the mRNAs from which they derived.

Figure 2 shows the distribution of Von Heijne scores for 5' ESTs in each of the categories described herein and the probability that these 5' ESTs encode a signal peptide.

Figure 3 summarizes a general method used to clone and sequence extended cDNAs containing sequences adjacent to 5' ESTs.

Figure 4 (description of promoters structure isolated from SignalTag 5' ESTs) provides a schematic description of promoters isolated and the way they are assembled with the corresponding 5' tags.

Detailed Description of the Preferred Embodiment

Table IV is an analysis of the 43 amino acids located at the N terminus of all human SwissProt proteins to determine the frequency of false positives and false negatives using the techniques for signal peptide identification described herein.

Table V shows the distribution of 5' ESTs in each category described herein and the number of 5' ESTs in each category having a given minimum Von Heijne's score.

Table VI shows the distribution of 5' ESTs in each category described herein with respect to the tissue from which the 5' ESTs of the corresponding mRNA were obtained.

Table VII describes the transcription factor binding sites present in each of these promoters.

I. General Methods for Obtaining 5' ESTs derived from mRNAs with intact 5' ends

In order to obtain the 5' ESTs of the present invention, mRNAs with intact 5' ends must be obtained. Currently, there are two approaches for obtaining such mRNAs with intact 5' ends as described below: either chemical (1) or enzymatic (2).

1. Chemical Methods for Obtaining mRNAs having Intact 5' Ends

One of these approaches is a chemical modification method involving derivatization of the 5' ends of the mRNAs and selection of the derivatized mRNAs. The 5' ends of eukaryotic mRNAs possess a structure referred to as a "cap" which comprises a guanosine

5 methylated at the 7 position. The cap is joined to the first transcribed base of the mRNA by a 5', 5'-triphosphate bond. In some instances, the 5' guanosine is methylated in both the 2 and 7 positions. Rarely, the 5' guanosine is trimethylated at the 2, 7 and 7 positions. In the chemical method for obtaining mRNAs having intact 5' ends, the 5' cap is specifically derivatized and coupled to a reactive group on an immobilizing substrate. This specific derivatization is based on the fact that only the ribose linked to the methylated guanosine at the 5' end of the mRNA and the ribose linked to the base at the 3' terminus of the mRNA, possess 2', 3'-cis diols.

10 Optionally, the 2', 3'-cis diol of the 3' terminal ribose may be chemically modified, substituted, converted, or eliminated, leaving only the ribose linked to the methylated guanosine at the 5' end of the mRNA with a 2', 3'-cis diol. A variety of techniques are available for eliminating the 2', 3'-cis diol on the 3' terminal ribose. For example, controlled alkaline hydrolysis may be used to generate mRNA fragments in which the 3' terminal ribose is a 3'-phosphate, 2'-phosphate or (2', 3')-cyclophosphate.

15 Thereafter, the fragment which includes the original 3' ribose may be eliminated from the mixture through chromatography on an oligodT column. Alternatively, a base which lacks the 2', 3'-cis diol may be added to the 3' end of the mRNA using an RNA ligase such as T4 RNA ligase. Example 1 below describes a method for ligation of a nucleoside diphosphate to the 3' end of messenger RNA.

20

EXAMPLE 1

Ligation of the Nucleoside Diphosphate pCp to the 3' End of mRNA

One μg of RNA was incubated in a final reaction medium of $10\ \mu\text{l}$ in the presence of 5 U of T₄ phage RNA ligase in the buffer provided by the manufacturer (Gibco - BRL), 40 U of the RNase inhibitor RNasin (Promega) and, 2 μl of ³²pCp (Amersham #PB 25 10208). The incubation was performed at 37°C for 2 hours or overnight at 7-8°C.

Following modification or elimination of the 2', 3'-cis diol at the 3' ribose, the 2', 3'-cis diol present at the 5' end of the mRNA may be oxidized using reagents such as NaBH₄, 30 NaBH₃CN, or sodium periodate, thereby converting the 2', 3'-cis diol to a dialdehyde.

Example 2 describes the oxidation of the 2', 3'-cis diol at the 5' end of the mRNA with sodium periodate.

EXAMPLE 2

5 Oxidation of 2', 3'-cis diol at the 5' End of the mRNA with Sodium Periodate

0.1 OD unit of either a capped oligoribonucleotide of 47 nucleotides (including the cap) or an uncapped oligoribonucleotide of 46 nucleotides were treated as follows. The oligoribonucleotides were produced by *in vitro* transcription using the transcription kit "AmpliScribe T7" (Epicentre Technologies). As indicated below, the DNA template for the
10 RNA transcript contained a single cytosine. To synthesize the uncapped RNA, all four NTPs were included in the *in vitro* transcription reaction. To obtain the capped RNA, GTP was replaced by an analogue of the cap, m7G(5')ppp(5')G. This compound, recognized by the polymerase, was incorporated into the 5' end of the nascent transcript during the initiation of transcription but was not incorporated during the extension step. Consequently, the resulting
15 RNA contained a cap at its 5' end. The sequences of the oligoribonucleotides produced by the *in vitro* transcription reaction were:

+Cap:

5'm7GpppGCAUCCUACUCCCAUCCAAUUCCACCCUAACUCCUCCCAUCUCCAC-
3' (SEQ ID NO:1)

20 -Cap:

5'-pppGCAUCCUACUCCCAUCCAAUUCCACCCUAACUCCUCCCAUCUCCAC-3'
(SEQ ID NO:2)

The oligoribonucleotides were dissolved in 9 µl of acetate buffer (0.1 M sodium acetate, pH 5.2) and 3 µl of freshly prepared 0.1 M sodium periodate solution. The mixture
25 was incubated for 1 hour in the dark at 4°C or room temperature. Thereafter, the reaction was stopped by adding 4 µl of 10% ethylene glycol. The product was ethanol precipitated, resuspended in at least 10 µl of water or appropriate buffer and dialyzed against water.

The resulting aldehyde groups may then be coupled to molecules having a reactive
30 amine group, such as hydrazine, carbazide, thiocarbazide or semicarbazide groups, in order to facilitate enrichment of the 5' ends of the mRNAs. Molecules having reactive amine groups

which are suitable for use in selecting mRNAs having intact 5' ends include avidin, proteins, antibodies, vitamins, ligands capable of specifically binding to receptor molecules, or oligonucleotides. Example 3 below describes the coupling of the resulting dialdehyde to biotin.

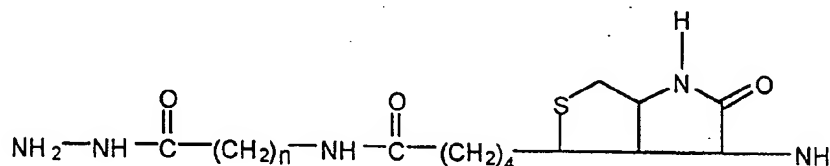
5

EXAMPLE 3

Coupling of the Dialdehyde at the 5' End of Transcripts with Biotin

The oxidation product obtained in Example 2 was dissolved in 50 μ l of sodium acetate at a pH between 5 and 5.2 and 50 μ l of freshly prepared 0.02 M solution of biotin hydrazide in a methoxyethanol/water mixture (1:1) of formula:

10



In the compound used in these experiments, $n=5$. However, it will be appreciated that other commercially available hydrazides may also be used, such as molecules of the above formula in which n varies from 0 to 5. The mixture was then incubated for 2 hours at 37°C, precipitated with ethanol and dialyzed against distilled water. Example 4 demonstrates the specificity of the biotinylation reaction.

15

EXAMPLE 4

20

Specificity of Biotinylation of Capped Transcripts

The specificity of the biotinylation for capped mRNAs was evaluated by gel electrophoresis of the following samples:

Sample 1. The 46 nucleotide uncapped *in vitro* transcript prepared as in Example 2 and labeled with 32 PpCp as described in Example 1.

25

Sample 2. The 46 nucleotide uncapped *in vitro* transcript prepared as in Example 2, labeled with 32 PpCp as described in Example 1, treated with the oxidation reaction of Example 2, and subjected to the biotinylation conditions of Example 3.

Sample 3. The 47 nucleotide capped *in vitro* transcript prepared as in Example 2 and labeled with 32 pCp as described in Example 1.

Sample 4. The 47 nucleotide capped *in vitro* transcript prepared as in Example 2, labeled with 32 pCp as described in Example 1, treated with the oxidation reaction of Example 2, and subjected to the biotinylation conditions of Example 3.

Samples 1 and 2 had identical migration rates, demonstrating that the uncapped RNAs were not oxidized and biotinylated. Sample 3 migrated more slowly than Samples 1 and 2, while Sample 4 exhibited the slowest migration. The difference in migration of the RNAs in Samples 3 and 4 demonstrates that the capped RNAs were specifically biotinylated.

In some cases, mRNAs having intact 5' ends may be enriched by binding the molecule containing a reactive amine group to a suitable solid phase substrate such as the inside of the vessel containing the mRNAs, magnetic beads, chromatography matrices, or nylon or nitrocellulose membranes. For example, where the molecule having a reactive amine group is biotin, the solid phase substrate may be coupled to avidin or streptavidin. Alternatively, where the molecule having the reactive amine group is an antibody or receptor ligand, the solid phase substrate may be coupled to the cognate antigen or receptor. Finally, where the molecule having a reactive amine group comprises an oligonucleotide, the solid phase substrate may comprise a complementary oligonucleotide.

The mRNAs having intact 5' ends may be released from the solid phase following the enrichment procedure. For example, where the dialdehyde is coupled to biotin hydrazide and the solid phase comprises streptavidin, the mRNAs may be released from the solid phase by simply heating to 95 degrees Celsius in 2% SDS. In some methods, the molecule having a reactive amine group may also be cleaved from the mRNAs having intact 5' ends following enrichment. Example 5 describes the capture of biotinylated mRNAs with streptavidin coated beads and the release of the biotinylated mRNAs from the beads following enrichment.

EXAMPLE 5

Capture and Release of Biotinylated mRNAs Using Streptavidin Coated Beads

The streptavidin coated magnetic beads were prepared according to the manufacturer's instructions (CPG Inc., USA). The biotinylated mRNAs were added to a

hybridization buffer (1.5 M NaCl, pH 5 - 6). After incubating for 30 minutes, the unbound and nonbiotinylated material was removed. The beads were then washed several times in water with 1% SDS. The beads thus obtained were incubated for 15 minutes at 95°C in water containing 2% SDS.

- 5 Example 6 demonstrates the efficiency with which biotinylated mRNAs were recovered from the streptavidin coated beads.

EXAMPLE 6

Efficiency of Recovery of Biotinylated mRNAs

- 10 The efficiency of the recovery procedure was evaluated as follows. Capped RNAs were labeled with ^{32}pCp , oxidized, biotinylated and bound to streptavidin coated beads as described above. Subsequently, the bound RNAs were incubated for 5, 15 or 30 minutes at 95°C in the presence of 2% SDS.

- 15 The products of the reaction were analyzed by electrophoresis on 12% polyacrylamide gels under denaturing conditions (7 M urea). The gels were subjected to autoradiography. During this manipulation, the hydrazone bonds were not reduced.

Increasing amounts of nucleic acids were recovered as incubation times in 2% SDS increased, demonstrating that biotinylated mRNAs were efficiently recovered.

- 20 In an alternative method for obtaining mRNAs having intact 5' ends, an oligonucleotide which has been derivatized to contain a reactive amine group is specifically coupled to mRNAs having an intact cap. Preferably, the 3' end of the mRNA is blocked prior to the step in which the aldehyde groups are joined to the derivatized oligonucleotide, as described above, so as to prevent the derivatized oligonucleotide from being joined to the 3' end of the mRNA. For example, pCp may be attached to the 3' end of the mRNA using T4 RNA ligase as described in example 1. However, as discussed above, blocking the 3' end of the mRNA is an optional step. Derivatized oligonucleotides may be prepared as described in Example 7.

EXAMPLE 7Derivatization of Oligonucleotides

An oligonucleotide phosphorylated at its 3' end was converted to a 3' hydrazide in 3' by treatment with an aqueous solution of hydrazine or of dihydrazide of the formula
5 $H_2N(R1)NH_2$ at about 1 to 3 M, and at pH 4.5 at a temperature of 8°C overnight. This incubation was performed in the presence of a carbodiimide type agent soluble in water such as 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide at a final concentration of 0.3 M.

The derivatized oligonucleotide was then separated from the other agents and products using a standard technique for isolating oligonucleotides.

10 As discussed above, the mRNAs to be enriched may be treated to eliminate the 3' OH groups which may be present thereon. This may be accomplished by enzymatic ligation of sequences lacking a 3' OH, such as pCp, as described in Example 1. Alternatively, the 3' OH groups may be eliminated by alkaline hydrolysis as described in Example 8 below.

15

EXAMPLE 8Elimination of 3' OH Groups of mRNA Using Alkaline Hydrolysis

In a total volume of 100 μ l of 0.1 N sodium hydroxide, 1.5 μ g mRNA is incubated for 40 to 60 minutes at 4°C. The solution is neutralized with acetic acid and precipitated with ethanol.

20 Following the optional elimination of the 3' OH groups, the diol groups at the 5' ends of the mRNAs are oxidized as described below in Example 9.

EXAMPLE 9Oxidation of Diols of mRNA

25 Up to 1 OD unit of RNA was dissolved in 9 μ l of buffer (0.1 M sodium acetate, pH 6-7) or water and 3 μ l of freshly prepared 0.1 M sodium periodate solution. The reaction was incubated for 1 h in the dark at 4°C or room temperature. Following the incubation, the reaction was stopped by adding 4 μ l of 10% ethylene glycol. Thereafter the mixture was incubated at room temperature for 15 minutes. After ethanol precipitation, the product was
30 resuspended in at least 10 μ l of water or appropriate buffer and dialyzed against water.

Following oxidation of the diol groups at the 5' ends of the mRNAs, the derivatized oligonucleotide was joined to the resulting aldehydes as described in Example 10.

EXAMPLE 10

5 Ligature of Aldehydes of mRNA to Derivatized Oligonucleotides

The oxidized mRNA was dissolved in an acidic medium such as 50 µl of sodium acetate pH 4-6. Fifty µl of a solution of the derivatized oligonucleotide were added in order to obtain an mRNA:derivatized oligonucleotide ratio of 1:20. The mixture was reduced with a borohydride and incubated for 2 h at 37°C or overnight (14 h) at 10°C. The mixture was
10 then ethanol precipitated, resuspended in 10 µl or more of water or appropriate buffer and dialyzed against distilled water. If desired, the resulting product may be analyzed using acrylamide gel electrophoresis, HPLC analysis, or other conventional techniques.

Following the attachment of the derivatized oligonucleotide to the mRNAs, a reverse
15 transcription reaction may be performed as described in Example 11 below.

EXAMPLE 11

Reverse Transcription of mRNAs Ligatured to Derivatized Oligonucleotides

An oligodeoxyribonucleotide was derivatized as follows. Three OD units of an
20 oligodeoxyribonucleotide of sequence 5'ATCAAGAATTCGCACGAGACCATTAA3' (SEQ ID NO:3) having 5'-OH and 3'-P ends were dissolved in 70 µl of a 1.5 M hydroxybenzotriazole solution, pH 5.3, prepared in dimethylformamide/water (75:25) containing 2 µg of 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide. The mixture was incubated for 2 h 30 min at 22°C and then precipitated twice in LiClO₄/acetone. The pellet
25 was resuspended in 200 µl of 0.25 M hydrazine and incubated at 8°C from 3 to 14 h. Following the hydrazine reaction, the mixture was precipitated twice in LiClO₄/acetone.

The messenger RNAs to be reverse transcribed were extracted from blocks of placenta having sides of 2 cm which had been stored at -80°C. The total RNA was extracted using conventional acidic phenol techniques. Oligo-dT chromatography was used to purify
30 the mRNAs. The integrity of the mRNAs was checked by Northern-blotting.

The diol groups on 7 μ g of the placental mRNAs were oxidized as described above in Example 9. The derivatized oligonucleotide was joined to the mRNAs as described in Example 10 above except that the precipitation step was replaced by an exclusion chromatography step to remove derivatized oligodeoxyribonucleotides which were not joined to mRNAs. Exclusion chromatography was performed as follows:

Ten ml of Ultrogel AcA34 (BioSeptra#230151) gel, a mix of agarose and acrylamide, were equilibrated in 50 ml of a solution of 10 mM Tris pH 8.0, 300 mM NaCl, 1 mM EDTA, and 0.05% SDS. The mixture was allowed to sediment. The supernatant was eliminated and the gel was resuspended in 50 ml of buffer. This procedure was repeated 2 or 3 times.

A glass bead (diameter 3 mm) was introduced into a 2 ml disposable pipette (length 25 cm). The pipette was filled with the gel suspension until the height of the gel stabilized at 1 cm from the top of the pipette. The column was then equilibrated with 20 ml of equilibration buffer (10 mM Tris HCl pH 7.4, 20 mM NaCl).

Ten μ l of the mRNA which had reacted with the derivatized oligonucleotide were mixed in 39 μ l of 10 mM urea and 2 μ l of blue-glycerol buffer, which had been prepared by dissolving 5 mg of bromophenol blue in 60% glycerol (v/v), and passing the mixture through a 0.45 μ m diameter filter.

The column was then loaded with the mRNAs coupled to the oligonucleotide. As soon as the sample had penetrated, equilibration buffer was added. Hundred μ l fractions were then collected. Derivatized oligonucleotide which had not been attached to mRNA appeared in fraction 16 and later fractions. Thus, fractions 3 to 15 were combined and precipitated with ethanol.

To determine whether the derivatized oligonucleotide was actually linked to mRNA, one tenth of the combined fractions were spotted twice on a nylon membrane and hybridized to a radioactive probe using conventional techniques. The 32 P labeled probe used in these hybridizations was an oligodeoxyribonucleotide of sequence 5'TAATGGTCTCGTGCGAATTCTTGAT3' (SEQ ID NO:4) anticomplementary to the derivatized oligonucleotide. A signal observed after autoradiography, indicated that the derivatized oligonucleotide had been truly joined to the mRNA.

The remaining nine tenth of the mRNAs which had reacted with the derivatized oligonucleotide was reverse transcribed as follows. A reverse transcription reaction was

carried out with reverse transcriptase following the manufacturer's instructions and 50 pmol of nonamers with random sequence as primers.

To ensure that reverse transcription had been carried out through the cap structure, two types of experiments were performed.

- 5 In the first approach, after elimination of RNA of the cDNA:RNA heteroduplexes obtained from the reverse transcription reaction by an alkaline hydrolysis, a portion of the resulting single stranded cDNAs was spotted on a positively charged membrane and hybridized, using conventional methods, to a ³²P labeled probe having a sequence identical to that of the derivatized oligonucleotide. Control spots containing, 1 pmol, 100 fmol, 50 fmol, 10 fmol and 1 fmol of a control oligodeoxyribonucleotide of sequence identical to that of the derivatized oligonucleotide were included. The signal observed in the spots containing the cDNA indicated that approximately 15 fmol of the derivatized oligonucleotide had been reverse transcribed. These results demonstrate that the reverse transcription can be performed through the cap and, in particular, that reverse transcriptase crosses the 5'-P-P-P-
10 5' bond of the cap of eukaryotic messenger RNAs.
15

- In the second type of experiment, the single stranded cDNAs obtained from the above first strand synthesis were used as template for PCR reactions. Two types of reactions were carried out. First, specific amplification of the mRNAs for alpha globin, dehydrogenase, pp15 and elongation factor E4 were carried out using the following pairs of
20 oligodeoxyribonucleotide primers.

alpha-globin

GLO-S: 5'CCG ACA AGA CCA ACG TCA AGG CCG C3' (SEQ ID NO:5)

GLO-As: 5'TCA CCA GCA GGC AGT GGC TTA GGA G 3' (SEQ ID NO:6)

25

dehydrogenase

3 DH-S: 5'AGT GAT TCC TGC TAC TTT GGA TGG C3' (SEQ ID NO:7)

3 DH-As: 5'GCT TGG TCT TGT TCT GGA GTT TAG A3' (SEQ ID NO:8)

30

pp15

PP15-S: 5'TCC AGA ATG GGA GAC AAG CCA ATT T3' (SEQ ID NO:9)

PP15-As: 5'AGG GAG GAG GAA ACA GCG TGA GTC C3' (SEQ ID NO:10)

Elongation factor E4

EFA1-S: 5'ATG GGA AAG GAA AAG ACT CAT ATC A3' (SEQ ID NO:11)

5 EF1A-As: 5'AGC AGC AAC AAT CAG GAC AGC ACA G3' (SEQ ID NO:12)

Second, non specific amplifications were also carried out with the antisense oligodeoxyribonucleotides of the pairs described above and with a primer derived from the sequence of the derivatized oligodeoxyribonucleotide
10 (5'ATCAAGAATTTCGCACGAGACCATTAA3') (SEQ ID NO:13).

One twentieth of the following RT-PCR product samples were run on a 1.5% agarose gel and stained with ethidium bromide.

Sample 1: The products of a PCR reaction using the globin primers of SEQ ID NOs 5 and 6 in the presence of cDNA.

15 Sample 2: The products of a PCR reaction using the globin primers of SEQ ID NOs 5 and 6 in the absence of added cDNA.

Sample 3: The products of a PCR reaction using the dehydrogenase primers of SEQ ID NOs 7 and 8 in the presence of cDNA.

Sample 4: The products of a PCR reaction using the dehydrogenase primers of SEQ
20 ID NOs 7 and 8 in the absence of added cDNA.

Sample 5: The products of a PCR reaction using the pp15 primers of SEQ ID NOs 9 and 10 in the presence of cDNA.

Sample 6: The products of a PCR reaction using the pp15 primers of SEQ ID NOs 9 and 10 in the absence of added cDNA.

25 Sample 7: The products of a PCR reaction using the EIF4 primers of SEQ ID NOs 11 and 12 in the presence of added cDNA.

Sample 8: The products of a PCR reaction using the EIF4 primers of SEQ ID NOs 11 and 12 in the absence of added cDNA.

A band of the size expected for the PCR product was observed only in samples 1, 3,
30 5 and 7, thus indicating the presence of the corresponding sequence in the cDNA population.

PCR reactions were also carried out with the antisense oligonucleotides of the globin and dehydrogenase primers (SEQ ID NOs 6 and 8) and an oligonucleotide whose sequence corresponds to that of the derivatized oligonucleotide. The presence of PCR products of the expected size in the samples equivalent to above samples 1 and 3 indicated that the
5 derivatized oligonucleotide had been linked to mRNA.

The above examples summarize the chemical procedure for enriching mRNAs for those having intact 5' ends as illustrated in Figure 1. Further detail regarding the chemical approaches for obtaining such mRNAs are disclosed in International Application No.
10 WO96/34981, published November 7, 1996, which is incorporated herein by reference. Strategies based on the above chemical modifications to the 5' cap structure may be utilized to generate cDNAs selected to include the 5' ends of the mRNAs from which they derived. In one version of such procedures, the 5' ends of the mRNAs are modified as described above. Thereafter, a reverse transcription reaction is conducted to extend a primer
15 complementary to the 5' end of the mRNA. Single stranded RNAs are eliminated to obtain a population of cDNA/mRNA heteroduplexes in which the mRNA includes an intact 5' end. The resulting heteroduplexes may be captured on a solid phase coated with a molecule capable of interacting with the molecule used to derivatize the 5' end of the mRNA. Thereafter, the strands of the heteroduplexes are separated to recover single stranded first
20 cDNA strands which include the 5' end of the mRNA. Second strand cDNA synthesis may then proceed using conventional techniques. For example, the procedures disclosed in WO 96/34981 or in Carninci. *et al.*, *Genomics* 37:327-336, 1996, the disclosures of which are incorporated herein by reference, may be employed to select cDNAs which include the sequence derived from the 5' end of the coding sequence of the mRNA.

25 Following ligation of the oligonucleotide tag to the 5' cap of the mRNA, a reverse transcription reaction is conducted to extend a primer complementary to the mRNA to the 5' end of the mRNA. Following elimination of the RNA component of the resulting heteroduplex using standard techniques, second strand cDNA synthesis is conducted with a primer complementary to the oligonucleotide tag.

2. Enzymatic Methods for Obtaining mRNAs having Intact 5' Ends

Other techniques for selecting cDNAs extending to the 5' end of the mRNA from which they are derived are fully enzymatic. Some versions of these techniques are disclosed in Dumas Milne Edwards J.B. (Doctoral Thesis of Paris VI University, Le clonage des ADNc complets: difficultes et perspectives nouvelles. Apports pour l'etude de la regulation de l'expression de la tryptophane hydroxylase de rat, 20 Dec. 1993), EP0 625572 and Kato *et al.*, *Gene* 150:243-250, 1994, the disclosures of which are incorporated herein by reference.

Briefly, in such approaches, isolated mRNA is treated with alkaline phosphatase to remove the phosphate groups present on the 5' ends of uncapped incomplete mRNAs. Following this procedure, the cap present on full length mRNAs is enzymatically removed with a decapping enzyme such as T4 polynucleotide kinase or tobacco acid pyrophosphatase. An oligonucleotide, which may be either a DNA oligonucleotide or a DNA-RNA hybrid oligonucleotide having RNA at its 3' end, is then ligated to the phosphate present at the 5' end of the decapped mRNA using T4 RNA ligase. The oligonucleotide may include a restriction site to facilitate cloning of the cDNAs following their synthesis. Example 12 below describes one enzymatic method based on the doctoral thesis of Dumas.

EXAMPLE 12

Enzymatic Approach for Obtaining 5' ESTs

Twenty micrograms of PolyA⁺ RNA were dephosphorylated using Calf Intestinal Phosphatase (Biolabs). After a phenol chloroform extraction, the cap structure of mRNA was hydrolysed using the Tobacco Acid Pyrophosphatase (purified as described by Shinshi *et al.*, *Biochemistry* 15: 2185-2190, 1976) and a hemi 5'DNA/RNA-3' oligonucleotide having an unphosphorylated 5' end, a stretch of adenosine ribophosphate at the 3' end, and an EcoRI site near the 5' end was ligated to the 5'P ends of mRNA using the T4 RNA ligase (Biolabs). Oligonucleotides suitable for use in this procedure are preferably 30 to 50 bases in length. Oligonucleotides having an unphosphorylated 5' end may be synthesized by adding a fluorochrome at the 5' end. The inclusion of a stretch of adenosine ribophosphates at the 3' end of the oligonucleotide increases ligation efficiency. It will be appreciated that the oligonucleotide may contain cloning sites other than EcoRI.

Following ligation of the oligonucleotide to the phosphate present at the 5' end of the decapped mRNA, first and second strand cDNA synthesis is carried out using conventional methods or those specified in EP0 625,572 and Kato *et al. supra*, and Dumas Milne Edwards, *supra*, the disclosures of which are incorporated herein by reference. The resulting cDNA may then be ligated into vectors such as those disclosed in Kato *et al. supra* or other nucleic acid vectors known to those skilled in the art using techniques such as those described in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual 2d Ed., Cold Spring Harbor Laboratory Press, 1989, the disclosure of which is incorporated herein by reference.

II. Obtention and Characterization of the 5' ESTs of the Present Invention

The 5' ESTs of the present invention were obtained using the aforementioned chemical and enzymatic approaches for enriching mRNAs for those having intact 5' ends as described below.

1. Obtention of 5' ESTS Using mRNAs with Intact 5' Ends

First, mRNAs were prepared as described in Example 13 below.

EXAMPLE 13

Preparation of mRNA With Intact 5' Ends

Total human RNAs or polyA⁺ RNAs derived from 29 different tissues were respectively purchased from LABIMO and CLONTECH and used to generate 44 cDNA libraries as follows. The purchased RNA had been isolated from cells or tissues using acid guanidium thiocyanate-phenol-chloroform extraction (Chomczynski and Sacchi, *Analytical Biochemistry* 162:156-159, 1987). PolyA⁺ RNA was isolated from total RNA (LABIMO) by two passes of oligo dT chromatography, as described by Aviv and Leder, *Proc. Natl. Acad. Sci. USA* 69:1408-1412, 1972 in order to eliminate ribosomal RNA.

The quality and the integrity of the polyA⁺ RNAs were checked. Northern blots hybridized with a globin probe were used to confirm that the mRNAs were not degraded. Contamination of the polyA⁺ mRNAs by ribosomal sequences was checked using Northern blots and a probe derived from the sequence of the 28S rRNA. Preparations of mRNAs with

less than 5% of rRNAs were used in library construction. To avoid constructing libraries with RNAs contaminated by exogenous sequences (prokaryotic or fungal), the presence of bacterial 16S ribosomal sequences or of two highly expressed fungal mRNAs was examined using PCR.

5 Following preparation of the mRNAs, the above described chemical and/or the enzymatic procedures for enriching mRNAs for those having intact 5' ends were employed to obtain 5' ESTs from various tissues. In both approaches, an oligonucleotide tag was attached to the 5' ends of the mRNAs. The oligonucleotide tag had an EcoRI site therein to facilitate later cloning procedures. To facilitate the processing of single stranded and double
10 stranded cDNA obtained in the construction of the libraries, the same nucleotidic sequence was used to design the ligated oligonucleotide in both chemical and enzymatic approaches. Nevertheless, in the chemical procedure, the tag used was an oligodeoxyribonucleotide which was linked to the cap of the mRNA whereas in the enzymatic ligation, the tag was a chimeric
15 hemi 5'DNA/RNA3' oligonucleotide which was ligated to the 5' end of decapped mRNA as described in example 12.

 Following attachment of the oligonucleotide tag to the mRNA by either the chemical or enzymatic methods, the integrity of the mRNA was examined by performing a Northern blot with 200 to 500 ng of mRNA using a probe complementary to the oligonucleotide tag before performing the first strand synthesis as described in example 14.

20

EXAMPLE 14

cDNA Synthesis Using mRNA Templates Having Intact 5' Ends

 For the mRNAs joined to oligonucleotide tags using both the chemical and enzymatic methods, first strand cDNA synthesis was performed using the Superscript II (Gibco BRL) or
25 the Rnase H Minus M-MLV (Promega) reverse transcriptase with random nonamers as primers. In order to protect internal EcoRI sites in the cDNA from digestion at later steps in the procedure, methylated dCTP was used for first strand synthesis. After removal of RNA by an alkaline hydrolysis, the first strand of cDNA was precipitated using isopropanol in order to eliminate residual primers.

30 For both the chemical and the enzymatic methods, the second strand of the cDNA was synthesized with a Klenow fragment using a primer corresponding to the 5' end of the

ligated oligonucleotide described in Example 12. Preferably, the primer is 20-25 bases in length. Methylated dCTP was also used for second strand synthesis in order to protect internal EcoRI sites in the cDNA from digestion during the cloning process.

Following cDNA synthesis, the cDNAs were cloned into pBlueScript as described in
5 Example 15 below.

EXAMPLE 15

Cloning of cDNAs derived from mRNA with intact 5' ends into BlueScript

Following second strand synthesis, the ends of the cDNA were blunted with T4 DNA
10 polymerase (Biolabs) and the cDNA was digested with EcoRI. Since methylated dCTP was used during cDNA synthesis, the EcoRI site present in the tag was the only hemi-methylated site, hence the only site susceptible to EcoRI digestion. The cDNA was then size fractionated using exclusion chromatography (AcA, Biosepra) and fractions corresponding to cDNAs of more than 150 bp were pooled and ethanol precipitated. The cDNA was directionally cloned
15 into the SmaI and EcoRI ends of the phagemid pBlueScript vector (Stratagene). The ligation mixture was electroporated into bacteria and propagated under appropriate antibiotic selection.

Clones containing the oligonucleotide tag attached were then selected as described in
Example 16 below.

20

EXAMPLE 16

Selection of Clones Having the Oligonucleotide Tag Attached Thereto

The plasmid DNAs containing 5' EST libraries made as described above were purified (Qiagen). A positive selection of the tagged clones was performed as follows.
25 Briefly, in this selection procedure, the plasmid DNA was converted to single stranded DNA using gene II endonuclease of the phage F1 in combination with an exonuclease (Chang *et al.*, *Gene* 127:95-8, 1993) such as exonuclease III or T7 gene 6 exonuclease. The resulting single stranded DNA was then purified using paramagnetic beads as described by Fry *et al.*, *Biotechniques*, 13: 124-131, 1992. In this procedure, the single stranded DNA was
30 hybridized with a biotinylated oligonucleotide having a sequence corresponding to the 3' end of the oligonucleotide described in Example 13. Preferably, the primer has a length of 20-25

bases. Clones including a sequence complementary to the biotinylated oligonucleotide were captured by incubation with streptavidin coated magnetic beads followed by magnetic selection. After capture of the positive clones, the plasmid DNA was released from the magnetic beads and converted into double stranded DNA using a DNA polymerase such as the ThermoSequenase obtained from Amersham Pharmacia Biotech. Alternatively, protocols such as the one described in the Gene Trapper kit available from Gibco BRL may be used. The double stranded DNA was then electroporated into bacteria. The percentage of positive clones having the 5' tag oligonucleotide was estimated to typically rank between 90 and 98% using dot blot analysis.

Following electroporation, the libraries were ordered in 384-microtiter plates (MTP). A copy of the MTP was stored for future needs. Then the libraries were transferred into 96 MTP and sequenced as described below.

EXAMPLE 17

Sequencing of Inserts in Selected Clones

Plasmid inserts were first amplified by PCR on PE 9600 thermocyclers (Perkin-Elmer, Applied Biosystems Division, Foster City, CA), using standard SETA-A and SETA-B primers (Genset SA), AmpliTaqGold (Perkin-Elmer), dNTPs (Boehringer), buffer and cycling conditions as recommended by the Perkin-Elmer Corporation.

PCR products were then sequenced using automatic ABI Prism 377 sequencers (Perkin Elmer). Sequencing reactions were performed using PE 9600 thermocyclers with standard dye-primer chemistry and ThermoSequenase (Amersham Pharmacia Biotech). The primers used were either T7 or 21M13 (available from Genset SA) as appropriate. The primers were labeled with the JOE, FAM, ROX and TAMRA dyes. The dNTPs and ddNTPs used in the sequencing reactions were purchased from Boehringer. Sequencing buffer, reagent concentrations and cycling conditions were as recommended by Amersham.

Following the sequencing reaction, the samples were precipitated with ethanol, resuspended in formamide loading buffer, and loaded on a standard 4% acrylamide gel. Electrophoresis was performed for 2.5 hours at 3000V on an ABI 377 sequencer, and the sequence data were collected and analyzed using the ABI Prism DNA Sequencing Analysis Software, version 2.1.2.

2. Computer analysis of the Obtained 5' ESTs: Construction of NetGene and SignalTag databases

The sequence data from the 44 cDNA libraries made as described above were transferred to a proprietary database, where quality control and validation steps were performed. A proprietary base-caller, working using a Unix system, automatically flagged suspect peaks, taking into account the shape of the peaks, the inter-peak resolution, and the noise level. The proprietary base-caller also performed an automatic trimming. Any stretch of 25 or fewer bases having more than 4 suspect peaks was considered unreliable and was discarded. Sequences corresponding to cloning vector or ligation oligonucleotides were automatically removed from the EST sequences. However, the resulting EST sequences may contain 1 to 5 bases belonging to the above mentioned sequences at their 5' end. If needed, these can easily be removed on a case to case basis.

Following sequencing as described above, the sequences of the 5' ESTs were entered in NetGene™, a proprietary database called for storage and manipulation as described below. It will be appreciated by those skilled in the art that the data could be stored and manipulated on any medium which can be read and accessed by a computer. Computer readable media include magnetically, optically, or electronically readable media. For example, the computer readable media may be a hard disc, a floppy disc, a magnetic tape, CD-ROM, RAM, or ROM as well as other types of other media known to those skilled in the art.

In addition, the sequence data may be stored and manipulated in a variety of data processor programs in a diversity of formats. For instance, the sequence data may be stored as text in a word processing file, such as Microsoft WORD or WORDPERFECT or as an ASCII file in a variety of database programs familiar to those of skill in the art, such as DB2, SYBASE, or ORACLE.

The computer readable media on which the sequence information is stored may be in a personal computer, a network, a server or other computer systems known to those skilled in the art. The computer or other system preferably includes the storage media described above, and a processor for accessing and manipulating the sequence data. Once the sequence data has been stored, it may be manipulated and searched to locate those stored sequences which contain a desired nucleic acid sequence or which encode a protein having a particular functional domain. For example, the stored sequence information may be compared to other

known sequences to identify homologies, motifs implicated in biological function, or structural motifs.

Programs which may be used to search or compare the stored sequences include the MacPattern (EMBL), BLAST, and BLAST2 program series (NCBI), basic local alignment search tool programs for nucleotide (BLASTN) and peptide (BLASTX) comparisons (Altschul *et al*, *J. Mol. Biol.* 215: 403, 1990) and FASTA (Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85: 2444, 1988). The BLAST programs then extend the alignments on the basis of defined match and mismatch criteria.

Motifs which may be detected using the above programs and those described in Example 28 include sequences encoding leucine zippers, helix-turn-helix motifs, glycosylation sites, ubiquitination sites, alpha helices, and beta sheets, signal sequences encoding signal peptides which direct the secretion of the encoded proteins, sequences implicated in transcription regulation such as homeoboxes, acidic stretches, enzymatic active sites, substrate binding sites, and enzymatic cleavage sites.

Before searching the cDNAs in the NetGene™ database for sequence motifs of interest, cDNAs derived from mRNAs which were not of interest were identified and eliminated from further consideration as described in Example 18 below.

EXAMPLE 18

Elimination of Undesired Sequences from Further Consideration

5' ESTs in the NetGene™ database which were derived from undesired sequences such as transfer RNAs, ribosomal RNAs, mitochondrial RNAs, prokaryotic RNAs, fungal RNAs, Alu sequences, L1 sequences, or repeat sequences were identified using the FASTA and BLASTN programs with the parameters listed in Table I.

To eliminate 5' ESTs encoding tRNAs from further consideration, the 5' EST sequences were compared to the sequences of 1190 known tRNAs obtained from EMBL release 38, of which 100 were human. The comparison was performed using FASTA on both strands of the 5' ESTs. Sequences having more than 80% homology over more than 60 nucleotides were identified as tRNA. Of the 144,341 sequences screened, 26 were identified as tRNAs and eliminated from further consideration.

To eliminate 5' ESTs encoding rRNAs from further consideration, the 5' EST sequences were compared to the sequences of 2497 known rRNAs obtained from EMBL release 38, of which 73 were human. The comparison was performed using BLASTN on both strands of the 5' ESTs with the parameter S=108. Sequences having more than 80%
5 homology over stretches longer than 40 nucleotides were identified as rRNAs. Of the 144,341 sequences screened, 3,312 were identified as rRNAs and eliminated from further consideration.

To eliminate 5' ESTs encoding mtRNAs from further consideration, the 5' EST sequences were compared to the sequences of the two known mitochondrial genomes for
10 which the entire genomic sequences are available and all sequences transcribed from these mitochondrial genomes including tRNAs, rRNAs, and mRNAs for a total of 38 sequences. The comparison was performed using BLASTN on both strands of the 5' ESTs with the parameter S=108. Sequences having more than 80% homology over stretches longer than 40 nucleotides were identified as mtRNAs. Of the 144,341 sequences screened, 6,110 were
15 identified as mtRNAs and eliminated from further consideration.

Sequences which might have resulted from exogenous contaminants were eliminated from further consideration by comparing the 5' EST sequences to release 46 of the EMBL bacterial and fungal divisions using BLASTN with the parameter S=144. All sequences having more than 90% homology over at least 40 nucleotides were identified as exogenous
20 contaminants. Of the 42 cDNA libraries examined, the average percentages of prokaryotic and fungal sequences contained therein were 0.2% and 0.5% respectively. Among these sequences, only one could be identified as a sequence specific to fungi. The others were either fungal or prokaryotic sequences having homologies with vertebrate sequences or including repeat sequences which had not been masked during the electronic comparison.

25 In addition, the 5' ESTs were compared to 6093 Alu sequences and 1115 L1 sequences to mask 5' ESTs containing such repeat sequences. 5' ESTs including THE and MER repeats, SSTR sequences or satellite, micro-satellite, or telomeric repeats were also eliminated from further consideration. On average, 11.5% of the sequences in the libraries contained repeat sequences. Of this 11.5%, 7% contained Alu repeats, 3.3% contained L1
30 repeats and the remaining 1.2% were derived from the other screened types of repetitive sequences. These percentages are consistent with those found in cDNA libraries prepared by

other groups. For example, the cDNA libraries of Adams *et al.* contained between 0% and 7.4% Alu repeats depending on the source of the RNA which was used to prepare the cDNA library (Adams *et al.*, *Nature* 377:174, 1996).

- 5 The sequences of those 5' ESTs remaining after the elimination of undesirable sequences were compared with the sequences of known human mRNAs to determine the accuracy of the sequencing procedures described above.

EXAMPLE 19

10 Measurement of Sequencing Accuracy by Comparison to Known Sequences

To further determine the accuracy of the sequencing procedure described above, the sequences of 5' ESTs derived from known sequences were identified and compared to the original known sequences. First, a FASTA analysis with overhangs shorter than 5 bp on both ends was conducted on the 5' ESTs to identify those matching an entry in the public human mRNA database. The 6655 5' ESTs which matched a known human mRNA were then realigned with their cognate mRNA and dynamic programming was used to include substitutions, insertions, and deletions in the list of "errors" which would be recognized. Errors occurring in the last 10 bases of the 5' EST sequences were ignored to avoid the inclusion of spurious cloning sites in the analysis of sequencing accuracy.

- 20 This analysis revealed that the sequences incorporated in the NetGene™ database had an accuracy of more than 99.5%.

To determine the efficiency with which the above selection procedures select cDNAs which include the 5' ends of their corresponding mRNAs, the following analysis was performed.

25

EXAMPLE 20

Determination of Efficiency of 5' EST Selection

- To determine the efficiency at which the above selection procedures isolated 5' ESTs which included sequences close to the 5' end of the mRNAs from which they derived, the sequences of the ends of the 5' ESTs derived from the elongation factor 1 subunit α and
- 30

ferritin heavy chain genes were compared to the known cDNA sequences of these genes. Since the transcription start sites of both genes are well characterized, they may be used to determine the percentage of derived 5' ESTs which included the authentic transcription start sites.

5 For both genes, more than 95% of the obtained 5' ESTs actually included sequences close to or upstream of the 5' end of the corresponding mRNAs.

To extend the analysis of the reliability of the procedures for isolating 5' ESTs from ESTs in the NetGene™ database, a similar analysis was conducted using a database composed of human mRNA sequences extracted from GenBank database release 97 for
10 comparison. The 5' ends of more than 85% of 5' ESTs derived from mRNAs included in the GeneBank database were located close to the 5' ends of the known sequence. As some of the mRNA sequences available in the GenBank database are deduced from genomic sequences, a 5' end matching with these sequences will be counted as an internal match. Thus, the method used here underestimates the yield of ESTs including the authentic 5' ends
15 of their corresponding mRNAs.

The EST libraries made above included multiple 5' ESTs derived from the same mRNA. The sequences of such 5' ESTs were compared to one another and the longest 5' ESTs for each mRNA were identified. Overlapping cDNAs were assembled into continuous
20 sequences (contigs). The resulting continuous sequences were then compared to public databases to gauge their similarity to known sequences, as described in Example 21 below.

EXAMPLE 21

Clustering of the 5' ESTs and Calculation of Novelty Indices for cDNA Libraries

25 For each sequenced EST library, the sequences were clustered by the 5' end. Each sequence in the library was compared to the others with BLASTN2 (direct strand, parameters S=107). ESTs with High Scoring Segment Pairs (HSPs) at least 25 bp long, having 95% identical bases and beginning closer than 10 bp from each EST 5' end were grouped. The longest sequence found in the cluster was used as representative of the group. A global
30 clustering between libraries was then performed leading to the definition of super-contigs.

To assess the yield of new sequences within the EST libraries, a novelty rate (NR) was defined as: $NR = 100 \times (\text{Number of new unique sequences found in the library} / \text{Total number of sequences from the library})$. Typically, novelty rating ranged between 10% and 41% depending on the tissue from which the EST library was obtained. For most of the libraries, the random sequencing of 5' EST libraries was pursued until the novelty rate reached 20%.

Following characterization as described above, the collection of 5' ESTs in NetGene™ was screened to identify those 5' ESTs bearing potential signal sequences as described in Example 22 below.

EXAMPLE 22

Identification of Potential Signal Sequences in 5' ESTs

The 5' ESTs in the NetGene™ database were screened to identify those having an uninterrupted open reading frame (ORF) longer than 45 nucleotides beginning with an ATG codon and extending to the end of the EST. Approximately half of the cDNA sequences in NetGene™ contained such an ORF. The ORFs of these 5' ESTs were then searched to identify potential signal motifs using slight modifications of the procedures disclosed in Von Heijne, *Nucleic Acids Res.* 14:4683-4690, 1986, the disclosure of which is incorporated herein by reference. Those 5' EST sequences encoding a stretch of at least 15 amino acid long with a score of at least 3.5 in the Von Heijne signal peptide identification matrix were considered to possess a signal sequence. Those 5' ESTs which matched a known human mRNA or EST sequence and had a 5' end more than 20 nucleotides downstream of the known 5' end were excluded from further analysis. The remaining cDNAs having signal sequences therein were included in a database called SignalTag™.

To confirm the accuracy of the above method for identifying signal sequences, the analysis of Example 23 was performed.

EXAMPLE 23

Confirmation of Accuracy of Identification of Potential Signal Sequences in 5' ESTs

The accuracy of the above procedure for identifying signal sequences encoding signal peptides was evaluated by applying the method to the 43 amino acids located at the N terminus of all human SwissProt proteins. The computed Von Heijne score for each protein was compared with the known characterization of the protein as being a secreted protein or a non-secreted protein. In this manner, the number of non-secreted proteins having a score higher than 3.5 (false positives) and the number of secreted proteins having a score lower than 3.5 (false negatives) could be calculated.

Using the results of the above analysis, the probability that a peptide encoded by the 5' region of the mRNA is in fact a genuine signal peptide based on its Von Heijne's score was calculated based on either the assumption that 10% of human proteins are secreted or the assumption that 20% of human proteins are secreted. The results of this analysis are shown in Figure 2 and table IV.

Using the above method of identification of secretory proteins, 5' ESTs of the following polypeptides known to be secreted were obtained: human glucagon, gamma interferon induced monokine precursor, secreted cyclophilin-like protein, human pleiotropin, and human biotinidase precursor. Thus, the above method successfully identified those 5' ESTs which encode a signal peptide.

To confirm that the signal peptide encoded by the 5' ESTs actually functions as a signal peptide, the signal sequences from the 5' ESTs may be cloned into a vector designed for the identification of signal peptides. Such vectors are designed to confer the ability to grow in selective medium only to host cells containing a vector with an operably linked signal sequence. For example, to confirm that a 5' EST encodes a genuine signal peptide, the signal sequence of the 5' EST may be inserted upstream and in frame with a non-secreted form of the yeast invertase gene in signal peptide selection vectors such as those described in U.S. Patent No. 5,536,637, the disclosure of which is incorporated herein by reference. Growth of host cells containing signal sequence selection vectors with the correctly inserted 5' EST signal sequence confirms that the 5' EST encodes a genuine signal peptide.

Alternatively, the presence of a signal peptide may be confirmed by cloning the extended cDNAs obtained using the ESTs into expression vectors such as pXT1 (as described below in example 30), or by constructing promoter-signal sequence-reporter gene vectors which encode fusion proteins between the signal peptide and an assayable reporter protein. After introduction of these vectors into a suitable host cell, such as COS cells or NIH 3T3 cells, the growth medium may be harvested and analyzed for the presence of the secreted protein. The medium from these cells is compared to the medium from control cells containing vectors lacking the signal sequence or extended cDNA insert to identify vectors which encode a functional signal peptide or an authentic secreted protein.

Those 5' ESTs which encoded a signal peptide, as determined by the method of Example 22 above, were further grouped into four categories based on their homology to known sequences as described in Example 24 below.

EXAMPLE 24

Categorization of 5' ESTs Encoding a Signal Peptide

Those 5' ESTs having a sequence not matching any known vertebrate sequence nor any publicly available EST sequence were designated "new." Of the sequences in the SignalTag™ database, 947 of the 5' ESTs having a Von Heijne's score of at least 3.5 fell into this category.

Those 5' ESTs having a sequence not matching any vertebrate sequence but matching a publicly known EST were designated "EST-ext", provided that the known EST sequence was extended by at least 40 nucleotides in the 5' direction. Of the sequences in the SignalTag™ database, 150 of the 5' ESTs having a Von Heijne's score of at least 3.5 fell into this category.

Those ESTs not matching any vertebrate sequence but matching a publicly known EST without extending the known EST by at least 40 nucleotides in the 5' direction were designated "EST." Of the sequences in the SignalTag™ database, 599 of the 5' ESTs having a Von Heijne's score of at least 3.5 fell into this category.

Those 5' ESTs matching a human mRNA sequence but extending the known sequence by at least 40 nucleotides in the 5' direction were designated "VERT-ext." Of the sequences in the SignalTag™ database, 23 of the 5' ESTs having a Von Heijne's score of at

least 3.5 fell into this category. Included in this category was a 5' EST which extended the known sequence of the human translocase mRNA by more than 200 bases in the 5' direction.

A 5' EST which extended the sequence of a human tumor suppressor gene in the 5' direction was also identified.

5 Table V shows the distribution of 5' ESTs in each category and the number of 5' ESTs in each category having a given minimum von Heijne's score.

3. Evaluation of Spatial and Temporal Expression of mRNAs Corresponding to the 5'ESTs or Extended cDNAs

10

Each of the 5' ESTs was also categorized based on the tissue from which its corresponding mRNA was obtained, as described below in Example 25.

EXAMPLE 25

15

Categorization of Expression Patterns

Table VI shows the distribution of 5' ESTs in each of the above defined category with respect to the tissue from which the 5'ESTs of the corresponding mRNA were obtained.

20 Table II provides the sequence identification numbers of 5' EST sequences derived from muscle and other mesodermal tissues, the categories in which these sequences fall, and the von Heijne's score of the signal peptides which they encode. The 5' EST sequences and the amino acid sequences they encode are provided in the appended sequence listings. Table III provides the sequence ID numbers of the 5' ESTs and the sequences of the signal peptides which they encode. The sequences of the 5' ESTs and the polypeptides they encode are provided in the sequence listing appended hereto.

25

The sequences of DNA SEQ ID NOs: 38-305 can readily be screened for any errors therein and any sequence ambiguities can be resolved by resequencing a fragment containing such errors or ambiguities on both strands. Such fragments may be obtained from the plasmids stored in the inventors' laboratory or can be isolated using the techniques described herein. Resolution of any such ambiguities or errors may be facilitated by using primers
30 which hybridize to sequences located close to the ambiguous or erroneous sequences. For example, the primers may hybridize to sequences within 50-75 bases of the ambiguity or

error. Upon resolution of an error or ambiguity, the corresponding corrections can be made in the protein sequences encoded by the DNA containing the error or ambiguity.

In addition to categorizing the 5' ESTs with respect to their tissue of origin, the spatial and temporal expression patterns of the mRNAs corresponding to the 5' ESTs, as well as their expression levels, may be determined as described in Example 26 below. Characterization of the spatial and temporal expression patterns and expression levels of these mRNAs is useful for constructing expression vectors capable of producing a desired level of gene product in a desired spatial or temporal manner, as will be discussed in more detail below.

Furthermore, 5' ESTs whose corresponding mRNAs are associated with disease states may also be identified. For example, a particular disease may result from the lack of expression, over expression, or under expression of an mRNA corresponding to a 5' EST. By comparing mRNA expression patterns and quantities in samples taken from healthy individuals with those from individuals suffering from a particular disease, 5' ESTs responsible for the disease may be identified.

It will be appreciated that the results of the above characterization procedures for 5' ESTs also apply to extended cDNAs (obtainable as described below) which contain sequences adjacent to the 5' ESTs. It will also be appreciated that if desired, characterization may be delayed until extended cDNAs have been obtained rather than characterizing the ESTs themselves.

EXAMPLE 26

Evaluation of Expression Levels and Patterns of mRNAs

Corresponding to 5' ESTs or Extended cDNAs

Expression levels and patterns of mRNAs corresponding to 5' ESTs or extended cDNAs (obtainable as described below in example 27) may be analyzed by solution hybridization with long probes as described in International Patent Application No. WO 97/05277, the entire contents of which are hereby incorporated by reference. Briefly, a 5' EST, extended cDNA, or fragment thereof corresponding to the gene encoding the mRNA to be characterized is inserted at a cloning site immediately downstream of a bacteriophage (T3,

T7 or SP6) RNA polymerase promoter to produce antisense RNA. Preferably, the 5' EST or extended cDNA has 100 or more nucleotides. The plasmid is linearized and transcribed in the presence of ribonucleotides comprising modified ribonucleotides (*i.e.* biotin-UTP and DIG-UTP). An excess of this doubly labeled RNA is hybridized in solution with mRNA isolated from cells or tissues of interest. The hybridizations are performed under standard stringent conditions (40-50°C for 16 hours in an 80% formamide, 0.4 M NaCl buffer, pH 7-8). The unhybridized probe is removed by digestion with ribonucleases specific for single-stranded RNA (*i.e.* RNases CL3, T1, Phy M, U2 or A). The presence of the biotin-UTP modification enables capture of the hybrid on a microtitration plate coated with streptavidin. The presence of the DIG modification enables the hybrid to be detected and quantified by ELISA using an anti-DIG antibody coupled to alkaline phosphatase.

The 5' ESTs, extended cDNAs, or fragments thereof may also be tagged with nucleotide sequences for the serial analysis of gene expression (SAGE) as disclosed in UK Patent Application No. 2 305 241 A, the entire contents of which are incorporated by reference. In this method, cDNAs are prepared from a cell, tissue, organism or other source of nucleic acid for which gene expression patterns must be determined. The resulting cDNAs are separated into two pools. The cDNAs in each pool are cleaved with a first restriction endonuclease, called an anchoring enzyme, having a recognition site which is likely to be present at least once in most cDNAs. The fragments which contain the 5' or 3' most region of the cleaved cDNA are isolated by binding to a capture medium such as streptavidin coated beads. A first oligonucleotide linker having a first sequence for hybridization of an amplification primer and an internal restriction site for a so-called tagging endonuclease is ligated to the digested cDNAs in the first pool. Digestion with the second endonuclease produces short tag fragments from the cDNAs.

A second oligonucleotide having a second sequence for hybridization of an amplification primer and an internal restriction site is ligated to the digested cDNAs in the second pool. The cDNA fragments in the second pool are also digested with the tagging endonuclease to generate short tag fragments derived from the cDNAs in the second pool. The tags resulting from digestion of the first and second pools with the anchoring enzyme and the tagging endonuclease are ligated to one another to produce so-called ditags. In some embodiments, the ditags are concatamerized to produce ligation products containing from 2

to 200 ditags. The tag sequences are then determined and compared to the sequences of the 5' ESTs or extended cDNAs to determine which 5' ESTs or extended cDNAs are expressed in the cell, tissue, organism, or other source of nucleic acids from which the tags were derived. In this way, the expression pattern of the 5' ESTs or extended cDNAs in the cell, tissue, organism, or other source of nucleic acids is obtained.

Quantitative analysis of gene expression may also be performed using arrays. As used herein, the term array means a one dimensional, two dimensional, or multidimensional arrangement of full length cDNAs (*i.e.* extended cDNAs which include the coding sequence for the signal peptide, the coding sequence for the mature protein, and a stop codon), extended cDNAs, 5' ESTs or fragments thereof of sufficient length to permit specific detection of gene expression. Preferably, the fragments are at least 15 nucleotides in length. More preferably, the fragments are at least 100 nucleotide long. More preferably, the fragments are more than 100 nucleotides in length. In some embodiments, the fragments may be more than 500 nucleotide long.

For example, quantitative analysis of gene expression may be performed with full length cDNAs as defined below, extended cDNAs, 5' ESTs, or fragments thereof in a complementary DNA microarray as described by Schena *et al.* (*Science* 270:467-470, 1995; *Proc. Natl. Acad. Sci. U.S.A.* 93:10614-10619, 1996). Full length cDNAs, extended cDNAs, 5' ESTs or fragments thereof are amplified by PCR and arrayed from 96-well microtiter plates onto silylated microscope slides using high-speed robotics. Printed arrays are incubated in a humid chamber to allow rehydration of the array elements and rinsed, once in 0.2% SDS for 1 min, twice in water for 1 min and once for 5 min in sodium borohydride solution. The arrays are submerged in water for 2 min at 95°C, transferred into 0.2% SDS for 1 min, rinsed twice with water, air dried and stored in the dark at 25°C.

Cell or tissue mRNA is isolated or commercially obtained and probes are prepared by a single round of reverse transcription. Probes are hybridized to 1 cm² microarrays under a 14 x 14 mm glass coverslip for 6-12 hours at 60°C. Arrays are washed for 5 min at 25°C in low stringency wash buffer (1 x SSC/0.2% SDS), then for 10 min at room temperature in high stringency wash buffer (0.1 x SSC/0.2% SDS). Arrays are scanned in 0.1 x SSC using a fluorescence laser scanning device fitted with a custom filter set. Accurate differential

expression measurements are obtained by taking the average of the ratios of two independent hybridizations.

Quantitative analysis of the expression of genes may also be performed with full length cDNAs, extended cDNAs, 5' ESTs, or fragments thereof in complementary DNA arrays as described by Pietu *et al.* (*Genome Research* 6:492-503, 1996). The full length cDNAs, extended cDNAs, 5' ESTs or fragments thereof are PCR amplified and spotted on membranes. Then, mRNAs originating from various tissues or cells are labeled with radioactive nucleotides. After hybridization and washing in controlled conditions, the hybridized mRNAs are detected by phospho-imaging or autoradiography. Duplicate experiments are performed and a quantitative analysis of differentially expressed mRNAs is then performed.

Alternatively, expression analysis of the 5' ESTs or extended cDNAs can be done through high density nucleotide arrays as described by Lockhart *et al.* (*Nature Biotechnology* 14: 1675-1680, 1996) and Sosnowsky *et al.* (*Proc. Natl. Acad. Sci.* 94:1119-1123, 1997). Oligonucleotides of 15-50 nucleotides corresponding to sequences of the 5' ESTs or extended cDNAs are synthesized directly on the chip (Lockhart *et al.*, *supra*) or synthesized and then addressed to the chip (Sosnowsky *et al.*, *supra*). Preferably, the oligonucleotides are about 20 nucleotides in length.

cDNA probes labeled with an appropriate compound, such as biotin, digoxigenin or fluorescent dye, are synthesized from the appropriate mRNA population and then randomly fragmented to an average size of 50 to 100 nucleotides. The said probes are then hybridized to the chip. After washing as described in Lockhart *et al.*, *supra* and application of different electric fields (Sonowsky *et al.*, *supra.*), the dyes or labeling compounds are detected and quantified. Duplicate hybridizations are performed. Comparative analysis of the intensity of the signal originating from cDNA probes on the same target oligonucleotide in different cDNA samples indicates a differential expression of the mRNA corresponding to the 5' EST or extended cDNA from which the oligonucleotide sequence has been designed.

III. Use of 5' ESTs to Clone Extended cDNAs and to Clone the Corresponding Genomic DNAs

Once 5' ESTs which include the 5' end of the corresponding mRNAs have been selected using the procedures described above, they can be utilized to isolate extended cDNAs which contain sequences adjacent to the 5' ESTs. The extended cDNAs may include the entire coding sequence of the protein encoded by the corresponding mRNA, including the authentic translation start site, the signal sequence, and the sequence encoding the mature protein remaining after cleavage of the signal peptide. Such extended cDNAs are referred to herein as "full length cDNAs." Alternatively, the extended cDNAs may include only the sequence encoding the mature protein remaining after cleavage of the signal peptide, or only the sequence encoding the signal peptide.

Example 27 below describes a general method for obtaining extended cDNAs using 5' ESTs. Example 28 below provides experimental results, using the method explained in example 27, describing several extended cDNAs including the entire coding sequence and authentic 5' end of the corresponding mRNA for several secreted proteins.

The methods of Examples 27, 28, and 29 can also be used to obtain extended cDNAs which encode less than the entire coding sequence of the secreted proteins encoded by the genes corresponding to the 5' ESTs. In some embodiments, the extended cDNAs isolated using these methods encode at least 10 amino acids of one of the proteins encoded by the sequences of SEQ ID NOs: 38-305. In further embodiments, the extended cDNAs encode at least 20 amino acids of the proteins encoded by the sequences of SEQ ID NOs: 38-305. In further embodiments, the extended cDNAs encode at least 30 amino acids of the sequences of SEQ ID NOs: 38-305. In a preferred embodiment, the extended cDNAs encode a full length protein sequence, which includes the protein coding sequences of SEQ ID NOs: 38-305.

EXAMPLE 27

General Method for Using 5' ESTs to Clone and Sequence cDNAs which Include the Entire Coding Region and the Authentic 5' End of the Corresponding mRNA

The following general method has been used to quickly and efficiently isolate extended cDNAs having the authentic 5' ends of their corresponding mRNAs as well as

the full protein coding sequence and including sequence adjacent to the sequences of the 5' ESTs used to obtain them. This method may be applied to obtain extended cDNAs for any 5' EST in the NetGene™ database, including those 5' ESTs encoding polypeptides belonging to secreted proteins. The method is summarized in figure 3.

5

1. Obtention of Extended cDNAs

a) First strand synthesis

The method takes advantage of the known 5' sequence of the mRNA. A reverse transcription reaction is conducted on purified mRNA with a poly 14dT primer containing a 49 nucleotide sequence at its 5' end allowing the addition of a known sequence at the end of the cDNA which corresponds to the 3' end of the mRNA. For example, the primer may have the following sequence: 5'-ATC GTT GAG ACT CGT ACC AGC AGA GTC ACG AGA GAG ACT ACA CGG TAC TGG TTT TTT TTT TTT TTVN -3' (SEQ ID NO:14). Those skilled in the art will appreciate that other sequences may also be added to the poly dT sequence and used to prime the first strand synthesis. Using this primer and a reverse transcriptase such as the Superscript II (Gibco BRL) or Rnase H Minus M-MLV (Promega) enzyme, a reverse transcript anchored at the 3' polyA site of the RNAs is generated.

15

20

After removal of the mRNA hybridized to the first cDNA strand by alkaline hydrolysis, the products of the alkaline hydrolysis and the residual poly dT primer are eliminated with an exclusion column such as an AcA34 (Biosepra) matrix as explained in Example 11.

b) Second strand synthesis

A pair of nested primers on each end is designed based on the known 5' sequence from the 5' EST and the known 3' end added by the poly dT primer used in the first strand synthesis. Softwares used to design primers are either based on GC content and melting temperatures of oligonucleotides, such as OSP (Illier and Green, *PCR Meth. Appl.* 1:124-128, 1991), or based on the octamer frequency disparity method (Griffais *et al.*, *Nucleic Acids Res.* 19: 3887-3891, 1991) such as PC-Rare (<http://bioinformatics.weizmann.ac.il/software/PC-Rare/doc/manuel.html>).

25

Preferably, the nested primers at the 5' end are separated from one another by four to nine bases. The 5' primer sequences may be selected to have melting temperatures and specificities suitable for use in PCR.

Preferably, the nested primers at the 3' end are separated from one another by four to nine bases. For example, the nested 3' primers may have the following sequences: (5'- CCA GCA GAG TCA CGA GAG AGA CTA CAC GG -3'(SEQ ID NO:15), and 5'- CAC GAG AGA GAC TAC ACG GTA CTG G -3' (SEQ ID NO:16). These primers were selected because they have melting temperatures and specificities compatible with their use in PCR. However, those skilled in the art will appreciate that other sequences may also be used as primers.

The first PCR run of 25 cycles is performed using the Advantage Tth Polymerase Mix (Clontech) and the outer primer from each of the nested pairs. A second 20 cycle PCR using the same enzyme and the inner primer from each of the nested pairs is then performed on 1/2500 of the first PCR product. Thereafter, the primers and nucleotides are removed.

2. Sequencing of Full Length Extended cDNAs or Fragments Thereof

Due to the lack of position constraints on the design of 5' nested primers compatible for PCR use using the OSP software, amplicons of two types are obtained. Preferably, the second 5' primer is located upstream of the translation initiation codon thus yielding a nested PCR product containing the whole coding sequence. Such a full length extended cDNA undergoes a direct cloning procedure as described in section a. However, in some cases, the second 5' primer is located downstream of the translation initiation codon, thereby yielding a PCR product containing only part of the ORF. Such incomplete PCR products are submitted to a modified procedure described in section b.

a) Nested PCR products containing complete ORFs

When the resulting nested PCR product contains the complete coding sequence, as predicted from the 5'EST sequence, it is cloned in an appropriate vector such as pED6dpc2, as described in section 3.

b) Nested PCR products containing incomplete ORFs

When the amplicon does not contain the complete coding sequence, intermediate steps are necessary to obtain both the complete coding sequence and a PCR product containing the full coding sequence. The complete coding sequence can be assembled from several partial sequences determined directly from different PCR products as described in the following section.

Once the full coding sequence has been completely determined, new primers compatible for PCR use are designed to obtain amplicons containing the whole coding region. However, in such cases, 3' primers compatible for PCR use are located inside the 3' UTR of the corresponding mRNA, thus yielding amplicons which lack part of this region, *i.e.* the polyA tract and sometimes the polyadenylation signal, as illustrated in figure 3. Such full length extended cDNAs are then cloned into an appropriate vector as described in section 3.

c) Sequencing extended cDNAs

Sequencing of extended cDNAs is performed using a Die Terminator approach with the AmpliTaq DNA polymerase FS kit available from Perkin Elmer.

In order to sequence PCR fragments, primer walking is performed using software such as OSP to choose primers and automated computer software such as ASMG (Sutton *et al.*, *Genome Science Technol.* 1: 9-19, 1995) to construct contigs of walking sequences including the initial 5' tag using minimum overlaps of 32 nucleotides. Preferably, primer walking is performed until the sequences of full length cDNAs are obtained.

Completion of the sequencing of a given extended cDNA fragment is assessed as follows. Since sequences located after a polyA tract are difficult to determine precisely in the case of uncloned products, sequencing and primer walking processes for PCR products are interrupted when a polyA tract is identified in extended cDNAs obtained as described in case b. The sequence length is compared to the size of the nested PCR product obtained as described above. Due to the limited accuracy of the determination of the PCR product size by gel electrophoresis, a sequence is considered complete if the size of the obtained sequence is at least 70 % the size of the first nested PCR product. If the length of the sequence determined from the computer analysis is not at least 70% of the length of the nested PCR product, these PCR products are cloned and the sequence of the insertion is determined. When Northern blot data are available, the size of the mRNA detected for a given PCR

product is used to finally assess that the sequence is complete. Sequences which do not fulfill the above criteria are discarded and will undergo a new isolation procedure.

Sequence data of all extended cDNAs are then transferred to a proprietary database, where quality controls and validation steps are carried out as described in
5 example 15.

3. Cloning of Full Length Extended cDNAs

The PCR product containing the full coding sequence is then cloned in an appropriate vector. For example, the extended cDNAs can be cloned into the expression vector
10 pED6dpc2 (DiscoverEase, Genetics Institute, Cambridge, MA) as follows. pED6dpc2 vector DNA is prepared with blunt ends by performing an EcoRI digestion followed by a fill in reaction. The blunt ended vector is dephosphorylated. After removal of PCR primers and ethanol precipitation, the PCR product containing the full coding sequence or the extended
15 cDNA obtained as described above is phosphorylated with a kinase subsequently removed by phenol-Sevag extraction and precipitation. The double stranded extended cDNA is then ligated to the vector and the resulting expression plasmid introduced into appropriate host cells.

Since the PCR products obtained as described above are blunt ended molecules that can be cloned in either direction, the orientation of several clones for each PCR product is
20 determined. Then, 4 to 10 clones are ordered in microtiter plates and subjected to a PCR reaction using a first primer located in the vector close to the cloning site and a second primer located in the portion of the extended cDNA corresponding to the 3' end of the mRNA. This second primer may be the antisense primer used in anchored PCR in the case of direct cloning (case a) or the antisense primer located inside the 3'UTR in the case of indirect cloning (case
25 b). Clones in which the start codon of the extended cDNA is operably linked to the promoter in the vector so as to permit expression of the protein encoded by the extended cDNA are conserved and sequenced. In addition to the ends of cDNA inserts, approximately 50 bp of vector DNA on each side of the cDNA insert are also sequenced.

The cloned PCR products are then entirely sequenced according to the
30 aforementioned procedure. In this case, contiguation of long fragments is then performed on walking sequences that have already contiguated for uncloned PCR products during

primer walking. Sequencing of cloned amplicons is complete when the resulting contigs include the whole coding region as well as overlapping sequences with vector DNA on both ends.

5 4. Computer analysis of Full Length Extended cDNA

Sequences of all full length extended cDNAs are then submitted to further analysis as described below. Before searching the extended full length cDNAs for sequences of interest, extended cDNAs which are not of interest (vector RNAs, transfer RNAs, ribosomal RNAs, mitochondrial RNAs, prokaryotic RNAs and fungal RNAs) are discarded using methods
10 essentially similar to those described for 5'ESTs in Example 18.

a) Identification of structural features

Structural features, e.g. polyA tail and polyadenylation signal, of the sequences of full length extended cDNAs are subsequently determined as follows.

15 A polyA tail is defined as a homopolymeric stretch of at least 11 A with at most one alternative base within it. The polyA tail search is restricted to the last 100 nt of the sequence and limited to stretches of 11 consecutive A's because sequencing reactions are often not readable after such a polyA stretch. Stretches having more than 90% homology over 8 nucleotides are identified as polyA tails using BLAST2N.

20 To search for a polyadenylation signal, the polyA tail is clipped from the full-length sequence. The 50 bp preceding the polyA tail are first searched for the canonic polyadenylation AAUAAA signal and, if the canonic signal is not detected, for the alternative AUUAAA signal (Sheets *et al.*, *Nuc. Acids Res.* 18: 5799-5805, 1990). If neither of these consensus polyadenylation signals is found, the canonic motif is searched again allowing one mismatch to account for possible sequencing errors. More than 85 %
25 of identified polyadenylation signals of either type actually ends 10 to 30 bp from the polyA tail. Alternative AUUAAA signals represents approximately 15 % of the total number of identified polyadenylation signals.

b) Identification of functional features

30 Functional features, e.g. ORFs and signal sequences, of the sequences of full length extended cDNAs were subsequently determined as follows.

The 3 upper strand frames of extended cDNAs are searched for ORFs defined as the maximum length fragments beginning with a translation initiation codon and ending with a stop codon. ORFs encoding at least 20 amino acids are preferred.

Each found ORF is then scanned for the presence of a signal peptide in the first 50 amino-acids or, where appropriate, within shorter regions down to 20 amino acids or less in the ORF, using the matrix method of von Heijne (*Nuc. Acids Res.* 14: 4683-4690, 1986), the disclosure of which is incorporated herein by reference as described in Example 22.

c) Homology to either nucleotidic or proteic sequences

Categorization of full-length sequences may be achieved using procedures essentially similar to those described for 5'ESTs in Example 24.

Extended cDNAs prepared as described above may be subsequently engineered to obtain nucleic acids which include desired portions of the extended cDNA using conventional techniques such as subcloning, PCR, or *in vitro* oligonucleotide synthesis. For example, nucleic acids which include only the full coding sequences (*i.e.* the sequences encoding the signal peptide and the mature protein remaining after the signal peptide is cleaved off) may be obtained using techniques known to those skilled in the art. Alternatively, conventional techniques may be applied to obtain nucleic acids which contain only the coding sequences for the mature protein remaining after the signal peptide is cleaved off or nucleic acids which contain only the coding sequences for the signal peptides.

Similarly, nucleic acids containing any other desired portion of the coding sequences for the secreted protein may be obtained. For example, the nucleic acid may contain at least 10 consecutive bases of an extended cDNA such as one of the extended cDNAs described below. In another embodiment, the nucleic acid may contain at least 15 consecutive bases of an extended cDNA such as one of the extended cDNAs described below. Alternatively, the nucleic acid may contain at least 20 consecutive bases of an extended cDNA such as one of the extended cDNAs described below. In another embodiment, the nucleic acid may contain at least 25 consecutive bases of an extended cDNA such as one of the extended cDNAs described below. In yet another embodiment, the nucleic acid may contain at least 40 consecutive bases of an extended cDNA such as one of the extended cDNAs described below.

Once an extended cDNA has been obtained, it can be sequenced to determine the amino acid sequence it encodes. Once the encoded amino acid sequence has been determined, one can create and identify any of the many conceivable cDNAs that will encode that protein by simply using the degeneracy of the genetic code. For example, allelic variants
5 or other homologous nucleic acids can be identified as described below. Alternatively, nucleic acids encoding the desired amino acid sequence can be synthesized *in vitro*.

In a preferred embodiment, the coding sequence may be selected using the known codon or codon pair preferences for the host organism in which the cDNA is to be expressed.

The extended cDNAs derived from the 5' ESTS of the present invention were
10 obtained as described in Example 28 below.

EXAMPLE 28

Characterization of cloned extended cDNAs obtained using 5' ESTs

The procedure described in Example 27 above was used to obtain the extended
15 cDNAs derived from the 5' ESTs of the present invention in a variety of tissues. The following list provides a few examples of thus obtained extended cDNAs.

Using this approach, the full length cDNA of SEQ ID NO:17 (internal identification number 48-19-3-G1-FL1) was obtained. This cDNA falls into the "EST-ext" category described above and encodes the signal peptide MKKVLLITAILAVAVG (SEQ ID NO:
20 18) having a von Heijne score of 8.2.

The full length cDNA of SEQ ID NO:19 (internal identification number 58-34-2-E7-FL2) was also obtained using this procedure. This cDNA falls into the "EST-ext" category described above and encodes the signal peptide MWWFQQGLSFLPSALVTWTS (SEQ ID NO:20) having a von Heijne score of 5.5.

25 Another full length cDNA obtained using the procedure described above has the sequence of SEQ ID NO:21 (internal identification number 51-27-1-E8-FL1). This cDNA, falls into the "EST-ext" category described above and encodes the signal peptide MVLTTLPANSANSPVNMPTTGPNLSYASSALSPCLT (SEQ ID NO:22) having a von Heijne score of 5.9.

30 The above procedure was also used to obtain a full length cDNA having the sequence of SEQ ID NO:23 (internal identification number 76-4-1-G5-FL1). This cDNA falls into the

"EST-ext" category described above and encodes the signal peptide ILSTVTALTFAXA (SEQ ID NO:24) having a von Heijne score of 5.5.

The full length cDNA of SEQ ID NO:25 (internal identification number 51-3-3-B10-FL3) was also obtained using this procedure. This cDNA falls into the "new" category
5 described above and encodes a signal peptide LVLTLCTLPLAVA (SEQ ID NO:26) having a von Heijne score of 10.1.

The full length cDNA of SEQ ID NO:27 (internal identification number 58-35-2-F10-FL2) was also obtained using this procedure. This cDNA falls into the "new" category described above and encodes a signal peptide LWLLFFLVTAIHA (SEQ ID NO:28) having
10 a von Heijne score of 10.7.

Bacterial clones containing plasmids containing the full length cDNAs described above are presently stored in the inventor's laboratories under the internal identification numbers provided above. The inserts may be recovered from the stored materials by growing an aliquot of the appropriate bacterial clone in the appropriate medium. The plasmid DNA
15 can then be isolated using plasmid isolation procedures familiar to those skilled in the art such as alkaline lysis minipreps or large scale alkaline lysis plasmid isolation procedures. If desired the plasmid DNA may be further enriched by centrifugation on a cesium chloride gradient, size exclusion chromatography, or anion exchange chromatography. The plasmid DNA obtained using these procedures may then be manipulated using standard cloning techniques
20 familiar to those skilled in the art. Alternatively, a PCR can be done with primers designed at both ends of the cDNA insertion. The PCR product which corresponds to the cDNA can then be manipulated using standard cloning techniques familiar to those skilled in the art.

The polypeptides encoded by the extended cDNAs may be screened for the presence of known structural or functional motifs or for the presence of signatures, small amino acid
25 sequences which are well conserved amongst the members of a protein family. The conserved regions have been used to derive consensus patterns or matrices included in the PROSITE data bank, in particular in the file prosite.dat (Release 13.0 of November 1995, located at <http://expasy.hcuge.ch/sprot/prosite.html>. Prosite_convert and prosite_scan programs (http://ulrec3.unil.ch/ftpserveur/prosite_scan) may be used to find signatures on the
30 extended cDNAs.

For each pattern obtained with the prosite_convert program from the prosite.dat file, the accuracy of the detection on a new protein sequence may be assessed by evaluating the frequency of irrelevant hits on the population of human secreted proteins included in the data bank SWISSPROT. The ratio between the number of hits on shuffled proteins (with a window size of 20 amino acids) and the number of hits on native (unshuffled) proteins may be used as an index. Every pattern for which the ratio is greater than 20% (one hit on shuffled proteins for 5 hits on native proteins) may be skipped during the search with prosite_scan. The program used to shuffle protein sequences (db_shuffle) and the program used to determine the statistics for each pattern in the protein data banks (prosite_statistics) are available on the ftp site http://ulrec3.unil.ch/ftpserveur/prosite_scan.

In addition to PCR based methods for obtaining extended cDNAs, traditional hybridization based methods may also be employed. These methods may also be used to obtain the genomic DNAs which encode the mRNAs from which the 5' ESTs were derived, mRNAs corresponding to the extended cDNAs, or nucleic acids which are homologous to extended cDNAs or 5' ESTs. Example 29 below provides examples of such methods.

EXAMPLE 29

Methods for Obtaining cDNAs which include the Entire Coding Region and the Authentic 5' End of the Corresponding mRNA

A full length cDNA library can be made using the strategies described in Examples 13, 14, 15, and 16 above by replacing the random nonamer used in Example 14 with an oligo-dT primer. For instance, the oligonucleotide of SEQ ID NO:14 may be used.

Alternatively, a cDNA library or genomic DNA library may be obtained from a commercial source or made using techniques familiar to those skilled in the art. Such cDNA or genomic DNA libraries may be used to isolate extended cDNAs obtained from 5' EST or nucleic acids homologous to extended cDNAs or 5' EST as follows. The cDNA library or genomic DNA library is hybridized to a detectable probe comprising at least 10 consecutive nucleotides from the 5' EST or extended cDNA using conventional techniques. Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST or extended cDNA. More preferably, the probe comprises at least 20 to 30 consecutive

nucleotides from the 5' EST or extended cDNA. In some embodiments, the probe comprises more than 30 nucleotides from the 5' EST or extended cDNA.

Techniques for identifying cDNA clones in a cDNA library which hybridize to a given probe sequence are disclosed in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual* 2d Ed., Cold Spring Harbor Laboratory Press, 1989, the disclosure of which is incorporated herein by reference. The same techniques may be used to isolate genomic DNAs.

Briefly, cDNA or genomic DNA clones which hybridize to the detectable probe are identified and isolated for further manipulation as follows. A probe comprising at least 10 consecutive nucleotides from the 5' EST or extended cDNA is labeled with a detectable label such as a radioisotope or a fluorescent molecule. Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST or extended cDNA. More preferably, the probe comprises 20 to 30 consecutive nucleotides from the 5' EST or extended cDNA. In some embodiments, the probe comprises more than 30 nucleotides from the 5' EST or extended cDNA.

Techniques for labeling the probe are well known and include phosphorylation with polynucleotide kinase, nick translation, *in vitro* transcription, and non radioactive techniques. The cDNAs or genomic DNAs in the library are transferred to a nitrocellulose or nylon filter and denatured. After blocking of non specific sites, the filter is incubated with the labeled probe for an amount of time sufficient to allow binding of the probe to cDNAs or genomic DNAs containing a sequence capable of hybridizing thereto.

By varying the stringency of the hybridization conditions used to identify extended cDNAs or genomic DNAs which hybridize to the detectable probe, extended cDNAs having different levels of homology to the probe can be identified and isolated as described below.

1. Identification of Extended cDNA or Genomic cDNA Sequences Having a High Degree of Homology to the Labeled Probe

To identify extended cDNAs or genomic DNAs having a high degree of homology to the probe sequence, the melting temperature of the probe may be calculated using the following formulas:

For probes between 14 and 70 nucleotides in length the melting temperature (T_m) is calculated using the formula: $T_m = 81.5 + 16.6(\log [Na^+]) + 0.41(\text{fraction G+C}) - (600/N)$ where N is the length of the probe.

5 If the hybridization is carried out in a solution containing formamide, the melting temperature may be calculated using the equation $T_m = 81.5 + 16.6(\log [Na^+]) + 0.41(\text{fraction G+C}) - (0.63\% \text{ formamide}) - (600/N)$ where N is the length of the probe.

Prehybridization may be carried out in 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100 μ g denatured fragmented salmon sperm DNA or 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100 μ g denatured fragmented salmon sperm DNA, 50% formamide. The formulas for
10 SSC and Denhardt's solutions are listed in Sambrook *et al.*, *supra*.

Hybridization is conducted by adding the detectable probe to the prehybridization solutions listed above. Where the probe comprises double stranded DNA, it is denatured before addition to the hybridization solution. The filter is contacted with the hybridization solution for a sufficient period of time to allow the probe to hybridize to extended cDNAs or
15 genomic DNAs containing sequences complementary thereto or homologous thereto. For probes over 200 nucleotides in length, the hybridization may be carried out at 15-25°C below the T_m . For shorter probes, such as oligonucleotide probes, the hybridization may be conducted at 15-25°C below the T_m . Preferably, for hybridizations in 6X SSC, the hybridization is conducted at approximately 68°C. Preferably, for hybridizations in 50%
20 formamide containing solutions, the hybridization is conducted at approximately 42°C.

All of the foregoing hybridizations would be considered to be under "stringent" conditions.

Following hybridization, the filter is washed in 2X SSC, 0.1% SDS at room temperature for 15 minutes. The filter is then washed with 0.1X SSC, 0.5% SDS at room
25 temperature for 30 minutes to 1 hour. Thereafter, the solution is washed at the hybridization temperature in 0.1X SSC, 0.5% SDS. A final wash is conducted in 0.1X SSC at room temperature.

Extended cDNAs, nucleic acids homologous to extended cDNAs or 5' ESTs, or genomic DNAs which have hybridized to the probe are identified by autoradiography or
30 other conventional techniques.

2. Obtention of Extended cDNA or Genomic cDNA Sequences Having Lower Degrees of Homology to the Labeled Probe

The above procedure may be modified to identify extended cDNAs, nucleic acids homologous to extended cDNAs, or genomic DNAs having decreasing levels of homology to the probe sequence. For example, to obtain extended cDNAs, nucleic acids homologous to extended cDNAs, or genomic DNAs of decreasing homology to the detectable probe, less stringent conditions may be used. For example, the hybridization temperature may be decreased in increments of 5°C from 68°C to 42°C in a hybridization buffer having a sodium concentration of approximately 1M. Following hybridization, the filter may be washed with 2X SSC, 0.5% SDS at the temperature of hybridization. These conditions are considered to be "moderate" conditions above 50°C and "low" conditions below 50°C.

Alternatively, the hybridization may be carried out in buffers, such as 6X SSC, containing formamide at a temperature of 42°C. In this case, the concentration of formamide in the hybridization buffer may be reduced in 5% increments from 50% to 0% to identify clones having decreasing levels of homology to the probe. Following hybridization, the filter may be washed with 6X SSC, 0.5% SDS at 50°C. These conditions are considered to be "moderate" conditions above 25% formamide and "low" conditions below 25% formamide.

Extended cDNAs, nucleic acids homologous to extended cDNAs, or genomic DNAs which have hybridized to the probe are identified by autoradiography.

3. Determination of the Degree of Homology Between the Obtained Extended cDNAs and the Labeled Probe

If it is desired to obtain nucleic acids homologous to extended cDNAs, such as allelic variants thereof or nucleic acids encoding proteins related to the proteins encoded by the extended cDNAs, the level of homology between the hybridized nucleic acid and the extended cDNA or 5' EST used as the probe may be further determined using BLAST2N; parameters may be adapted depending on the sequence length and degree of homology studied. To determine the level of homology between the hybridized nucleic acid and the extended cDNA or 5'EST from which the probe was derived, the nucleotide sequences of the hybridized nucleic acid and the extended cDNA or 5'EST from which the probe was derived are compared. For example, using the above methods, nucleic acids having at least 95%

nucleic acid homology to the extended cDNA or 5'EST from which the probe was derived may be obtained and identified. Similarly, by using progressively less stringent hybridization conditions one can obtain and identify nucleic acids having at least 90%, at least 85%, at least 80% or at least 75% homology to the extended cDNA or 5'EST from which the probe was
5 derived.

To determine whether a clone encodes a protein having a given amount of homology to the protein encoded by the extended cDNA or 5' EST, the amino acid sequence encoded by the extended cDNA or 5' EST is compared to the amino acid sequence encoded by the hybridizing nucleic acid. Homology is determined to exist when an amino acid sequence in
10 the extended cDNA or 5' EST is closely related to an amino acid sequence in the hybridizing nucleic acid. A sequence is closely related when it is identical to that of the extended cDNA or 5' EST or when it contains one or more amino acid substitutions therein in which amino acids having similar characteristics have been substituted for one another. Using the above methods and algorithms such as FASTA with parameters depending on the sequence length
15 and degree of homology studied, one can obtain nucleic acids encoding proteins having at least 95%, at least 90%, at least 85%, at least 80% or at least 75% homology to the proteins encoded by the extended cDNA or 5'EST from which the probe was derived.

In addition to the above described methods, other protocols are available to obtain
20 extended cDNAs using 5' ESTs as outlined in the following paragraphs.

Extended cDNAs may be prepared by obtaining mRNA from the tissue, cell, or organism of interest using mRNA preparation procedures utilizing polyA selection procedures or other techniques known to those skilled in the art. A first primer capable of hybridizing to the polyA tail of the mRNA is hybridized to the mRNA and a reverse
25 transcription reaction is performed to generate a first cDNA strand.

The first cDNA strand is hybridized to a second primer containing at least 10 consecutive nucleotides of the sequences of SEQ ID NOs 38-305. Preferably, the primer comprises at least 12, 15, or 17 consecutive nucleotides from the sequences of SEQ ID NOs 38-305. More preferably, the primer comprises 20 to 30 consecutive nucleotides from the
30 sequences of SEQ ID NOs 38-305. In some embodiments, the primer comprises more than 30 nucleotides from the sequences of SEQ ID NOs 38-305. If it is desired to obtain extended

cDNAs containing the full protein coding sequence, including the authentic translation initiation site, the second primer used contains sequences located upstream of the translation initiation site. The second primer is extended to generate a second cDNA strand complementary to the first cDNA strand. Alternatively, RT-PCR may be performed as described above using primers from both ends of the cDNA to be obtained.

Extended cDNAs containing 5' fragments of the mRNA may be prepared by hybridizing an mRNA comprising the sequence of the 5'EST for which an extended cDNA is desired with a primer comprising at least 10 consecutive nucleotides of the sequences complementary to the 5'EST and reverse transcribing the hybridized primer to make a first cDNA strand from the mRNAs. Preferably, the primer comprises at least 12, 15, or 17 consecutive nucleotides from the 5'EST. More preferably, the primer comprises 20 to 30 consecutive nucleotides from the 5'EST.

Thereafter, a second cDNA strand complementary to the first cDNA strand is synthesized. The second cDNA strand may be made by hybridizing a primer complementary to sequences in the first cDNA strand to the first cDNA strand and extending the primer to generate the second cDNA strand.

The double stranded extended cDNAs made using the methods described above are isolated and cloned. The extended cDNAs may be cloned into vectors such as plasmids or viral vectors capable of replicating in an appropriate host cell. For example, the host cell may be a bacterial, mammalian, avian, or insect cell.

Techniques for isolating mRNA, reverse transcribing a primer hybridized to mRNA to generate a first cDNA strand, extending a primer to make a second cDNA strand complementary to the first cDNA strand, isolating the double stranded cDNA and cloning the double stranded cDNA are well known to those skilled in the art and are described in *Current Protocols in Molecular Biology*, John Wiley and Sons, Inc. 1997 and Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, 1989, the entire disclosures of which are incorporated herein by reference.

Alternatively, procedures such as the one described in Example 29 may be used for obtaining full length cDNAs or extended cDNAs. In this approach, full length or extended cDNAs are prepared from mRNA and cloned into double stranded phagemids as follows. The cDNA library in the double stranded phagemids is then rendered single stranded by

treatment with an endonuclease, such as the Gene II product of the phage F1, and an exonuclease (Chang *et al.*, *Gene* 127:95-8, 1993). A biotinylated oligonucleotide comprising the sequence of a 5' EST, or a fragment containing at least 10 nucleotides thereof, is hybridized to the single stranded phagemids. Preferably, the fragment comprises at least 12,
5 15, or 17 consecutive nucleotides from the 5' EST. More preferably, the fragment comprises 20-30 consecutive nucleotides from the 5' EST. In some procedures, the fragment may comprise more than 30 consecutive nucleotides from the 5' EST.

Hybrids between the biotinylated oligonucleotide and phagemids having inserts containing the 5' EST sequence are isolated by incubating the hybrids with streptavidin
10 coated paramagnetic beads and retrieving the beads with a magnet (Fry *et al.*, *Biotechniques*, 13: 124-131, 1992). Thereafter, the resulting phagemids containing the 5' EST sequence are released from the beads and converted into double stranded DNA using a primer specific for the 5' EST sequence. Alternatively, protocols such as the Gene Trapper kit (Gibco BRL) may be used. The resulting double stranded DNA is transformed into bacteria. Extended
15 cDNAs containing the 5' EST sequence are identified by colony PCR or colony hybridization.

Using any of the above described methods in section III, a plurality of extended cDNAs containing full length protein coding sequences or sequences encoding only the mature protein remaining after the signal peptide is cleaved off may be provided as
20 cDNA libraries for subsequent evaluation of the encoded proteins or use in diagnostic assays as described below.

IV. Expression of Proteins Encoded by Extended cDNAs Isolated Using 5' ESTs

Extended cDNAs containing the full protein coding sequences of their corresponding
25 mRNAs or portions thereof, such as cDNAs encoding the mature protein, may be used to express the encoded secreted proteins or portions thereof as described in Example 30 below. If desired, the extended cDNAs may contain the sequences encoding the signal peptide to facilitate secretion of the expressed protein. It will be appreciated that a plurality of extended cDNAs containing the full protein coding sequences or portions thereof may be
30 simultaneously cloned into expression vectors to create an expression library for analysis of the encoded proteins as described below.

EXAMPLE 30**Expression of the Proteins Encoded by the Genes Corresponding
to 5'ESTS or Portions Thereof**

To express the proteins encoded by the genes corresponding to 5' ESTs (or portions thereof), full length cDNAs containing the entire protein coding region or extended cDNAs containing sequences adjacent to the 5' ESTs (or portions thereof) are obtained as described in Examples 27-29 and cloned into a suitable expression vector. If desired, the nucleic acids may contain the sequences encoding the signal peptide to facilitate secretion of the expressed protein. The nucleic acids inserted into the expression vectors may also contain sequences upstream of the sequences encoding the signal peptide, such as sequences which regulate expression levels or sequences which confer tissue specific expression.

The nucleic acid encoding the protein or polypeptide to be expressed is operably linked to a promoter in an expression vector using conventional cloning technology. The expression vector may be any of the mammalian, yeast, insect or bacterial expression systems known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Genetics Institute (Cambridge, MA), Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon context and codon pairing of the sequence may be optimized for the particular expression organism in which the expression vector is introduced, as explained by Hatfield, *et al.*, U.S. Patent No. 5,082,767, incorporated herein by this reference.

The cDNA cloned into the expression vector may encode the entire protein (*i.e.* the signal peptide and the mature protein), the mature protein (*i.e.* the protein created by cleaving the signal peptide off), only the signal peptide or any other portion thereof.

The following is provided as one exemplary method to express the proteins encoded by the extended cDNAs corresponding to the 5' ESTs or the nucleic acids described above. First, the methionine initiation codon for the gene and the polyA signal of the gene are identified. If the nucleic acid encoding the polypeptide to be expressed lacks a methionine to serve as the initiation site, an initiating methionine can be introduced next to the first codon of the nucleic acid using conventional techniques. Similarly, if the extended cDNA lacks a polyA signal, this sequence can be added to the construct by, for example, splicing out the

polyA signal from pSG5 (Stratagene) using BglII and SalI restriction endonuclease enzymes and incorporating it into the mammalian expression vector pXT1 (Stratagene). pXT1 contains the LTRs and a portion of the *gag* gene from Moloney Murine Leukemia Virus. The position of the LTRs in the construct allow efficient stable transfection. The vector
5 includes the Herpes Simplex thymidine kinase promoter and the selectable neomycin gene. The extended cDNA or portion thereof encoding the polypeptide to be expressed is obtained by PCR from the bacterial vector using oligonucleotide primers complementary to the extended cDNA or portion thereof and containing restriction endonuclease sequences for Pst I incorporated into the 5' primer and BglII at the 5' end of the corresponding cDNA 3' primer,
10 taking care to ensure that the extended cDNA is positioned with the poly A signal. The purified fragment obtained from the resulting PCR reaction is digested with PstI, blunt ended with an exonuclease, digested with Bgl II, purified and ligated to pXT1 containing a poly A signal and prepared for this ligation (blunt/BglII).

The ligated product is transfected into mouse NIH 3T3 cells using Lipofectin (Life
15 Technologies, Inc., Grand Island, New York) under conditions outlined in the product specification. Positive transfectants are selected after growing the transfected cells in 600 µg/ml G418 (Sigma, St. Louis, Missouri). Preferably the expressed protein is released into the culture medium, thereby facilitating purification.

Alternatively, the extended cDNAs may be cloned into pED6dpc2 as described
20 above. The resulting pED6dpc2 constructs may be transfected into a suitable host cell, such as COS 1 cells. Methotrexate resistant cells are selected and expanded. Preferably, the protein expressed from the extended cDNA is released into the culture medium thereby facilitating purification.

Proteins in the culture medium are separated by gel electrophoresis. If desired, the
25 proteins may be ammonium sulfate precipitated or separated based on size or charge prior to electrophoresis.

As a control, the expression vector lacking a cDNA insert is introduced into host cells or organisms and the proteins in the medium are harvested. The secreted proteins present in the medium are detected using techniques familiar to those skilled in the art such as
30 Coomassie blue or silver staining or using antibodies against the protein encoded by the extended cDNA.

Antibodies capable of specifically recognizing the protein of interest may be generated using synthetic 15-mer peptides having a sequence encoded by the appropriate 5' EST, extended cDNA, or portion thereof. The synthetic peptides are injected into mice to generate antibody to the polypeptide encoded by the 5' EST, extended cDNA, or portion thereof.

5 Secreted proteins from the host cells or organisms containing an expression vector which contains the extended cDNA derived from a 5' EST or a portion thereof are compared to those from the control cells or organism. The presence of a band in the medium from the cells containing the expression vector which is absent in the medium from the control cells indicates that the extended cDNA encodes a secreted protein. Generally, the band
10 corresponding to the protein encoded by the extended cDNA will have a mobility near that expected based on the number of amino acids in the open reading frame of the extended cDNA. However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

 Alternatively, if the protein expressed from the above expression vectors does not
15 contain sequences directing its secretion, the proteins expressed from host cells containing an expression vector with an insert encoding a secreted protein or portion thereof can be compared to the proteins expressed in control host cells containing the expression vector without an insert. The presence of a band in samples from cells containing the expression
20 vector with an insert which is absent in samples from cells containing the expression vector without an insert indicates that the desired protein or portion thereof is being expressed. Generally, the band will have the mobility expected for the secreted protein or portion thereof. However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

 The protein encoded by the extended cDNA may be purified using standard
25 immunochromatography techniques. In such procedures, a solution containing the secreted protein, such as the culture medium or a cell extract, is applied to a column having antibodies against the secreted protein attached to the chromatography matrix. The secreted protein is allowed to bind the immunochromatography column. Thereafter, the column is washed to remove non-specifically bound proteins. The specifically bound secreted protein is then
30 released from the column and recovered using standard techniques.

If antibody production is not possible, the extended cDNA sequence or portion thereof may be incorporated into expression vectors designed for use in purification schemes employing chimeric polypeptides. In such strategies, the coding sequence of the extended cDNA or portion thereof is inserted in frame with the gene encoding the other half of the chimera. The other half of the chimera may be β -globin or a nickel binding polypeptide. A chromatography matrix having antibody to β -globin or nickel attached thereto is then used to purify the chimeric protein. Protease cleavage sites may be engineered between the β -globin gene or the nickel binding polypeptide and the extended cDNA or portion thereof. Thus, the two polypeptides of the chimera may be separated from one another by protease digestion.

One useful expression vector for generating β -globin chimerics is pSG5 (Stratagene), which encodes rabbit β -globin. Intron II of the rabbit β -globin gene facilitates splicing of the expressed transcript, and the polyadenylation signal incorporated into the construct increases the level of expression. These techniques as described are well known to those skilled in the art of molecular biology. Standard methods are published in methods texts such as Davis *et al.*, (*Basic Methods in Molecular Biology*, Davis, Dignner, and Battey, ed., Elsevier Press, NY, 1986) and many of the methods are available from Stratagene, Life Technologies, Inc., or Promega. Polypeptide may additionally be produced from the construct using *in vitro* translation systems such as the *In vitro* ExpressTM Translation Kit (Stratagene).

Following expression and purification of the secreted proteins encoded by the 5' ESTs, extended cDNAs, or fragments thereof, the purified proteins may be tested for the ability to bind to the surface of various cell types as described in Example 31 below. It will be appreciated that a plurality of proteins expressed from these cDNAs may be included in a panel of proteins to be simultaneously evaluated for the activities specifically described below, as well as other biological roles for which assays for determining activity are available.

EXAMPLE 31

Analysis of Secreted Proteins to Determine Whether they Bind to the Cell Surface

The proteins encoded by the 5' ESTs, extended cDNAs, or fragments thereof are cloned into expression vectors such as those described in Example 30. The proteins are purified by size, charge, immunochromatography or other techniques familiar to those skilled

in the art. Following purification, the proteins are labeled using techniques known to those skilled in the art. The labeled proteins are incubated with cells or cell lines derived from a variety of organs or tissues to allow the proteins to bind to any receptor present on the cell surface. Following the incubation, the cells are washed to remove non-specifically bound protein. The labeled proteins are detected by autoradiography. Alternatively, unlabeled proteins may be incubated with the cells and detected with antibodies having a detectable label, such as a fluorescent molecule, attached thereto.

Specificity of cell surface binding may be analyzed by conducting a competition analysis in which various amounts of unlabeled protein are incubated along with the labeled protein. The amount of labeled protein bound to the cell surface decreases as the amount of competitive unlabeled protein increases. As a control, various amounts of an unlabeled protein unrelated to the labeled protein is included in some binding reactions. The amount of labeled protein bound to the cell surface does not decrease in binding reactions containing increasing amounts of unrelated unlabeled protein, indicating that the protein encoded by the cDNA binds specifically to the cell surface.

As discussed above, secreted proteins have been shown to have a number of important physiological effects and, consequently, represent a valuable therapeutic resource. The secreted proteins encoded by the extended cDNAs or portions thereof made according to Examples 27-29 may be evaluated to determine their physiological activities as described below.

EXAMPLE 32

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Cytokine,

Cell Proliferation or Cell Differentiation Activity

As discussed above, secreted proteins may act as cytokines or may affect cellular proliferation or differentiation. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein encoded by the extended cDNAs is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D,

DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M⁺ (preB M⁺), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7c and CMK. The proteins encoded by the above extended cDNAs or portions thereof may be evaluated for their ability to regulate T cell or thymocyte proliferation in assays such as those described above or in the following references, which are
5 incorporated herein by reference: *Current Protocols in Immunology*, Ed. by Coligan *et al.*, Greene Publishing Associates and Wiley-Interscience; Takai *et al.* *J. Immunol.* 137:3494-3500, 1986.; Bertagnolli *et al.*, *J. Immunol.* 145:1706-1712, 1990.; Bertagnolli *et al.*, *Cell. Immunol.* 133:327-341, 1991; Bertagnolli, *et al.*, *J. Immunol.* 149:3778-3783, 1992; Bowman *et al.*, *J. Immunol.* 152:1756-1761, 1994.

10 In addition, numerous assays for cytokine production and/or the proliferation of spleen cells, lymph node cells and thymocytes are known. These include the techniques disclosed in *Current Protocols in Immunology*, *supra* 1:3.12.1-3.12.14; and Schreiber In *Current Protocols in Immunology*, *supra* 1 : 6.8.1-6.8.8.

The proteins encoded by the cDNAs may also be assayed for the ability to regulate
15 the proliferation and differentiation of hematopoietic or lymphopoietic cells. Many assays for such activity are familiar to those skilled in the art, including the assays in the following references, which are incorporated herein by reference: Bottomly *et al.*, In *Current Protocols in Immunology*, *supra* 1 : 6.3.1-6.3.12.; deVries *et al.*, *J. Exp. Med.* 173:1205-1211, 1991; Moreau *et al.*, *Nature* 36:690-692, 1988; Greenberger *et al.*, *Proc. Natl. Acad. Sci. U.S.A.*
20 80:2931-2938, 1983; Nordan, R., In *Current Protocols in Immunology*, *supra* 1 : 6.6.1-6.6.5; Smith *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 83:1857-1861, 1986; Bennett *et al.*, in *Current Protocols in Immunology supra* 1 : 6.15.1; Ciarletta *et al.*, In *Current Protocols in Immunology supra* 1 : 6.13.1.

The proteins encoded by the cDNAs may also be assayed for their ability to regulate
25 T-cell responses to antigens. Many assays for such activity are familiar to those skilled in the art, including the assays described in the following references, which are incorporated herein by reference: Chapter 3 (*In Vitro* Assays for Mouse Lymphocyte Function), Chapter 6 (Cytokines and Their Cellular Receptors) and Chapter 7, (Immunologic Studies in Humans) in *Current Protocols in Immunology supra*; Weinberger *et al.*, *Proc. Natl. Acad. Sci. USA*
30 77:6091-6095, 1980; Weinberger *et al.*, *Eur. J. Immun.* 11:405-411, 1981; Takai *et al.*, *J. Immunol.* 137:3494-3500, 1986; Takai *et al.*, *J. Immunol.* 140:508-512, 1988.

Those proteins which exhibit cytokine, cell proliferation, or cell differentiation activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which induction of cell proliferation or differentiation is beneficial. Alternatively, as described in more detail below, genes encoding these proteins or nucleic acids regulating the expression of these proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 33

Assaying the Proteins Expressed from Extended cDNAs or Portions

Thereof for Activity as Immune System Regulators

The proteins encoded by the cDNAs may also be evaluated for their effects as immune regulators. For example, the proteins may be evaluated for their activity to influence thymocyte or splenocyte cytotoxicity. Numerous assays for such activity are familiar to those skilled in the art including the assays described in the following references, which are incorporated herein by reference: Chapter 3 (*In Vitro* Assays for Mouse Lymphocyte Function 3.1-3.19) and Chapter 7 (Immunologic studies in Humans) in *Current Protocols in Immunology*, Coligan *et al.*, Eds, Greene Publishing Associates and Wiley-Interscience; Herrmann *et al.*, *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann *et al.*, *J. Immunol.* 128:1968-1974, 1982; Handa *et al.*, *J. Immunol.* 135:1564-1572, 1985; Takai *et al.*, *J. Immunol.* 137:3494-3500, 1986; Takai *et al.*, *J. Immunol.* 140:508-512, 1988; Bowman *et al.*, *J. Virology* 61:1992-1998; Bertagnoli *et al.*, *Cell. Immunol.* 133:327-341, 1991; Brown *et al.*, *J. Immunol.* 153:3079-3092, 1994.

The proteins encoded by the cDNAs may also be evaluated for their effects on T-cell dependent immunoglobulin responses and isotype switching. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Maliszewski, *J. Immunol.* 144:3028-3033, 1990; Mond *et al.* in *Current Protocols in Immunology*, 1:3.8.1-3.8.16, *supra*.

The proteins encoded by the cDNAs may also be evaluated for their effect on immune effector cells, including their effect on Th1 cells and cytotoxic lymphocytes. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Chapter 3 (*In Vitro* Assays

for Mouse Lymphocyte Function 3.1-3.19) and Chapter 7 (Immunologic Studies in Humans) in *Current Protocols in Immunology*, *supra*; Takai *et al.*, *J. Immunol.* 137:3494-3500, 1986; Takai *et al.*, *J. Immunol.* 140:508-512, 1988; Bertagnolli *et al.*, *J. Immunol.* 149:3778-3783, 1992.

5 The proteins encoded by the cDNAs may also be evaluated for their effect on dendritic cell mediated activation of naive T-cells. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Guery *et al.*, *J. Immunol.* 134:536-544, 1995; Inaba *et al.*, *J. Exp. Med.* 173:549-559, 1991; Macatonia *et al.*, *J. Immunol.* 154:5071-5079, 1995; Porgador *et al.*, *J. Exp. Med.* 182:255-260, 1995; Nair *et al.*, *J. Virol.* 67:4062-4069, 10 1993; Huang *et al.*, *Science* 264:961-965, 1994; Macatonia *et al.*, *J. Exp. Med.* 169:1255-1264, 1989; Bhardwaj *et al.*, *Journal of Clinical Investigation* 94:797-807, 1994; and Inaba *et al.*, *J. Exp. Med.* 172:631-640, 1990.

 The proteins encoded by the cDNAs may also be evaluated for their influence on the lifetime of lymphocytes. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Darzynkiewicz *et al.*, *Cytometry* 13:795-808, 1992; Gorczyca *et al.*, *Leukemia* 7:659-670, 1993; Gorczyca *et al.*, *Cancer Res.* 53:1945-1951, 1993; Itoh *et al.*, *Cell* 66:233-243, 1991; Zacharchuk, *J. Immunol.* 145:4037-4045, 1990; Zamai *et al.*, *Cytometry* 14:891-20 897, 1993; Gorczyca *et al.*, *Int. J. Oncol.* 1:639-648, 1992.

 The proteins encoded by the cDNAs may also be evaluated for their influence on early steps of T-cell commitment and development. Numerous assays for such activity are familiar to those skilled in the art, including without limitation the assays disclosed in the following references, which are incorporated herein by references: Antica *et al.*, *Blood* 25 84:111-117, 1994; Fine *et al.*, *Cell. Immunol.* 155:111-122, 1994; Galy *et al.*, *Blood* 85:2770-2778, 1995; Toki *et al.*, *Proc. Nat. Acad. Sci. USA* 88:7548-7551, 1991.

 Those proteins which exhibit activity as immune system regulators activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of immune activity is beneficial. For example, the protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency), 30 e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well

as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., plasmodium and various fungal infections such as candidiasis. Of course, in this regard, a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Alternatively, proteins encoded by extended cDNAs derived from the 5' ESTs of the present invention may be used in treatment of autoimmune disorders including, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses either up or down.

Down regulation may involve inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T-cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active non-antigen-specific process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after the end of exposure to the tolerizing agent. Operationally, tolerance can be

demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions, such as, for example, B7 costimulation), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation, can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this manner prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, *Science* 257:789-792, 1992 and Turka *et al.*, *Proc. Natl. Acad. Sci USA*, 89:11102-11105, 1992. In addition, murine models of GVHD (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor/ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which potentially involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/pr/pr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in OD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., *supra*, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may involve either enhancing an existing immune response or eliciting an initial immune response as shown by the following examples. For instance, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory form of B lymphocyte antigens systemically.

Alternatively, antiviral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide encoded by extended cDNAs derived from the 5' ESTs of the present invention or together with a stimulatory form of a soluble peptide encoded by extended cDNAs derived from the 5' ESTs of the present invention and reintroducing the *in vitro* primed T cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to T cells *in vivo*, thereby activating the T cells.

In another application, upregulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide encoded by extended cDNAs derived from the 5' ESTs of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide encoded by extended cDNAs derived from the 5' ESTs of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules can be transfected with nucleic acids encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain and β_2 microglobulin or an MHC class II α chain and an MHC class II β chain to thereby express MHC class I or MHC class II proteins on the cell surface, respectively. Expression of the appropriate MHC class I or class II molecules in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject. Alternatively, as described in more detail below, genes encoding these immune system regulator proteins or nucleic acids regulating the expression of

such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 34

5 Assaying the Proteins Expressed from Extended cDNAs
 or Portions Thereof for Hematopoiesis Regulating Activity

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their hematopoiesis regulating activity. For example, the effect of the proteins on embryonic stem cell differentiation may be evaluated. Numerous assays for such activity
10 are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Johansson *et al.* *Cell. Biol.* 15:141-151, 1995; Keller *et al.*, *Mol. Cell. Biol.* 13:473-486, 1993; McClanahan *et al.*, *Blood* 81:2903-2915, 1993.

The proteins encoded by the extended cDNAs or portions thereof may also be
15 evaluated for their influence on the lifetime of stem cells and stem cell differentiation. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Freshney, Methylcellulose Colony Forming Assays, in *Culture of Hematopoietic Cells.*, Freshney, *et al.* Eds. pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama *et al.*, *Proc. Natl. Acad.*
20 *Sci. USA* 89:5907-5911, 1992; McNiece and Briddell, in *Culture of Hematopoietic Cells*, *supra*; Neben *et al.*, *Exp. Hematol.* 22:353-359, 1994; Ploemacher and Cobblestone In *Culture of Hematopoietic Cells*, *supra* 1-21, Spooncer *et al.*, in *Culture of Hematopoietic Cells*, *supra* 163-179 and Sutherland in *Culture of Hematopoietic Cells*, *supra*. 139-162.

Those proteins which exhibit hematopoiesis regulatory activity may then be
25 formulated as pharmaceuticals and used to treat clinical conditions in which regulation of hematopoeisis is beneficial, such as in the treatment of myeloid or lymphoid cell deficiencies. Involvement in regulating hematopoiesis is indicated even by marginal biological activity in support of colony forming cells or of factor-dependent cell lines. For example, proteins supporting the growth and proliferation of erythroid progenitor cells alone or in combination
30 with other cytokines, indicates utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors

and/or erythroid cells. Proteins supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) may be useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelosuppression. Proteins supporting the growth and proliferation of megakaryocytes and consequently of platelets allows prevention or treatment of various platelet disorders such as thrombocytopenia, and generally may be used in place of or complementary to platelet transfusions. Proteins supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells may therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in vivo* or *ex vivo* (*i.e.*, in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy. Alternatively, as described in more detail below, genes encoding hematopoiesis regulating activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 35

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Regulation of Tissue Growth

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their effect on tissue growth. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in International Patent Publication No. WO95/16035, International Patent Publication No. WO95/05846 and International Patent Publication No. WO91/07491, which are incorporated herein by reference.

Assays for wound healing activity include, without limitation, those described in: Winter, *Epidermal Wound Healing*, pps. 71-112, Maibach and Rovee, eds., Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, *J. Invest. Dermatol.* 71:382-84, 1978, which are incorporated herein by reference.

Those proteins which are involved in the regulation of tissue growth may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of tissue growth is beneficial. For example, a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein encoded by extended cDNAs derived from the 5' ESTs of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone synthesis induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of bone-forming cell progenitors. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein encoded by extended cDNAs derived from the 5' ESTs of the present invention is tendon/ligament formation. A protein encoded by extended cDNAs derived from the 5' ESTs of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. *De novo* tendon/ligament-like tissue

formation induced by a composition encoded by extended cDNAs derived from the 5' ESTs of the present invention contributes to the repair of tendon or ligaments defects of congenital, traumatic or other origin and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions encoded by extended cDNAs derived from the 5' ESTs of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.*, for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium) muscle (smooth, skeletal or cardiac) and vascular (including vascular

endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to generate. A protein of the invention may also exhibit angiogenic activity.

5 A protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also be useful for promoting or inhibiting differentiation of tissues described
10 above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Alternatively, as described in more detail below, genes encoding tissue growth regulating activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

15

EXAMPLE 36

Assaying the Proteins Expressed from Extended cDNAs or Portions

Thereof for Regulation of Reproductive Hormones

The proteins encoded by the extended cDNAs or portions thereof may also be
20 evaluated for their ability to regulate reproductive hormones, such as follicle stimulating hormone. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Vale *et al.*, *Endocrinol.* 91:562-572, 1972; Ling *et al.*, *Nature* 321:779-782, 1986; Vale *et al.*, *Nature* 321:776-779, 1986; Mason *et al.*, *Nature* 318:659-663, 1985; Forage *et al.*,
25 *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986, Chapter 6.12 in *Current Protocols in Immunology*, Coligan *et al.* Eds. Greene Publishing Associates and Wiley-Interscience; Taub *et al.*, *J. Clin. Invest.* 95:1370-1376, 1995; Lind *et al.*, *APMIS* 103:140-146, 1995; Muller *et al.*, *Eur. J. Immunol.* 25:1744-1748; Gruber *et al.*, *J. Immunol.* 152:5860-5867, 1994; Johnston *et al.*, *J Immunol.* 153:1762-1768, 1994.

30 Those proteins which exhibit activity as reproductive hormones or regulators of cell movement may then be formulated as pharmaceuticals and used to treat clinical conditions in

which regulation of reproductive hormones are beneficial. For example, a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of FSH. Thus, a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-B group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885, the disclosure of which is incorporated herein by reference. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

Alternatively, as described in more detail below, genes encoding reproductive hormone regulating activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 37

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Chemotactic/Chemokinetic Activity

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for chemotactic/chemokinetic activity. For example, a protein encoded by extended cDNAs derived from the 5' ESTs of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins

provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

5 A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell
10 chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of
15 cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: *Current Protocols in Immunology*, Ed by Coligan, Kruisbeek, Margulies, Shevach and Strober, Pub. Greene Publishing Associates and Wiley-Interscience, Chapter 6.12: 6.12.1-6.12.28; Taub *et al.*, *J. Clin. Invest.* 95:1370-1376, 1995;
20 Lind *et al.*, *APMIS* 103:140-146, 1995; Mueller *et al.*, *Eur. J. Immunol.* 25:1744-1748; Gruber *et al.*, *J. Immunol.* 152:5860-5867, 1994; Johnston *et al.* *J. Immunol.*, 153:1762-1768, 1994.

EXAMPLE 38

25 Assaying the Proteins Expressed from Extended cDNAs or
 Portions Thereof for Regulation of Blood Clotting

The proteins encoded by the extended cDNAs or portions thereof may also be evaluated for their effects on blood clotting. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references, which are
30 incorporated herein by reference: Linet *et al.*, *J. Clin. Pharmacol.* 26:131-140, 1986; Burdick

et al., *Thrombosis Res.* 45:413-419, 1987; Humphrey *et al.*, *Fibrinolysis* 5:71-79, 1991; Schaub, *Prostaglandins* 35:467-474, 1988.

Those proteins which are involved in the regulation of blood clotting may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of blood clotting is beneficial. For example, a protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulations disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as infarction of cardiac and central nervous system vessels (e.g., stroke)). Alternatively, as described in more detail below, genes encoding blood clotting activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 39

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Involvement in Receptor/Ligand Interactions

The proteins encoded by the extended cDNAs or a portion thereof may also be evaluated for their involvement in receptor/ligand interactions. Numerous assays for such involvement are familiar to those skilled in the art, including the assays disclosed in the following references, which are incorporated herein by reference: Chapter 7. 7.28.1-7.28.22 in *Current Protocols in Immunology*, Coligan *et al.* Eds. Greene Publishing Associates and Wiley-Interscience; Takai *et al.*, *Proc. Natl. Acad. Sci. USA* 84:6864-6868, 1987; Bierer *et al.*, *J. Exp. Med.* 168:1145-1156, 1988; Rosenstein *et al.*, *J. Exp. Med.* 169:149-160, 1989; Stoltenborg *et al.*, *J. Immunol. Methods* 175:59-68, 1994; Stitt *et al.*, *Cell* 80:661-670, 1995; Gyuris *et al.*, *Cell* 75:791-803, 1993.

For example, the proteins encoded by extended cDNAs derived from the 5' ESTs of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include,

without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen
5 recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein encoded by extended cDNAs derived from the 5' ESTs of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions. Alternatively,
10 as described in more detail below, genes encoding proteins involved in receptor/ligand interactions or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 40

Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof
for Anti-Inflammatory Activity

The proteins encoded by the extended cDNAs or a portion thereof may also be evaluated for anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions, including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine- or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Alternatively, as described in more detail below, genes encoding anti-inflammatory activity proteins or nucleic

acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 41

5 Assaying the Proteins Expressed from Extended cDNAs or Portions Thereof for Tumor Inhibition Activity

10 The proteins encoded by the extended cDNAs or a portion thereof may also be evaluated for tumor inhibition activity. In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or
15 inhibiting factors, agents or cell types which promote tumor growth. Alternatively, as described in more detail below, genes tumor inhibition activity proteins or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

20 A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or
25 body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral
30 characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors;

providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein. Alternatively, as described in more detail below, genes encoding proteins involved in any of the above mentioned activities or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

EXAMPLE 42

Identification of Proteins which Interact with Polypeptides Encoded by Extended cDNAs

Proteins which interact with the polypeptides encoded by cDNAs derived from the 5' ESTs or fragments thereof, such as receptor proteins, may be identified using two hybrid systems such as the Matchmaker Two Hybrid System 2 (Catalog No. K1604-1, Clontech). As described in the manual accompanying the kit which is incorporated herein by reference, the the cDNAs derived from 5' ESTs, or fragments thereof, are inserted into an expression vector such that they are in frame with DNA encoding the DNA binding domain of the yeast transcriptional activator GAL4. cDNAs in a cDNA library which encode proteins which might interact with the polypeptides encoded by the extended cDNAs or portions thereof are inserted into a second expression vector such that they are in frame with DNA encoding the activation domain of GAL4. The two expression plasmids are transformed into yeast and the yeast are plated on selection medium which selects for expression of selectable markers on each of the expression vectors as well as GAL4 dependent expression of the HIS3 gene. Transformants capable of growing on medium lacking histidine are screened for GAL4 dependent lacZ expression. Those cells which are positive in both the histidine selection and the lacZ assay contain plasmids encoding proteins which interact with the polypeptide encoded by the extended cDNAs or portions thereof.

Alternatively, the system described in Lustig *et al.*, *Methods in Enzymology* 283: 83-99, 1997, and in U.S. Patent No. 5,654,150, the disclosure of which is incorporated herein by reference, may be used for identifying molecules which interact with the polypeptides encoded by extended cDNAs. In such systems, *in vitro* transcription reactions are performed
5 on a pool of vectors containing extended cDNA inserts cloned downstream of a promoter which drives *in vitro* transcription. The resulting pools of mRNAs are introduced into *Xenopus laevis* oocytes. The oocytes are then assayed for a desired activity.

Alternatively, the pooled *in vitro* transcription products produced as described above may be translated *in vitro*. The pooled *in vitro* translation products can be assayed for a
10 desired activity or for interaction with a known polypeptide.

Proteins or other molecules interacting with polypeptides encoded by extended cDNAs can be found by a variety of additional techniques. In one method, affinity columns containing the polypeptide encoded by the extended cDNA or a portion thereof can be constructed. In some versions, of this method the affinity column contains
15 chimeric proteins in which the protein encoded by the extended cDNA or a portion thereof is fused to glutathione S-transferase. A mixture of cellular proteins or pool of expressed proteins as described above and is applied to the affinity column. Proteins interacting with the polypeptide attached to the column can then be isolated and analyzed on 2-D electrophoresis gel as described in Ramunsen *et al.*, *Electrophoresis* 18:588-598,
20 1997, the disclosure of which is incorporated herein by reference. Alternatively, the proteins retained on the affinity column can be purified by electrophoresis based methods and sequenced. The same method can be used to isolate antibodies, to screen phage display products, or to screen phage display human antibodies.

Proteins interacting with polypeptides encoded by extended cDNAs or portions
25 thereof can also be screened by using an Optical Biosensor as described in Edwards and Leatherbarrow, *Analytical Biochemistry* 246:1-6, 1997, the disclosure of which is incorporated herein by reference. The main advantage of the method is that it allows the determination of the association rate between the protein and other interacting molecules. Thus, it is possible to specifically select interacting molecules with a high or
30 low association rate. Typically a target molecule is linked to the sensor surface (through a carboxymethyl dextran matrix) and a sample of test molecules is placed in contact with

the target molecules. The binding of a test molecule to the target molecule causes a change in the refractive index and/ or thickness. This change is detected by the Biosensor provided it occurs in the evanescent field (which extend a few hundred nanometers from the sensor surface). In these screening assays, the target molecule can be one of the polypeptides encoded by extended cDNAs or a portion thereof and the test sample can be a collection of proteins extracted from tissues or cells, a pool of expressed proteins, combinatorial peptide and/ or chemical libraries, or phage displayed peptides. The tissues or cells from which the test proteins are extracted can originate from any species.

10 In other methods, a target protein is immobilized and the test population is a collection of unique polypeptides encoded by the extended cDNAs or portions thereof.

To study the interaction of the proteins encoded by the extended cDNAs or portions thereof with drugs, the microdialysis coupled to HPLC method described by Wang *et al.*, *Chromatographia* 44:205-208, 1997 or the affinity capillary electrophoresis method described by Busch *et al.*, *J. Chromatogr.* 777:311-328, 1997, the disclosures of which are incorporated herein by reference can be used.

It will be appreciated by those skilled in the art that the proteins expressed from the extended cDNAs or portions may be assayed for numerous activities in addition to those specifically enumerated above. For example, the expressed proteins may be evaluated for applications involving control and regulation of inflammation, tumor proliferation or metastasis, infection, or other clinical conditions. In addition, the proteins expressed from the extended cDNAs or portions thereof may be useful as nutritional agents or cosmetic agents.

The proteins expressed from the cDNAs or portions thereof may be used to generate antibodies capable of specifically binding to the expressed protein or fragments thereof as described in Example 40 below. The antibodies may capable of binding a full length protein encoded by a cDNA derived from a 5' EST, a mature protein (*i.e.* the protein generated by cleavage of the signal peptide) encoded by a cDNA derived from a 5' EST, or a signal peptide encoded by a cDNA derived from a 5' EST. Alternatively, the antibodies may be capable of binding fragments of at least 10 amino acids of the proteins encoded by the above cDNAs. In some embodiments, the antibodies may be capable of binding fragments of at

least 15 amino acids of the proteins encoded by the above cDNAs. In other embodiments, the antibodies may be capable of binding fragments of at least 25 amino acids of the proteins expressed from the extended cDNAs which comprise at least 25 amino acids of the proteins encoded by the above cDNAs. In further embodiments, the antibodies may be capable of binding fragments of at least 40 amino acids of the proteins encoded by the above cDNAs.

EXAMPLE 43

Production of an Antibody to a Human Protein

Substantially pure protein or polypeptide is isolated from the transfected or transformed cells as described in Example 30. The concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few $\mu\text{g/ml}$. Monoclonal or polyclonal antibody to the protein can then be prepared as follows:

1. Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the peptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, and Milstein, *Nature* 256:495, 1975 or derivative methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein or peptides derived therefrom over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall, *Meth. Enzymol.* 70:419, 1980, the disclosure of which is incorporated herein by reference and derivative methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis *et al.* in *Basic Methods in Molecular Biology*

Elsevier, New York. Section 21-2, the disclosure of which is incorporated herein by reference.

2. Polyclonal Antibody Production by Immunization

5 Polyclonal antiserum containing antibodies to heterogenous epitopes of a single protein can be prepared by immunizing suitable animals with the expressed protein or peptides derived therefrom, which can be unmodified or modified to enhance immunogenicity. Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less
10 immunogenic than others and may require the use of carriers and adjuvant. Also, host animals response vary depending on site of inoculations and doses, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis, *et al*, *J. Clin. Endocrinol. Metab.* 33:988-991 (1971), the disclosure of which is incorporated herein by reference.

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, *et al.*, Chap. 19 in: *Handbook of Experimental Immunology* D. Wier (ed) Blackwell (1973), the disclosure of which is incorporated herein by reference. Plateau
20 concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 μ M). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, 2d Ed. (Rose and Friedman, Eds.) Amer. Soc. For Microbiol., Washington, D.C. (1980), the
25 disclosure of which is incorporated herein by reference.

Antibody preparations prepared according to either protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample. The antibodies may also be used in
30 therapeutic compositions for killing cells expressing the protein or reducing the levels of the protein in the body.

V. Use of 5' ESTs or Sequences Obtainable Therefrom or Portions Thereof as Reagents

The 5' ESTs of the present invention (or cDNAs or genomic DNAs obtainable therefrom) may be used as reagents in isolation procedures, diagnostic assays, and forensic procedures. For example, sequences from the 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom) may be detectably labeled and used as probes to isolate other sequences capable of hybridizing to them. In addition, sequences from 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom) may be used to design PCR primers to be used in isolation, diagnostic, or forensic procedures.

1. Use of 5' ESTs or Sequences Obtainable Therefrom or Portions Thereof in Isolation, Diagnostic and Forensic Procedures

EXAMPLE 44

Preparation of PCR Primers and Amplification of DNA

The 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom) may be used to prepare PCR primers for a variety of applications, including isolation procedures for cloning nucleic acids capable of hybridizing to such sequences, diagnostic techniques and forensic techniques. The PCR primers are at least 10 bases, and preferably at least 12, 15, or 17 bases in length. More preferably, the PCR primers are at least 20-30 bases in length. In some embodiments, the PCR primers may be more than 30 bases in length. It is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. A variety of PCR techniques are familiar to those skilled in the art. For a review of PCR technology, see *Molecular Cloning to Genetic Engineering*, White Ed. *in Methods in Molecular Biology* 67: Humana Press, Totowa 1997, the disclosure of which is incorporated herein by reference. In each of these PCR procedures, PCR primers on either side of the nucleic acid sequences to be amplified are added to a suitably prepared nucleic acid sample along with dNTPs and a thermostable polymerase such as Taq polymerase, Pfu polymerase, or Vent polymerase. The nucleic acid in the sample is denatured and the PCR primers are specifically hybridized to complementary nucleic acid sequences in the sample. The hybridized primers are extended. Thereafter, another cycle of denaturation,

hybridization, and extension is initiated. The cycles are repeated multiple times to produce an amplified fragment containing the nucleic acid sequence between the primer sites.

EXAMPLE 45

Use of 5' ESTs as Probes

5 Probes derived from 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom), including full length cDNAs or genomic sequences, may be labeled with detectable labels familiar to those skilled in the art, including radioisotopes and non-radioactive labels, to provide a detectable probe. The detectable probe may be single stranded or double stranded
10 and may be made using techniques known in the art, including *in vitro* transcription, nick translation, or kinase reactions. A nucleic acid sample containing a sequence capable of hybridizing to the labeled probe is contacted with the labeled probe. If the nucleic acid in the sample is double stranded, it may be denatured prior to contacting the probe. In some applications, the nucleic acid sample may be immobilized on a surface such as a nitrocellulose
15 or nylon membrane. The nucleic acid sample may comprise nucleic acids obtained from a variety of sources, including genomic DNA, cDNA libraries, RNA, or tissue samples.

Procedures used to detect the presence of nucleic acids capable of hybridizing to the detectable probe include well known techniques such as Southern blotting, Northern blotting, dot blotting, colony hybridization, and plaque hybridization. In some applications, the nucleic
20 acid capable of hybridizing to the labeled probe may be cloned into vectors such as expression vectors, sequencing vectors, or *in vitro* transcription vectors to facilitate the characterization and expression of the hybridizing nucleic acids in the sample. For example, such techniques may be used to isolate and clone sequences in a genomic library or cDNA library which are capable of hybridizing to the detectable probe as described in Example 30 above.

25 PCR primers made as described in Example 44 above may be used in forensic analyses, such as the DNA fingerprinting techniques described in Examples 46-50 below. Such analyses may utilize detectable probes or primers based on the sequences of the the 5' ESTs or of cDNAs or genomic DNAs isolated using the 5' ESTs.

EXAMPLE 46**Forensic Matching by DNA Sequencing**

In one exemplary method, DNA samples are isolated from forensic specimens of, for example, hair, semen, blood or skin cells by conventional methods. A panel of PCR primers based on a number of the 5' ESTs of Example 25, or cDNAs or genomic DNAs isolated therefrom as described above, is then utilized in accordance with Example 44 to amplify DNA of approximately 100-200 bases in length from the forensic specimen. Corresponding sequences are obtained from a test subject. Each of these identification DNAs is then sequenced using standard techniques, and a simple database comparison determines the differences, if any, between the sequences from the subject and those from the sample. Statistically significant differences between the suspect's DNA sequences and those from the sample conclusively prove a lack of identity. This lack of identity can be proven, for example, with only one sequence. Identity, on the other hand, should be demonstrated with a large number of sequences, all matching. Preferably, a minimum of 50 statistically identical sequences of 100 bases in length are used to prove identity between the suspect and the sample.

EXAMPLE 47**Positive Identification by DNA Sequencing**

The technique outlined in the previous example may also be used on a larger scale to provide a unique fingerprint-type identification of any individual. In this technique, primers are prepared from a large number of 5'EST sequences from Example 25, or cDNA or genomic DNA sequences obtainable therefrom. Preferably, 20 to 50 different primers are used. These primers are used to obtain a corresponding number of PCR-generated DNA segments from the individual in question in accordance with Example 44. Each of these DNA segments is sequenced, using the methods set forth in Example 46. The database of sequences generated through this procedure uniquely identifies the individual from whom the sequences were obtained. The same panel of primers may then be used at any later time to absolutely correlate tissue or other biological specimen with that individual.

EXAMPLE 48**Southern Blot Forensic Identification**

The procedure of Example 47 is repeated to obtain a panel of at least 10 amplified sequences from an individual and a specimen. Preferably, the panel contains at least 50 amplified sequences. More preferably, the panel contains 100 amplified sequences. In some embodiments, the panel contains 200 amplified sequences. This PCR-generated DNA is then digested with one or a combination of, preferably, four base specific restriction enzymes. Such enzymes are commercially available and known to those of skill in the art. After digestion, the resultant gene fragments are size separated in multiple duplicate wells on an agarose gel and transferred to nitrocellulose using Southern blotting techniques well known to those with skill in the art. For a review of Southern blotting see Davis *et al.* (Basic Methods in Molecular Biology, 1986, Elsevier Press. pp 62-65) , the disclosure of which is incorporated herein by reference..

A panel of probes based on the sequences of 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom), or fragments thereof of at least 10 bases, are radioactively or colorimetrically labeled using methods known in the art, such as nick translation or end labeling, and hybridized to the Southern blot using techniques known in the art (Davis *et al.*, supra). Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST (or cDNAs or genomic DNAs obtainable therefrom). More preferably, the probe comprises at least 20-30 consecutive nucleotides from the 5' EST (or cDNAs or genomic DNAs obtainable therefrom). In some embodiments, the probe comprises more than 30 nucleotides from the 5' EST (or cDNAs or genomic DNAs obtainable therefrom).

Preferably, at least 5 to 10 of these labeled probes are used, and more preferably at least about 20 or 30 are used to provide a unique pattern. The resultant bands appearing from the hybridization of a large sample of 5' EST (or cDNAs or genomic DNAs obtainable therefrom) will be a unique identifier. Since the restriction enzyme cleavage will be different for every individual, the band pattern on the Southern blot will also be unique. Increasing the number of 5' EST (or cDNAs or genomic DNAs obtainable therefrom) probes will provide a statistically higher level of confidence in the identification since there will be an increased number of sets of bands used for identification.

EXAMPLE 49

Dot Blot Identification Procedure

Another technique for identifying individuals using the 5' EST sequences disclosed herein utilizes a dot blot hybridization technique.

5 Genomic DNA is isolated from nuclei of subject to be identified. Oligonucleotide probes of approximately 30 bp in length are synthesized that correspond to at least 10, preferably 50 sequences from the 5' ESTs or cDNAs or genomic DNAs obtainable therefrom. The probes are used to hybridize to the genomic DNA through conditions known to those in the art. The oligonucleotides are end labeled with P³² using polynucleotide kinase
10 (Pharmacia). Dot Blots are created by spotting the genomic DNA onto nitrocellulose or the like using a vacuum dot blot manifold (BioRad, Richmond California). The nitrocellulose filter containing the genomic sequences is baked or UV linked to the filter, prehybridized and hybridized with labeled probe using techniques known in the art (Davis *et al.*, *supra*). The ³²P labeled DNA fragments are sequentially hybridized with successively stringent conditions to
15 detect minimal differences between the 30 bp sequence and the DNA. Tetramethylammonium chloride is useful for identifying clones containing small numbers of nucleotide mismatches (Wood *et al.*, *Proc. Natl. Acad. Sci. USA* 82(6):1585-1588, 1985) which is hereby incorporated by reference. A unique pattern of dots distinguishes one individual from another individual.

20 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom) or oligonucleotides containing at least 10 consecutive bases from these sequences can be used as probes in the following alternative fingerprinting technique. Preferably, the probe comprises at least 12, 15, or 17 consecutive nucleotides from the 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom). More preferably, the probe comprises at least 20-30
25 consecutive nucleotides from the 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom). In some embodiments, the probe comprises more than 30 nucleotides from the 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom).

Preferably, a plurality of probes having sequences from different genes are used in the alternative fingerprinting technique. Example 50 below provides a representative alternative
30 fingerprinting procedure in which the probes are derived from 5'EST.

EXAMPLE 50Alternative "Fingerprint" Identification Technique

20-mer oligonucleotides are prepared from a large number, e.g. 50, 100, or 200, of 5'EST using commercially available oligonucleotide services such as Genset, Paris, France.

5 Cell samples from the test subject are processed for DNA using techniques well known to those with skill in the art. The nucleic acid is digested with restriction enzymes such as EcoRI and XbaI. Following digestion, samples are applied to wells for electrophoresis. The procedure, as known in the art, may be modified to accommodate polyacrylamide electrophoresis, however in this example, samples containing 5 ug of DNA are loaded into

10 wells and separated on 0.8% agarose gels. The gels are transferred onto nitrocellulose using standard Southern blotting techniques.

10 ng of each of the oligonucleotides are pooled and end-labeled with ^{32}P . The nitrocellulose is prehybridized with blocking solution and hybridized with the labeled probes. Following hybridization and washing, the nitrocellulose filter is exposed to X-Omat AR X-ray

15 film. The resulting hybridization pattern will be unique for each individual.

It is additionally contemplated within this example that the number of probe sequences used can be varied for additional accuracy or clarity.

The proteins encoded by the extended cDNAs may also be used to generate

20 antibodies as explained in Examples 30 and 43 in order to identify the tissue type or cell species from which a sample is derived as described in example 51.

EXAMPLE 51Identification of Tissue Types or Cell Species by Means of

25 Labeled Tissue Specific Antibodies

Identification of specific tissues is accomplished by the visualization of tissue specific antigens by means of antibody preparations according to Examples 30 and 43 which are conjugated, directly or indirectly to a detectable marker. Selected labeled antibody species bind to their specific antigen binding partner in tissue sections, cell suspensions, or in extracts

30 of soluble proteins from a tissue sample to provide a pattern for qualitative or semi-qualitative interpretation.

Antisera for these procedures must have a potency exceeding that of the native preparation, and for that reason, antibodies are concentrated to a mg/ml level by isolation of the gamma globulin fraction, for example, by ion-exchange chromatography or by ammonium sulfate fractionation. Also, to provide the most specific antisera, unwanted antibodies, for example to common proteins, must be removed from the gamma globulin fraction, for example by means of insoluble immunoabsorbents, before the antibodies are labeled with the marker. Either monoclonal or heterologous antisera is suitable for either procedure.

A. *Immunohistochemical techniques*

Purified, high-titer antibodies, prepared as described above, are conjugated to a detectable marker, as described, for example, by Fudenberg, Chap. 26 in: *Basic and Clinical Immunology*, 3rd Ed. Lange, Los Altos, California, 1980, or Rose, *et al.*, Chap. 12 in: *Methods in Immunodiagnosis*, 2d Ed. John Wiley and Sons, New York (1980), the disclosures of which are incorporated herein by reference.

A fluorescent marker, either fluorescein or rhodamine, is preferred, but antibodies can also be labeled with an enzyme that supports a color producing reaction with a substrate, such as horseradish peroxidase. Markers can be added to tissue-bound antibody in a second step, as described below. Alternatively, the specific antitissue antibodies can be labeled with ferritin or other electron dense particles, and localization of the ferritin coupled antigen-antibody complexes achieved by means of an electron microscope. In yet another approach, the antibodies are radiolabeled, with, for example ^{125}I , and detected by overlaying the antibody treated preparation with photographic emulsion.

Preparations to carry out the procedures can comprise monoclonal or polyclonal antibodies to a single protein or peptide identified as specific to a tissue type, for example, brain tissue, or antibody preparations to several antigenically distinct tissue specific antigens can be used in panels, independently or in mixtures, as required.

Tissue sections and cell suspensions are prepared for immunohistochemical examination according to common histological techniques. Multiple cryostat sections (about 4 μm , unfixed) of the unknown tissue and known control, are mounted and each slide covered with different dilutions of the antibody preparation. Sections of known and unknown tissues should also be treated with preparations to provide a positive control, a negative

control, for example, pre-immune sera, and a control for non-specific staining, for example, buffer.

5 Treated sections are incubated in a humid chamber for 30 min at room temperature, rinsed, then washed in buffer for 30-45 min. Excess fluid is blotted away, and the marker developed.

If the tissue specific antibody was not labeled in the first incubation, it can be labeled at this time in a second antibody-antibody reaction, for example, by adding fluorescein- or enzyme-conjugated antibody against the immunoglobulin class of the antiserum-producing species, for example, fluorescein labeled antibody to mouse IgG. Such labeled sera are
10 commercially available.

The antigen found in the tissues by the above procedure can be quantified by measuring the intensity of color or fluorescence on the tissue section, and calibrating that signal using appropriate standards.

B. Identification of tissue specific soluble proteins

15 The visualization of tissue specific proteins and identification of unknown tissues from that procedure is carried out using the labeled antibody reagents and detection strategy as described for immunohistochemistry; however the sample is prepared according to an electrophoretic technique to distribute the proteins extracted from the tissue in an orderly array on the basis of molecular weight for detection.

20 A tissue sample is homogenized using a Virtis apparatus; cell suspensions are disrupted by Dounce homogenization or osmotic lysis, using detergents in either case as required to disrupt cell membranes, as is the practice in the art. Insoluble cell components such as nuclei, microsomes, and membrane fragments are removed by ultracentrifugation, and the soluble protein-containing fraction concentrated if necessary and reserved for analysis.

25 A sample of the soluble protein solution is resolved into individual protein species by conventional SDS polyacrylamide electrophoresis as described, for example, by Davis, *et al.*, Section 19-2 in: *Basic Methods in Molecular Biology*, Leder ed., Elsevier, New York, 1986, the disclosure of which is incorporated herein by reference, using a range of amounts of polyacrylamide in a set of gels to resolve the entire molecular weight range of proteins to be
30 detected in the sample. A size marker is run in parallel for purposes of estimating molecular weights of the constituent proteins. Sample size for analysis is a convenient volume of from 5

to 55 μ l, and containing from about 1 to 100 μ g protein. An aliquot of each of the resolved proteins is transferred by blotting to a nitrocellulose filter paper, a process that maintains the pattern of resolution. Multiple copies are prepared. The procedure, known as Western Blot Analysis, is well described in Davis, L. *et al.*, *supra* Section 19-3. One set of nitrocellulose blots is stained with Coomassie blue dye to visualize the entire set of proteins for comparison with the antibody bound proteins. The remaining nitrocellulose filters are then incubated with a solution of one or more specific antisera to tissue specific proteins prepared as described in Examples 30 and 43. In this procedure, as in procedure A above, appropriate positive and negative sample and reagent controls are run.

10 In either procedure A or B, a detectable label can be attached to the primary tissue antigen-primary antibody complex according to various strategies and permutations thereof. In a straightforward approach, the primary specific antibody can be labeled; alternatively, the unlabeled complex can be bound by a labeled secondary anti-IgG antibody. In other approaches, either the primary or secondary antibody is conjugated to a biotin molecule, 15 which can, in a subsequent step, bind an avidin conjugated marker. According to yet another strategy, enzyme labeled or radioactive protein A, which has the property of binding to any IgG, is bound in a final step to either the primary or secondary antibody.

The visualization of tissue specific antigen binding at levels above those seen in control tissues to one or more tissue specific antibodies, prepared from the gene sequences 20 identified from extended cDNA sequences, can identify tissues of unknown origin, for example, forensic samples, or differentiated tumor tissue that has metastasized to foreign bodily sites.

In addition to their applications in forensics and identification, 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom) may be mapped to their chromosomal 25 locations. Example 52 below describes radiation hybrid (RH) mapping of human chromosomal regions using 5'ESTs. Example 53 below describes a representative procedure for mapping an 5' EST to its location on a human chromosome. Example 54 below describes mapping of 5' ESTs on metaphase chromosomes by Fluorescence In Situ Hybridization (FISH). Those skilled in the art will appreciate that the method of 30 Examples 52-54 may also be used to map cDNAs or genomic DNAs obtainable from the 5' ESTs to their chromosomal locations.

2. Use of 5' ESTs or Sequences Obtainable Therefrom or Portions Thereof in Chromosome Mapping

EXAMPLE 52

Radiation hybrid mapping of 5'ESTs to the human genome

5 Radiation hybrid (RH) mapping is a somatic cell genetic approach that can be used for high resolution mapping of the human genome. In this approach, cell lines containing one or more human chromosomes are lethally irradiated, breaking each chromosome into fragments whose size depends on the radiation dose. These fragments are rescued by fusion with cultured rodent cells, yielding subclones containing different portions of the human
10 genome. This technique is described by Benham *et al.*, *Genomics* 4:509-517, 1989; and Cox *et al.*, *Science* 250:245-250, 1990, the entire contents of which are hereby incorporated by reference. The random and independent nature of the subclones permits efficient mapping of any human genome marker. Human DNA isolated from a panel of 80-100 cell lines provides a mapping reagent for ordering 5'EST. In this approach, the frequency of breakage between
15 markers is used to measure distance, allowing construction of fine resolution maps as has been done using conventional ESTs (Schuler *et al.*, *Science* 274:540-546, 1996, hereby incorporated by reference).

 RH mapping has been used to generate a high-resolution whole genome radiation hybrid map of human chromosome 17q22-q25.3 across the genes for growth hormone (GH)
20 and thymidine kinase (TK) (Foster *et al.*, *Genomics* 33:185-192, 1996), the region surrounding the Gorlin syndrome gene (Obermayr *et al.*, *Eur. J. Hum. Genet.* 4:242-245, 1996), 60 loci covering the entire short arm of chromosome 12 (Raeymaekers *et al.*, *Genomics* 29:170-178, 1995), the region of human chromosome 22 containing the neurofibromatosis type 2 locus (Frazer *et al.*, *Genomics* 14:574-584, 1992) and 13 loci on the
25 long arm of chromosome 5 (Warrington *et al.*, *Genomics* 11:701-708, 1991).

EXAMPLE 53

Mapping of 5'ESTs to Human Chromosomes using PCR techniques

 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom) may be assigned to
30 human chromosomes using PCR based methodologies. In such approaches, oligonucleotide primer pairs are designed from the 5' ESTs (or cDNAs or genomic DNAs obtainable

therefrom) to minimize the chance of amplifying through an intron. Preferably, the oligonucleotide primers are 18-23 bp in length and are designed for PCR amplification. The creation of PCR primers from known sequences is well known to those with skill in the art. For a review of PCR technology see Erlich in *PCR Technology, Principles and Applications for DNA Amplification*, Freeman and Co., New York, 1992, the disclosure of which is
5 incorporated herein by reference.

The primers are used in polymerase chain reactions (PCR) to amplify templates from total human genomic DNA. PCR conditions are as follows: 60 ng of genomic DNA is used as a template for PCR with 80 ng of each oligonucleotide primer, 0.6 unit of Taq polymerase,
10 and 1 μ Cu of a 32 P-labeled deoxycytidine triphosphate. The PCR is performed in a microplate thermocycler (Techne) under the following conditions: 30 cycles of 94°C, 1.4 min; 55°C, 2 min; and 72°C, 2 min; with a final extension at 72°C for 10 min. The amplified products are analyzed on a 6% polyacrylamide sequencing gel and visualized by autoradiography. If the length of the resulting PCR product is identical to the distance
15 between the ends of the primer sequences in the extended cDNA from which the primers are derived, then the PCR reaction is repeated with DNA templates from two panels of human-rodent somatic cell hybrids, BIOS PCRable DNA (BIOS Corporation) and NIGMS Human-Rodent Somatic Cell Hybrid Mapping Panel Number 1 (NIGMS, Camden, NJ).

PCR is used to screen a series of somatic cell hybrid cell lines containing defined sets
20 of human chromosomes for the presence of a given 5' EST (or cDNA or genomic DNA obtainable therefrom). DNA is isolated from the somatic hybrids and used as starting templates for PCR reactions using the primer pairs from the 5' EST (or cDNA or genomic DNA obtainable therefrom). Only those somatic cell hybrids with chromosomes containing the human gene corresponding to the 5' EST (or cDNA or genomic DNA obtainable
25 therefrom) will yield an amplified fragment. The 5' EST (or cDNA or genomic DNA obtainable therefrom) are assigned to a chromosome by analysis of the segregation pattern of PCR products from the somatic hybrid DNA templates. The single human chromosome present in all cell hybrids that give rise to an amplified fragment is the chromosome containing that 5'EST (or cDNA or genomic DNA obtainable therefrom). For a review of techniques
30 and analysis of results from somatic cell gene mapping experiments, see Ledbetter *et al.*, *Genomics* 6:475-481, 1990, the disclosure of which is incorporated herein by reference.

EXAMPLE 54**Mapping of Extended 5' ESTs to Chromosomes Using Fluorescence *In Situ*****Hybridization**

Fluorescence in situ hybridization allows the 5'EST (or cDNA or genomic DNA obtainable therefrom) to be mapped to a particular location on a given chromosome. The chromosomes to be used for fluorescence in situ hybridization techniques may be obtained from a variety of sources including cell cultures, tissues, or whole blood.

In a preferred embodiment, chromosomal localization of an 5'EST (or cDNA or genomic DNA obtainable therefrom) is obtained by FISH as described by Cherif *et al.* (*Proc. Natl. Acad. Sci. U.S.A.*, 87:6639-6643, 1990), the disclosure of which is incorporated herein by reference. Metaphase chromosomes are prepared from phytohemagglutinin (PHA)-stimulated blood cell donors. PHA-stimulated lymphocytes from healthy males are cultured for 72 h in RPMI-1640 medium. For synchronization, methotrexate (10 μ M) is added for 17 h, followed by addition of 5-bromodeoxyuridine (5-BrdU, 0.1 mM) for 6 h. Colcemid (1 μ g/ml) is added for the last 15 min before harvesting the cells. Cells are collected, washed in RPMI, incubated with a hypotonic solution of KCl (75 mM) at 37°C for 15 min and fixed in three changes of methanol:acetic acid (3:1). The cell suspension is dropped onto a glass slide and air dried. The 5'EST (or cDNA or genomic DNA obtainable therefrom) is labeled with biotin-16 dUTP by nick translation according to the manufacturer's instructions (Bethesda Research Laboratories, Bethesda, MD), purified using a Sephadex G-50 column (Pharmacia, Upsala, Sweden) and precipitated. Just prior to hybridization, the DNA pellet is dissolved in hybridization buffer (50% formamide, 2 X SSC, 10% dextran sulfate, 1 mg/ml sonicated salmon sperm DNA, pH 7) and the probe is denatured at 70°C for 5-10 min.

Slides kept at -20°C are treated for 1 h at 37°C with RNase A (100 μ g/ml), rinsed three times in 2 X SSC and dehydrated in an ethanol series. Chromosome preparations are denatured in 70% formamide, 2 X SSC for 2 min at 70°C, then dehydrated at 4°C. The slides are treated with proteinase K (10 μ g/100 ml in 20 mM Tris-HCl, 2 mM CaCl₂) at 37°C for 8 min and dehydrated. The hybridization mixture containing the probe is placed on the slide, covered with a coverslip, sealed with rubber cement and incubated overnight in a humid chamber at 37°C. After hybridization and post-hybridization washes, the biotinylated probe is detected by avidin-FITC and amplified with additional layers of biotinylated goat anti-avidin

and avidin-FITC. For chromosomal localization, fluorescent R-bands are obtained as previously described (Cherif *et al.*, *supra.*). The slides are observed under a LEICA fluorescence microscope (DMRXA). Chromosomes are counterstained with propidium iodide and the fluorescent signal of the probe appears as two symmetrical yellow-green spots on both chromatids of the fluorescent R-band chromosome (red). Thus, a particular 5'EST (or cDNA or genomic DNA obtainable therefrom) may be localized to a particular cytogenetic R-band on a given chromosome.

Once the 5'EST (or cDNA or genomic DNA obtainable therefrom) have been assigned to particular chromosomes using the techniques described in Examples 52-54 above, they may be utilized to construct a high resolution map of the chromosomes on which they are located or to identify the chromosomes in a sample.

EXAMPLE 55

Use of 5'EST to Construct or Expand Chromosome Maps

Chromosome mapping involves assigning a given unique sequence to a particular chromosome as described above. Once the unique sequence has been mapped to a given chromosome, it is ordered relative to other unique sequences located on the same chromosome. One approach to chromosome mapping utilizes a series of yeast artificial chromosomes (YACs) bearing several thousand long inserts derived from the chromosomes of the organism from which the extended cDNAs (or genomic DNAs obtainable therefrom) are obtained. This approach is described in Nagaraja *et al.*, *Genome Research* 7:210-222, 1997, the disclosure of which is incorporated herein by reference. Briefly, in this approach each chromosome is broken into overlapping pieces which are inserted into the YAC vector. The YAC inserts are screened using PCR or other methods to determine whether they include the 5'EST (or cDNA or genomic DNA obtainable therefrom) whose position is to be determined. Once an insert has been found which includes the 5'EST (or cDNA or genomic DNA obtainable therefrom), the insert can be analyzed by PCR or other methods to determine whether the insert also contains other sequences known to be on the chromosome or in the region from which the 5'EST (or cDNA or genomic DNA obtainable therefrom) was derived. This process can be repeated for each insert in the YAC library to determine the

location of each of the extended cDNAs (or genomic DNAs obtainable therefrom) relative to one another and to other known chromosomal markers. In this way, a high resolution map of the distribution of numerous unique markers along each of the organisms chromosomes may be obtained.

5

As described in Example 56 below extended cDNAs (or genomic DNAs obtainable therefrom) may also be used to identify genes associated with a particular phenotype, such as hereditary disease or drug response.

10 3. Use of 5'ESTs or Sequences Obtained Therefrom or Fragments Thereof in Gene Identification

EXAMPLE 56

Identification of genes associated with hereditary diseases or drug response

15 This example illustrates an approach useful for the association of 5'ESTs (or cDNA or genomic DNA obtainable therefrom) with particular phenotypic characteristics. In this example, a particular 5'EST (or cDNA or genomic DNA obtainable therefrom) is used as a test probe to associate that 5'EST (or cDNA or genomic DNA obtainable therefrom) with a particular phenotypic characteristic.

20 5'ESTs (or cDNA or genomic DNA obtainable therefrom) are mapped to a particular location on a human chromosome using techniques such as those described in Examples 52 and 53 or other techniques known in the art. A search of Mendelian Inheritance in Man (McKusick in *Mendelian Inheritance in Man* (available on line through Johns Hopkins University Welch Medical Library) reveals the region of the human chromosome which contains the 5'EST (or cDNA or genomic DNA obtainable therefrom) to be a very gene rich
25 region containing several known genes and several diseases or phenotypes for which genes have not been identified. The gene corresponding to this 5'EST (or cDNA or genomic DNA obtainable therefrom) thus becomes an immediate candidate for each of these genetic diseases.

30 Cells from patients with these diseases or phenotypes are isolated and expanded in culture. PCR primers from the 5'EST (or cDNA or genomic DNA obtainable therefrom) are used to screen genomic DNA, mRNA or cDNA obtained from the

patients. 5'ESTs (or cDNA or genomic DNA obtainable therefrom) that are not amplified in the patients can be positively associated with a particular disease by further analysis. Alternatively, the PCR analysis may yield fragments of different lengths when the samples are derived from an individual having the phenotype associated with the disease than when the sample is derived from a healthy individual, indicating that the gene containing the 5'EST may be responsible for the genetic disease.

VI. Use of 5'EST (or cDNA or Genomic DNA Obtainable Therefrom) to Construct Vectors

The present 5'ESTs (or cDNA or genomic DNA obtainable therefrom) may also be used to construct secretion vectors capable of directing the secretion of the proteins encoded by genes therein. Such secretion vectors may facilitate the purification or enrichment of the proteins encoded by genes inserted therein by reducing the number of background proteins from which the desired protein must be purified or enriched. Exemplary secretion vectors are described in Example 57 below.

1. Construction of Secretion Vectors

EXAMPLE 57

Construction of Secretion Vectors

The secretion vectors include a promoter capable of directing gene expression in the host cell, tissue, or organism of interest. Such promoters include the Rous Sarcoma Virus promoter, the SV40 promoter, the human cytomegalovirus promoter, and other promoters familiar to those skilled in the art.

A signal sequence from a 5' EST (or cDNAs or genomic DNAs obtainable therefrom) is operably linked to the promoter such that the mRNA transcribed from the promoter will direct the translation of the signal peptide. The host cell, tissue, or organism may be any cell, tissue, or organism which recognizes the signal peptide encoded by the signal sequence in the 5' EST (or cDNA or genomic DNA obtainable therefrom). Suitable hosts include mammalian cells, tissues or organisms, avian cells, tissues, or organisms, insect cells, tissues or organisms, or yeast.

In addition, the secretion vector contains cloning sites for inserting genes encoding the proteins which are to be secreted. The cloning sites facilitate the cloning of the insert gene in frame with the signal sequence such that a fusion protein in which the signal peptide is fused to the protein encoded by the inserted gene is expressed from the mRNA transcribed from the promoter. The signal peptide directs the extracellular secretion of the fusion protein.

The secretion vector may be DNA or RNA and may integrate into the chromosome of the host, be stably maintained as an extrachromosomal replicon in the host, be an artificial chromosome, or be transiently present in the host. Many nucleic acid backbones suitable for use as secretion vectors are known to those skilled in the art, including retroviral vectors, SV40 vectors, Bovine Papilloma Virus vectors, yeast integrating plasmids, yeast episomal plasmids, yeast artificial chromosomes, human artificial chromosomes, P element vectors, baculovirus vectors, or bacterial plasmids capable of being transiently introduced into the host.

The secretion vector may also contain a polyA signal such that the polyA signal is located downstream of the gene inserted into the secretion vector.

After the gene encoding the protein for which secretion is desired is inserted into the secretion vector, the secretion vector is introduced into the host cell, tissue, or organism using calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection, viral particles or as naked DNA. The protein encoded by the inserted gene is then purified or enriched from the supernatant using conventional techniques such as ammonium sulfate precipitation, immunoprecipitation, immunochromatography, size exclusion chromatography, ion exchange chromatography, and HPLC. Alternatively, the secreted protein may be in a sufficiently enriched or pure state in the supernatant or growth media of the host to permit it to be used for its intended purpose without further enrichment.

The signal sequences may also be inserted into vectors designed for gene therapy. In such vectors, the signal sequence is operably linked to a promoter such that mRNA transcribed from the promoter encodes the signal peptide. A cloning site is located downstream of the signal sequence such that a gene encoding a protein whose secretion is desired may readily be inserted into the vector and fused to the signal sequence. The vector is introduced into an appropriate host cell. The protein expressed from the promoter is secreted extracellularly, thereby producing a therapeutic effect.

The 5' ESTs may also be used to clone sequences located upstream of the 5' ESTs which are capable of regulating gene expression, including promoter sequences, enhancer sequences, and other upstream sequences which influence transcription or translation levels. Once identified and cloned, these upstream regulatory sequences may be used in expression vectors designed to direct the expression of an inserted gene in a desired spatial, temporal, developmental, or quantitative fashion. Example 58 describes a method for cloning sequences upstream of the extended cDNAs or 5' ESTs.

2. Identification of Upstream Sequences With Promoting or Regulatory Activities

10

EXAMPLE 58

Use of Extended cDNAs or 5' ESTs to Clone Upstream Sequences from Genomic DNA

Sequences derived from extended cDNAs or 5' ESTs may be used to isolate the promoters of the corresponding genes using chromosome walking techniques. In one chromosome walking technique, which utilizes the GenomeWalker™ kit available from Clontech, five complete genomic DNA samples are each digested with a different restriction enzyme which has a 6 base recognition site and leaves a blunt end. Following digestion, oligonucleotide adapters are ligated to each end of the resulting genomic DNA fragments.

For each of the five genomic DNA libraries, a first PCR reaction is performed according to the manufacturer's instructions (which are incorporated herein by reference) using an outer adaptor primer provided in the kit and an outer gene specific primer. The gene specific primer should be selected to be specific for the extended cDNA or 5' EST of interest and should have a melting temperature, length, and location in the extended cDNA or 5' EST which is consistent with its use in PCR reactions. Each first PCR reaction contains 5 ng of genomic DNA, 5 µl of 10X Tth reaction buffer, 0.2 mM of each dNTP, 0.2 µM each of outer adaptor primer and outer gene specific primer, 1.1 mM of Mg(OAc)₂, and 1 µl of the Tth polymerase 50X mix in a total volume of 50 µl. The reaction cycle for the first PCR reaction is as follows: 1 min - 94°C / 2 sec - 94°C, 3 min - 72°C (7 cycles) / 2 sec - 94°C, 3 min - 67°C (32 cycles) / 5 min - 67°C.

The product of the first PCR reaction is diluted and used as a template for a second PCR reaction according to the manufacturer's instructions using a pair of nested primers which are located internally on the amplicon resulting from the first PCR

reaction. For example, 5 µl of the reaction product of the first PCR reaction mixture may be diluted 180 times. Reactions are made in a 50 µl volume having a composition identical to that of the first PCR reaction except the nested primers are used. The first nested primer is specific for the adaptor, and is provided with the GenomeWalker™ kit.

5 The second nested primer is specific for the particular extended cDNA or 5' EST for which the promoter is to be cloned and should have a melting temperature, length, and location in the extended cDNA or 5' EST which is consistent with its use in PCR reactions. The reaction parameters of the second PCR reaction are as follows: 1 min - 94°C / 2 sec - 94°C, 3 min - 72°C (6 cycles) / 2 sec - 94°C, 3 min - 67°C (25 cycles) / 5

10 min - 67°C. The product of the second PCR reaction is purified, cloned, and sequenced using standard techniques.

Alternatively, two or more human genomic DNA libraries can be constructed by using two or more restriction enzymes. The digested genomic DNA is cloned into vectors which can be converted into single stranded, circular, or linear DNA. A biotinylated

15 oligonucleotide comprising at least 15 nucleotides from the extended cDNA or 5' EST sequence is hybridized to the single stranded DNA. Hybrids between the biotinylated oligonucleotide and the single stranded DNA containing the extended cDNA or EST sequence are isolated as described in Example 29 above. Thereafter, the single stranded DNA containing the extended cDNA or EST sequence is released from the beads and

20 converted into double stranded DNA using a primer specific for the extended cDNA or 5' EST sequence or a primer corresponding to a sequence included in the cloning vector. The resulting double stranded DNA is transformed into bacteria. DNAs containing the 5' EST or extended cDNA sequences are identified by colony PCR or colony hybridization.

25 Once the upstream genomic sequences have been cloned and sequenced as described above, prospective promoters and transcription start sites within the upstream sequences may be identified by comparing the sequences upstream of the extended cDNAs or 5' ESTs with databases containing known transcription start sites, transcription factor binding sites, or promoter sequences.

30 In addition, promoters in the upstream sequences may be identified using promoter reporter vectors as described in Example .

EXAMPLE 59

Identification of Promoters in Cloned Upstream Sequences

The genomic sequences upstream of the extended cDNAs or 5' ESTs are cloned into
5 a suitable promoter reporter vector, such as the pSEAP-Basic, pSEAP-Enhancer, p β gal-
Basic, p β gal-Enhancer, or pEGFP-1 Promoter Reporter vectors available from Clontech.
Briefly, each of these promoter reporter vectors include multiple cloning sites positioned
upstream of a reporter gene encoding a readily assayable protein such as secreted alkaline
phosphatase, β galactosidase, or green fluorescent protein. The sequences upstream of the
10 extended cDNAs or 5' ESTs are inserted into the cloning sites upstream of the reporter gene
in both orientations and introduced into an appropriate host cell. The level of reporter protein
is assayed and compared to the level obtained from a vector which lacks an insert in the
cloning site. The presence of an elevated expression level in the vector containing the insert
with respect to the control vector indicates the presence of a promoter in the insert. If
15 necessary, the upstream sequences can be cloned into vectors which contain an enhancer for
augmenting transcription levels from weak promoter sequences. A significant level of
expression above that observed with the vector lacking an insert indicates that a promoter
sequence is present in the inserted upstream sequence.

Appropriate host cells for the promoter reporter vectors may be chosen based on the
20 results of the above described determination of expression patterns of the extended cDNAs
and ESTs. For example, if the expression pattern analysis indicates that the mRNA
corresponding to a particular extended cDNA or 5' EST is expressed in fibroblasts, the
promoter reporter vector may be introduced into a human fibroblast cell line.

Promoter sequences within the upstream genomic DNA may be further defined by
25 constructing nested deletions in the upstream DNA using conventional techniques such as
Exonuclease III digestion. The resulting deletion fragments can be inserted into the promoter
reporter vector to determine whether the deletion has reduced or obliterated promoter
activity. In this way, the boundaries of the promoters may be defined. If desired, potential
individual regulatory sites within the promoter may be identified using site directed
30 mutagenesis or linker scanning to obliterate potential transcription factor binding sites within
the promoter individually or in combination. The effects of these mutations on transcription

levels may be determined by inserting the mutations into the cloning sites in the promoter reporter vectors.

EXAMPLE 60

5 Cloning and Identification of Promoters

Using the method described in Example 58 above with 5' ESTs, sequences upstream of several genes were obtained. Using the primer pairs GGG AAG ATG GAG ATA GTA TTG CCT G (SEQ ID NO:29) and CTG CCA TGT ACA TGA TAG AGA GAT TC (SEQ ID NO:30), the promoter having the internal designation P13H2 (SEQ ID NO:31) was
10 obtained.

Using the primer pairs GTA CCA GGGG ACT GTG ACC ATT GC (SEQ ID NO:32) and CTG TGA CCA TTG CTC CCA AGA GAG (SEQ ID NO:33), the promoter having the internal designation P15B4 (SEQ ID NO:34) was obtained.

Using the primer pairs CTG GGA TGG AAG GCA CGG TA (SEQ ID NO:35) and
15 GAG ACC ACA CAG CTA GAC AA (SEQ ID NO:36), the promoter having the internal designation P29B6 (SEQ ID NO:37) was obtained.

Figure 4 provides a schematic description of the promoters isolated and the way they are assembled with the corresponding 5' tags. The upstream sequences were screened for the presence of motifs resembling transcription factor binding sites or known transcription start
20 sites using the computer program MatInspector release 2.0, August 1996.

Table VII describes the transcription factor binding sites present in each of these promoters. The columns labeled matrice provides the name of the MatInspector matrix used. The column labeled position provides the 5' position of the promoter site. Numeration of the sequence starts from the transcription site as determined by matching the genomic sequence with the 5' EST sequence. The column labeled "orientation" indicates the DNA strand on
25 which the site is found, with the + strand being the coding strand as determined by matching the genomic sequence with the sequence of the 5' EST. The column labeled "score" provides the MatInspector score found for this site. The column labeled "length" provides the length of the site in nucleotides. The column labeled "sequence" provides the sequence of the site
30 found.

Bacterial clones containing plasmids containing the promoter sequences described above described above are presently stored in the inventor's laboratories under the internal identification numbers provided above. The inserts may be recovered from the deposited materials by growing an aliquot of the appropriate bacterial clone in the appropriate medium.

5 The plasmid DNA can then be isolated using plasmid isolation procedures familiar to those skilled in the art such as alkaline lysis minipreps or large scale alkaline lysis plasmid isolation procedures. If desired the plasmid DNA may be further enriched by centrifugation on a cesium chloride gradient, size exclusion chromatography, or anion exchange chromatography. The plasmid DNA obtained using these procedures may then be manipulated using standard
10 cloning techniques familiar to those skilled in the art. Alternatively, a PCR can be done with primers designed at both ends of the EST insertion. The PCR product which corresponds to the 5' EST can then be manipulated using standard cloning techniques familiar to those skilled in the art.

The promoters and other regulatory sequences located upstream of the extended
15 cDNAs or 5' ESTs may be used to design expression vectors capable of directing the expression of an inserted gene in a desired spatial, temporal, developmental, or quantitative manner. A promoter capable of directing the desired spatial, temporal, developmental, and quantitative patterns may be selected using the results of the expression analysis described in Example 26 above. For example, if a promoter which confers a high level of expression in
20 muscle is desired, the promoter sequence upstream of an extended cDNA or 5' EST derived from an mRNA which is expressed at a high level in muscle, as determined by the method of Example 26, may be used in the expression vector.

Preferably, the desired promoter is placed near multiple restriction sites to facilitate the cloning of the desired insert downstream of the promoter, such that the promoter is able
25 to drive expression of the inserted gene. The promoter may be inserted in conventional nucleic acid backbones designed for extrachromosomal replication, integration into the host chromosomes or transient expression. Suitable backbones for the present expression vectors include retroviral backbones, backbones from eukaryotic episomes such as SV40 or Bovine Papilloma Virus, backbones from bacterial episomes, or artificial chromosomes.

Preferably, the expression vectors also include a polyA signal downstream of the multiple restriction sites for directing the polyadenylation of mRNA transcribed from the gene inserted into the expression vector.

Following the identification of promoter sequences using the procedures of Examples 58-60, proteins which interact with the promoter may be identified as described in Example 61 below.

EXAMPLE 61

Identification of Proteins Which Interact with Promoter Sequences, Upstream

Regulatory Sequences, or mRNA

Sequences within the promoter region which are likely to bind transcription factors may be identified by homology to known transcription factor binding sites or through conventional mutagenesis or deletion analyses of reporter plasmids containing the promoter sequence. For example, deletions may be made in a reporter plasmid containing the promoter sequence of interest operably linked to an assayable reporter gene. The reporter plasmids carrying various deletions within the promoter region are transfected into an appropriate host cell and the effects of the deletions on expression levels is assessed. Transcription factor binding sites within the regions in which deletions reduce expression levels may be further localized using site directed mutagenesis, linker scanning analysis, or other techniques familiar to those skilled in the art.

Nucleic acids encoding proteins which interact with sequences in the promoter may be identified using one-hybrid systems such as those described in the manual accompanying the Matchmaker One-Hybrid System kit available from Clontech (Catalog No. K1603-1), the disclosure of which is incorporated herein by reference. Briefly, the Matchmaker One-hybrid system is used as follows. The target sequence for which it is desired to identify binding proteins is cloned upstream of a selectable reporter gene and integrated into the yeast genome. Preferably, multiple copies of the target sequences are inserted into the reporter plasmid in tandem. A library comprised of fusions between cDNAs to be evaluated for the ability to bind to the promoter and the activation domain of a yeast transcription factor, such as GAL4, is transformed into the yeast strain containing the integrated reporter sequence. The yeast are plated on selective media to

select cells expressing the selectable marker linked to the promoter sequence. The colonies which grow on the selective media contain genes encoding proteins which bind the target sequence. The inserts in the genes encoding the fusion proteins are further characterized by sequencing. In addition, the inserts may be inserted into expression
5 vectors or *in vitro* transcription vectors. Binding of the polypeptides encoded by the inserts to the promoter DNA may be confirmed by techniques familiar to those skilled in the art, such as gel shift analysis or DNase protection analysis.

10 VII. Use of 5' ESTs (or cDNAs or Genomic DNAs Obtainable Therefrom) in Gene Therapy

The present invention also comprises the use of 5'ESTs (or cDNA or genomic DNA obtainable therefrom) in gene therapy strategies, including antisense and triple helix strategies as described in Examples 62 and 63 below. In antisense approaches, nucleic acid sequences complementary to an mRNA are hybridized to the mRNA intracellularly, thereby blocking the
15 expression of the protein encoded by the mRNA. The antisense sequences may prevent gene expression through a variety of mechanisms. For example, the antisense sequences may inhibit the ability of ribosomes to translate the mRNA. Alternatively, the antisense sequences may block transport of the mRNA from the nucleus to the cytoplasm, thereby limiting the amount of mRNA available for translation. Another mechanism through which antisense
20 sequences may inhibit gene expression is by interfering with mRNA splicing. In yet another strategy, the antisense nucleic acid may be incorporated in a ribozyme capable of specifically cleaving the target mRNA.

EXAMPLE 62

25 Preparation and Use of Antisense Oligonucleotides

The antisense nucleic acid molecules to be used in gene therapy may be either DNA or RNA sequences. They may comprise a sequence complementary to the sequence of the 5'EST (or cDNA or genomic DNA obtainable therefrom). The antisense nucleic acids should have a length and melting temperature sufficient to permit formation of an intracellular
30 duplex with sufficient stability to inhibit the expression of the mRNA in the duplex. Strategies for designing antisense nucleic acids suitable for use in gene therapy are disclosed in Green *et*

al., *Ann. Rev. Biochem.* 55:569-597, 1986; and Izant and Weintraub, *Cell* 36:1007-1015, 1984, which are hereby incorporated by reference.

5 In some strategies, antisense molecules are obtained from a nucleotide sequence encoding a protein by reversing the orientation of the coding region with respect to a promoter so as to transcribe the opposite strand from that which is normally transcribed in the cell. The antisense molecules may be transcribed using *in vitro* transcription systems such as those which employ T7 or SP6 polymerase to generate the transcript. Another approach involves transcription of the antisense nucleic acids *in vivo* by operably linking DNA containing the antisense sequence to a promoter in an expression vector.

10 Alternatively, oligonucleotides which are complementary to the strand normally transcribed in the cell may be synthesized *in vitro*. Thus, the antisense nucleic acids are complementary to the corresponding mRNA and are capable of hybridizing to the mRNA to create a duplex. In some embodiments, the antisense sequences may contain modified sugar phosphate backbones to increase stability and make them less sensitive to RNase activity.
15 Examples of modifications suitable for use in antisense strategies are described by Rossi *et al.*, *Pharmacol. Ther.* 50(2):245-254, 1991, which is hereby incorporated by reference.

Various types of antisense oligonucleotides complementary to the sequence of the 5'EST (or cDNA or genomic DNA obtainable therefrom) may be used. In one preferred embodiment, stable and semi-stable antisense oligonucleotides described in International
20 Application No. PCT WO94/23026, hereby incorporated by reference, are used. In these molecules, the 3' end or both the 3' and 5' ends are engaged in intramolecular hydrogen bonding between complementary base pairs. These molecules are better able to withstand exonuclease attacks and exhibit increased stability compared to conventional antisense oligonucleotides.

25 In another preferred embodiment, the antisense oligodeoxynucleotides against herpes simplex virus types 1 and 2 described in International Application No. WO 95/04141, hereby incorporated by reference, are used.

In yet another preferred embodiment, the covalently cross-linked antisense oligonucleotides described in International Application No. WO 96/31523, hereby
30 incorporated by reference, are used. These double- or single-stranded oligonucleotides comprise one or more, respectively, inter- or intra-oligonucleotide covalent cross-linkages,

wherein the linkage consists of an amide bond between a primary amine group of one strand and a carboxyl group of the other strand or of the same strand, respectively, the primary amine group being directly substituted in the 2' position of the strand nucleotide monosaccharide ring, and the carboxyl group being carried by an aliphatic spacer group substituted on a nucleotide or nucleotide analog of the other strand or the same strand, respectively.

The antisense oligodeoxynucleotides and oligonucleotides disclosed in International Application No. WO 92/18522, incorporated by reference, may also be used. These molecules are stable to degradation and contain at least one transcription control recognition sequence which binds to control proteins and are effective as decoys therefore. These molecules may contain "hairpin" structures, "dumbbell" structures, "modified dumbbell" structures, "cross-linked" decoy structures and "loop" structures.

In another preferred embodiment, the cyclic double-stranded oligonucleotides described in European Patent Application No. 0 572 287 A2, hereby incorporated by reference are used. These ligated oligonucleotide "dumbbells" contain the binding site for a transcription factor and inhibit expression of the gene under control of the transcription factor by sequestering the factor.

Use of the closed antisense oligonucleotides disclosed in International Application No. WO 92/19732, hereby incorporated by reference, is also contemplated. Because these molecules have no free ends, they are more resistant to degradation by exonucleases than are conventional oligonucleotides. These oligonucleotides may be multifunctional, interacting with several regions which are not adjacent to the target mRNA.

The appropriate level of antisense nucleic acids required to inhibit gene expression may be determined using *in vitro* expression analysis. The antisense molecule may be introduced into the cells by diffusion, injection, infection, transfection or h-region-mediated import using procedures known in the art. For example, the antisense nucleic acids can be introduced into the body as a bare or naked oligonucleotide, oligonucleotide encapsulated in lipid, oligonucleotide sequence encapsulated by viral protein, or as an oligonucleotide operably linked to a promoter contained in an expression vector. The expression vector may be any of a variety of expression vectors known in the art, including retroviral or viral vectors,

vectors capable of extrachromosomal replication, or integrating vectors. The vectors may be DNA or RNA.

The antisense molecules are introduced onto cell samples at a number of different concentrations preferably between 1×10^{-10} M to 1×10^{-4} M. Once the minimum concentration that can adequately control gene expression is identified, the optimized dose is translated into a dosage suitable for use *in vivo*. For example, an inhibiting concentration in culture of 1×10^{-7} translates into a dose of approximately 0.6 mg/kg bodyweight. Levels of oligonucleotide approaching 100 mg/kg bodyweight or higher may be possible after testing the toxicity of the oligonucleotide in laboratory animals. It is additionally contemplated that cells from the vertebrate are removed, treated with the antisense oligonucleotide, and reintroduced into the vertebrate.

It is further contemplated that the antisense oligonucleotide sequence is incorporated into a ribozyme sequence to enable the antisense to specifically bind and cleave its target mRNA. For technical applications of ribozyme and antisense oligonucleotides see Rossi *et al.*, *supra*.

In a preferred application of this invention, the polypeptide encoded by the gene is first identified, so that the effectiveness of antisense inhibition on translation can be monitored using techniques that include but are not limited to antibody-mediated tests such as RIAs and ELISA, functional assays, or radiolabeling.

The 5' ESTs of the present invention (or cDNAs or genomic DNAs obtainable therefrom) may also be used in gene therapy approaches based on intracellular triple helix formation. Triple helix oligonucleotides are used to inhibit transcription from a genome. They are particularly useful for studying alterations in cell activity as it is associated with a particular gene. The 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom) of the present invention or, more preferably, a portion of those sequences, can be used to inhibit gene expression in individuals having diseases associated with expression of a particular gene. Similarly, a portion of 5' EST sequences (or cDNAs or genomic DNAs obtainable therefrom) can be used to study the effect of inhibiting transcription of a particular gene within a cell. Traditionally, homopurine sequences were considered the most useful for triple helix strategies. However, homopyrimidine sequences can also inhibit gene expression. Such homopyrimidine oligonucleotides bind to the major groove at

homopurine:homopyrimidine sequences. Thus, both types of sequences from the 5'EST or from the gene corresponding to the 5'EST are contemplated within the scope of this invention.

5

EXAMPLE 63

Preparation and Use of Triple Helix Probes

The sequences of the 5' ESTs (or cDNAs or genomic DNAs obtainable therefrom) are scanned to identify 10-mer to 20-mer homopyrimidine or homopurine stretches which could be used in triple-helix based strategies for inhibiting gene expression. Following
10 identification of candidate homopyrimidine or homopurine stretches, their efficiency in inhibiting gene expression is assessed by introducing varying amounts of oligonucleotides containing the candidate sequences into tissue culture cells which normally express the target gene. The oligonucleotides may be prepared on an oligonucleotide synthesizer or they may be purchased commercially from a company specializing in custom oligonucleotide synthesis,
15 such as GENSET, Paris, France.

The oligonucleotides may be introduced into the cells using a variety of methods known to those skilled in the art, including but not limited to calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection or native uptake.

Treated cells are monitored for altered cell function or reduced gene expression using
20 techniques such as Northern blotting, RNase protection assays, or PCR based strategies to monitor the transcription levels of the target gene in cells which have been treated with the oligonucleotide. The cell functions to be monitored are predicted based upon the homologies of the target gene corresponding to the extended cDNA from which the oligonucleotide was derived with known gene sequences that have been associated with a particular function. The
25 cell functions can also be predicted based on the presence of abnormal physiologies within cells derived from individuals with a particular inherited disease, particularly when the extended cDNA is associated with the disease using techniques described in Example 56.

The oligonucleotides which are effective in inhibiting gene expression in tissue culture cells may then be introduced *in vivo* using the techniques described above and in Example 62
30 at a dosage calculated based on the *in vitro* results, as described in Example 62.

In some embodiments, the natural (beta) anomers of the oligonucleotide units can be replaced with alpha anomers to render the oligonucleotide more resistant to nucleases. Further, an intercalating agent such as ethidium bromide, or the like, can be attached to the 3' end of the alpha oligonucleotide to stabilize the triple helix. For information on the generation of oligonucleotides suitable for triple helix formation see Griffin *et al.*, *Science* 245:967-971, 1989, which is hereby incorporated by this reference.

EXAMPLE 64

Use of cDNAs Obtained Using the 5' ESTs to Express an Encoded Protein in a Host

10

Organism

The cDNAs obtained as described above using the 5' ESTs of the present invention may also be used to express an encoded protein in a host organism to produce a beneficial effect. In such procedures, the encoded protein may be transiently expressed in the host organism or stably expressed in the host organism. The encoded protein may have any of the activities described above. The encoded protein may be a protein which the host organism lacks or, alternatively, the encoded protein may augment the existing levels of the protein in the host organism.

A full length extended cDNA encoding the signal peptide and the mature protein, or an extended cDNA encoding only the mature protein is introduced into the host organism. The extended cDNA may be introduced into the host organism using a variety of techniques known to those of skill in the art. For example, the extended cDNA may be injected into the host organism as naked DNA such that the encoded protein is expressed in the host organism, thereby producing a beneficial effect.

Alternatively, the extended cDNA may be cloned into an expression vector downstream of a promoter which is active in the host organism. The expression vector may be any of the expression vectors designed for use in gene therapy, including viral or retroviral vectors. The expression vector may be directly introduced into the host organism such that the encoded protein is expressed in the host organism to produce a beneficial effect. In another approach, the expression vector may be introduced into cells *in vitro*. Cells containing the expression vector are thereafter selected and introduced into the host organism, where they express the encoded protein to produce a beneficial effect.

EXAMPLE 65

Use of Signal Peptides Encoded by 5' ESTs or Sequences obtained Therefrom
to Import Proteins Into Cells

The short core hydrophobic region (h) of signal peptides encoded by the 5'ESTS or
5 extended cDNAs derived from SEQ ID NOs: 38-305 may also be used as a carrier to import
a peptide or a protein of interest, so-called cargo, into tissue culture cells (Lin *et al.*, *J. Biol.
Chem.*, 270: 14225-14258, 1995; Du *et al.*, *J. Peptide Res.*, 51: 235-243, 1998; Rojas *et al.*,
Nature Biotech., 16: 370-375, 1998).

When cell permeable peptides of limited size (approximately up to 25 amino acids)
10 are to be translocated across cell membrane, chemical synthesis may be used in order to add
the h region to either the C-terminus or the N-terminus to the cargo peptide of interest.
Alternatively, when longer peptides or proteins are to be imported into cells, nucleic acids can
be genetically engineered, using techniques familiar to those skilled in the art, in order to link
the extended cDNA sequence encoding the h region to the 5' or the 3' end of a DNA
15 sequence coding for a cargo polypeptide. Such genetically engineered nucleic acids are then
translated either *in vitro* or *in vivo* after transfection into appropriate cells, using conventional
techniques to produce the resulting cell permeable polypeptide. Suitable hosts cells are then
simply incubated with the cell permeable polypeptide which is then translocated across the
membrane.

20 This method may be applied to study diverse intracellular functions and cellular
processes. For instance, it has been used to probe functionally relevant domains of
intracellular proteins and to examine protein-protein interactions involved in signal
transduction pathways (Lin *et al.*, *supra*; Lin *et al.*, *J. Biol. Chem.*, 271: 5305-5308, 1996;
Rojas *et al.*, *J. Biol. Chem.*, 271: 27456-27461, 1996; Liu *et al.*, *Proc. Natl. Acad. Sci. USA*,
25 93: 11819-11824, 1996; Rojas *et al.*, *Bioch. Biophys. Res. Commun.*, 234: 675-680, 1997).

Such techniques may be used in cellular therapy to import proteins producing
therapeutic effects. For instance, cells isolated from a patient may be treated with imported
therapeutic proteins and then re-introduced into the host organism.

Alternatively, the h region of signal peptides of the present invention could be used in
30 combination with a nuclear localization signal to deliver nucleic acids into cell nucleus. Such
oligonucleotides may be antisense oligonucleotides or oligonucleotides designed to form

triple helixes, as described in examples 62 and 63 respectively, in order to inhibit processing and/or maturation of a target cellular RNA.

As discussed above, the cDNAs or portions thereof obtained using the 5' ESTs of the present invention can be used for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination for expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris *et al.*, *Cell* 75:791-803, 1993, the disclosure of which is hereby incorporated by reference) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins or polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins

involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

5 Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation *Molecular Cloning: A Laboratory Manual*, 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, Fritsch and Maniatis eds., 1989, and *Methods in Enzymology: Guide to Molecular Cloning Techniques*, Academic Press, Berger and Kimmel eds., 1987.

10 Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid
15 preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

 Although this invention has been described in terms of certain preferred embodiments, other embodiments which will be apparent to those of ordinary skill in the art in view of the
20 disclosure herein are also within the scope of this invention. Accordingly, the scope of the invention is intended to be defined only by reference to the appended claims. All documents cited herein are incorporated herein by reference in their entirety.

Step	Search characteristic		Selection Characteristics		
	Program	Strand	Parameters	Identity (%)	Length (bp)
miscellaneous	blastn	both	S=61 X=16	90	17
tRNA	fasta	both	-	80	60
rRNA	blastn	both	S=108	80	40
mtRNA	blastn	both	S=108	80	40
Prokaryotic	blastn	both	S=144	90	40
Fungal	blastn	both	S=144	90	40
Alu	fasta*	both	-	70	40
L1	blastn	both	S=72	70	40
Repeats	blastn	both	S=72	70	40
Promoters	blastn	top	S=54 X=16	90	15†
Vertebrate	fasta*	both	S=108	90	30
ESTs	blastn	both	S=108 X=16	90	30
Proteins	blastx α	top	E = 0.001	-	-

Table 1: Parameters used for each step of EST analysis

- * use "Quick Fast" Database scanner
- † alignment further constrained to begin closer than 10bp to EST's end
- α using BLOSUM62 substitution matrix

TABLE II

<u>SEQ. ID NO.</u>	<u>CATEGORY</u>	<u>VON HEIJNE SCORE</u>	<u>TISSUE SOURCE</u>	<u>INTERNAL DESIGNATION</u>
ID38	new	15.8	Heart	25-13-1-H10-PU
ID39	new	14	Fetal kidney	58-47-2-B11-PU
ID40	new	12.3	Dystrophic muscle	29-3-3-H8-PU
ID41	new	12.2	Fetal kidney	58-4-2-A3-PU
ID42	new	11.9	Kidney	21-10-4-G1-PU
ID43	new	11.3	Fetal kidney	58-27-3-B10-PU
ID44	new	10.7	Fetal kidney	58-35-2-F10-PU
ID45	new	10.7	Fetal kidney	58-37-2-G10-PU
ID46	new	10.6	Dystrophic muscle	29-11-1-C11-PU
ID47	new	10	Fetal kidney	58-20-4-G7-PU
ID48	new	10	Fetal kidney	58-2-4-E9-PU
ID49	new	9.6	Fetal kidney	58-37-3-D8-PU
ID50	new	9.5	Fetal kidney	58-46-1-F1-PU
ID51	new	9.2	Dystrophic muscle	29-9-4-D8-PU
ID52	new	9.2	Muscle	27-10-4-C6-PU
ID53	new	8.3	Heart	67-5-4-H9-PU
ID54	new	8.1	Fetal kidney	58-4-3-H4-PU
ID55	new	8	Muscle	27-16-3-D12-PU
ID56	new	7.9	Fetal kidney	58-54-2-C2-PU
ID57	new	7.9	Heart	25-9-3-A3-PU
ID58	new	7.9	Dystrophic muscle	29-11-3-F1-PU
ID59	new	7.9	Fetal kidney	58-32-3-G6-PU
ID60	new	7.8	Fetal kidney	58-22-2-H8-PU
ID61	new	7.8	Fetal kidney	58-2-4-H4-PU
ID62	new	7.8	Heart	67-4-3-G3-PU
ID63	new	7.8	Fetal kidney	58-24-1-G11-PU
ID64	new	7.7	Fetal kidney	58-19-3-H1-PU
ID65	new	7.5	Fetal kidney	58-45-4-B11-PU
ID66	new	7.3	Fetal kidney	58-44-2-D3-PU
ID67	new	7.2	Dystrophic muscle	29-3-3-E7-PU
ID68	new	7.1	Dystrophic muscle	29-12-3-A3-PU
ID69	new	7.1	Fetal kidney	58-14-2-B3-PU
ID70	new	7.1	Fetal kidney	58-10-3-D12-PU
ID71	new	7	Fetal kidney	58-6-2-E5-PU
ID72	new	7	Dystrophic muscle	29-7-1-C1-PU
ID73	new	6.9	Fetal kidney	58-26-4-A12-PU
ID74	new	6.9	Fetal kidney	58-7-2-H9-PU
ID75	new	6.9	Fetal kidney	58-14-2-D5-PU
ID76	new	6.7	Fetal kidney	58-3-4-E1-PU
ID77	new	6.7	Fetal kidney	58-43-4-G3-PU
ID78	new	6.7	Fetal kidney	58-11-1-G10-PU
ID79	new	6.6	Fetal kidney	58-4-4-G2-PU
ID80	new	6.6	Fetal kidney	58-41-3-D6-PU
ID81	new	6.6	Heart	25-8-2-H10-PU
ID82	new	6.5	Muscle	27-18-4-E5-PU
ID83	new	6.4	Dystrophic muscle	29-4-1-G6-PU
ID84	new	6.4	Muscle	27-10-2-B1-PU
ID85	new	6.4	Fetal kidney	58-38-1-E5-PU
ID86	new	6.3	Muscle	27-4-3-D9-PU

<u>SEQ. ID NO.</u>	<u>CATEGORY</u>	<u>VON HEINE SCORE</u>	<u>TISSUE SOURCE</u>	<u>INTERNAL DESIGNATION</u>
ID87	new	6.3	Fetal kidney	58-53-1-G1-PU
ID88	new	6.3	Fetal kidney	58-7-3-F6-PU
ID89	new	6.3	Heart	25-7-2-B12-PU
ID90	new	6.1	Fetal kidney	58-16-3-E11-PU
ID91	new	6	Fetal kidney	58-15-4-C2-PU
ID92	new	6	Fetal kidney	58-34-3-A9-PU
ID93	new	5.9	Fetal kidney	58-16-1-E1-PU
ID94	new	5.9	Fetal kidney	58-4-3-E6-PU
ID95	new	5.9	Fetal kidney	58-37-3-B11-PU
ID96	new	5.9	Fetal kidney	58-35-3-C6-PU
ID97	new	5.8	Fetal kidney	58-35-1-D9-PU
ID98	new	5.8	Fetal kidney	58-26-3-B2-PU
ID99	new	5.7	Fetal kidney	58-48-1-F8-PU
ID100	new	5.7	Fetal kidney	58-27-4-A6-PU
ID101	new	5.7	Fetal kidney	58-26-3-D1-PU
ID102	new	5.7	Muscle	27-19-4-B4-PU
ID103	new	5.6	Fetal kidney	58-23-3-B2-PU
ID104	new	5.5	Heart	25-1-2-C1-PU
ID105	new	5.5	Fetal kidney	58-14-3-F10-PU
ID106	new	5.5	Fetal kidney	58-25-1-E11-PU
ID107	new	5.5	Muscle	27-9-4-A10-PU
ID108	new	5.5	Heart	25-4-2-D8-PU
ID109	new	5.4	Fetal kidney	58-29-3-G8-PU
ID110	new	5.4	Fetal kidney	58-4-4-E5-PU
ID111	new	5.4	Fetal kidney	58-24-2-H2-PU
ID112	new	5.4	Muscle	27-11-2-C8-PU
ID113	new	5.4	Fetal kidney	58-41-2-E3-PU
ID114	new	5.3	Muscle	27-22-1-G8-PU
ID115	new	5.3	Dystrophic muscle	29-1-1-C9-PU
ID116	new	5.3	Fetal kidney	58-22-2-A3-PU
ID117	new	5.2	Fetal kidney	58-42-2-G1-PU
ID118	new	5.2	Fetal kidney	58-52-2-E5-PU
ID119	new	5.2	Fetal kidney	58-24-2-G2-PU
ID120	new	5.2	Fetal kidney	58-29-1-A3-PU
ID121	new	5.1	Fetal kidney	58-26-1-G8-PU
ID122	new	5.1	Fetal kidney	58-29-4-G12-PU
ID123	new	5.1	Dystrophic muscle	29-8-3-E8-PU
ID124	new	5.1	Dystrophic muscle	29-3-4-C1-PU
ID125	new	5	Fetal kidney	58-17-2-H1-PU
ID126	new	5	Fetal kidney	58-9-3-E3-PU
ID127	new	5	Muscle	27-19-3-G7-PU
ID128	new	5	Fetal kidney	58-41-3-B4-PU
ID129	new	5	Dystrophic muscle	29-7-4-G7-PU
ID130	new	5	Muscle	27-9-3-D4-PU
ID131	new	4.9	Kidney	21-3-4-C5-PU
ID132	new	4.9	Heart	25-11-2-D6-PU
ID133	new	4.9	Heart	67-7-2-F3-PU
ID134	new	4.8	Fetal kidney	58-4-3-D3-PU
ID135	new	4.8	Fetal kidney	58-49-3-B5-PU
ID136	new	4.8	Fetal kidney	58-28-3-G12-PU
ID137	new	4.7	Fetal kidney	58-53-1-A5-PU

<u>SEQ. ID NO.</u>	<u>CATEGORY</u>	<u>VON HEIJNE SCORE</u>	<u>TISSUE SOURCE</u>	<u>INTERNAL DESIGNATION</u>
ID138	new	4.7	Fetal kidney	58-3-3-E10-PU
ID139	new	4.7	Fetal kidney	58-8-1-G7-PU
ID140	new	4.6	Fetal kidney	58-23-1-G9-PU
ID141	new	4.6	Fetal kidney	58-21-1-H8-PU
ID142	new	4.6	Fetal kidney	58-54-2-E10-PU
ID143	new	4.6	Fetal kidney	58-46-3-E4-PU
ID144	new	4.6	Fetal kidney	58-6-3-G3-PU
ID145	new	4.6	Fetal kidney	58-41-2-B5-PU
ID146	new	4.6	Dystrophic muscle	29-7-3-F2-PU
ID147	new	4.5	Fetal kidney	58-2-4-G12-PU
ID148	new	4.5	Fetal kidney	58-11-2-G8-PU
ID149	new	4.4	Fetal kidney	58-17-1-C4-PU
ID150	new	4.4	Fetal kidney	58-46-1-G7-PU
ID151	new	4.4	Heart	67-3-2-F4-PU
ID152	new	4.4	Fetal kidney	58-8-4-E12-PU
ID153	new	4.4	Fetal kidney	58-4-2-D9-PU
ID154	new	4.4	Fetal kidney	58-25-1-B5-PU
ID155	new	4.4	Fetal kidney	58-15-1-C10-PU
ID156	new	4.3	Dystrophic muscle	29-4-4-A10-PU
ID157	new	4.3	Fetal kidney	58-32-3-H7-PU
ID158	new	4.3	Kidney	21-4-4-D12-PU
ID159	new	4.3	Fetal kidney	58-45-4-G9-PU
ID160	new	4.3	Fetal kidney	58-1-2-E2-PU
ID161	new	4.2	Fetal kidney	58-25-4-E6-PU
ID162	new	4.2	Fetal kidney	58-36-4-C6-PU
ID163	new	4.2	Dystrophic muscle	29-9-3-D5-PU
ID164	new	4.2	Fetal kidney	58-3-3-B8-PU
ID165	new	4.2	Heart	25-4-4-B4-PU
ID166	new	4.2	Kidney	21-10-3-A3-PU
ID167	new	4.2	Muscle	27-19-4-B5-PU
ID168	new	4.2	Fetal kidney	58-23-3-D10-PU
ID169	new	4.1	Fetal kidney	58-41-1-F8-PU
ID170	new	4.1	Heart	25-7-2-B1-PU
ID171	new	4.1	Fetal kidney	58-53-3-G4-PU
ID172	new	4.1	Fetal kidney	58-52-2-C2-PU
ID173	new	4	Muscle	27-21-4-E12-PU
ID174	new	4	Fetal kidney	58-22-2-B8-PU
ID175	new	4	Fetal kidney	58-9-3-A8-PU
ID176	new	4	Muscle	27-5-4-C10-PU
ID177	new	4	Fetal kidney	58-38-1-G5-PU
ID178	new	4	Fetal kidney	58-34-4-F6-PU
ID179	new	4	Heart	25-1-4-D2-PU
ID180	new	4	Fetal kidney	58-48-2-D6-PU
ID181	new	3.9	Fetal kidney	58-9-3-C10-PU
ID182	new	3.9	Fetal kidney	58-9-4-F2-PU
ID183	new	3.9	Fetal kidney	58-32-3-G3-PU
ID184	new	3.9	Fetal kidney	58-52-1-F6-PU
ID185	new	3.9	Fetal kidney	58-29-1-E1-PU
ID186	new	3.9	Muscle	27-3-4-A3-PU
ID187	new	3.9	Muscle	27-16-3-H2-PU
ID188	new	3.9	Fetal kidney	58-1-3-E1-PU

<u>SEQ. ID NO.</u>	<u>CATEGORY</u>	<u>VON HEIJNE SCORE</u>	<u>TISSUE SOURCE</u>	<u>INTERNAL DESIGNATION</u>
ID189	new	3.8	Kidney	21-5-4-F10-PU
ID190	new	3.8	Kidney	21-1-3-C9-PU
ID191	new	3.8	Fetal kidney	58-1-2-C7-PU
ID192	new	3.8	Fetal kidney	58-10-3-B6-PU
ID193	new	3.8	Fetal kidney	58-11-4-C8-PU
ID194	new	3.8	Heart	67-6-4-B12-PU
ID195	new	3.8	Fetal kidney	58-7-3-B5-PU
ID196	new	3.8	Fetal kidney	58-46-3-C6-PU
ID197	new	3.7	Dystrophic muscle	29-2-4-D8-PU
ID198	new	3.7	Fetal kidney	58-7-1-D10-PU
ID199	new	3.7	Kidney	21-2-4-A11-PU
ID200	new	3.6	Fetal kidney	58-45-3-B7-PU
ID201	new	3.6	Fetal kidney	58-29-1-D7-PU
ID202	new	3.6	Fetal kidney	58-16-3-B3-PU
ID203	new	3.6	Dystrophic muscle	29-7-3-C3-PU
ID204	new	3.6	Fetal kidney	58-42-3-C2-PU
ID205	new	3.5	Fetal kidney	58-38-3-G8-PU
ID206	new	3.5	Dystrophic muscle	29-6-2-B12-PU
ID207	new	3.5	Fetal kidney	58-8-1-D1-PU
ID208	new	3.5	Fetal kidney	58-24-1-H2-PU
ID209	new	3.5	Fetal kidney	58-41-4-G9-PU
ID210	ext-est-not-vrt	12.7	Muscle	27-22-3-H1-PU
ID211	ext-est-not-vrt	10.5	Fetal kidney	58-29-1-F11-PU
ID212	ext-est-not-vrt	8	Fetal kidney	58-14-2-B12-PU
ID213	ext-est-not-vrt	7.7	Fetal kidney	58-5-1-C4-PU
ID214	ext-est-not-vrt	7.1	Fetal kidney	58-37-4-C7-PU
ID215	ext-est-not-vrt	6.7	Muscle	27-21-2-C8-PU
ID216	ext-est-not-vrt	6.7	Heart	67-1-1-C8-PU
ID217	ext-est-not-vrt	6.3	Fetal kidney	58-26-3-G6-PU
ID218	ext-est-not-vrt	6.2	Fetal kidney	58-15-3-B12-PU
ID219	ext-est-not-vrt	6	Muscle	27-5-2-G11-PU
ID220	ext-est-not-vrt	6	Fetal kidney	58-8-1-H10-PU
ID221	ext-est-not-vrt	5.8	Fetal kidney	58-38-4-D2-PU
ID222	ext-est-not-vrt	5.6	Fetal kidney	58-53-2-E6-PU
ID223	ext-est-not-vrt	5.6	Fetal kidney	58-52-2-C7-PU
ID224	ext-est-not-vrt	5.5	Fetal kidney	58-34-2-E7-PU
ID225	ext-est-not-vrt	5.4	Fetal kidney	58-4-1-A2-PU
ID226	ext-est-not-vrt	5.2	Fetal kidney	58-11-1-D3-PU
ID227	ext-est-not-vrt	5.2	Fetal kidney	58-34-3-C9-PU
ID228	ext-est-not-vrt	5.2	Fetal kidney	58-35-4-H11-PU
ID229	ext-est-not-vrt	4.6	Fetal kidney	58-3-4-H7-PU
ID230	ext-est-not-vrt	4.5	Fetal kidney	58-25-1-F3-PU
ID231	ext-est-not-vrt	4.5	Fetal kidney	58-4-4-A8-PU
ID232	ext-est-not-vrt	4.4	Fetal kidney	58-11-1-C1-PU
ID233	ext-est-not-vrt	3.9	Muscle	27-19-2-F5-PU
ID234	ext-est-not-vrt	3.5	Dystrophic muscle	29-2-2-A2-PU
ID235	est-not-ext	14.1	Fetal kidney	58-29-2-B9-PU
ID236	est-not-ext	11.4	Dystrophic muscle	29-11-2-E4-PU
ID237	est-not-ext	11.2	Fetal kidney	58-7-2-A7-PU
ID238	est-not-ext	10.8	Muscle	27-22-3-G4-PU
ID239	est-not-ext	9.9	Fetal kidney	58-9-1-G1-PU

<u>SEQ. ID NO.</u>	<u>CATEGORY</u>	<u>VON HELINE SCORE</u>	<u>TISSUE SOURCE</u>	<u>INTERNAL DESIGNATION</u>
ID240	est-not-ext	9.7	Dystrophic muscle	29-8-1-H5-PU
ID241	est-not-ext	9.6	Fetal kidney	58-40-1-F5-PU
ID242	est-not-ext	9.5	Fetal kidney	58-6-4-G2-PU
ID243	est-not-ext	9.2	Fetal kidney	58-25-2-E7-PU
ID244	est-not-ext	8.9	Fetal kidney	58-48-1-A11-PU
ID245	est-not-ext	8.8	Fetal kidney	58-35-2-B6-PU
ID246	est-not-ext	8.5	Kidney	21-7-4-C7-PU
ID247	est-not-ext	8.4	Fetal kidney	58-45-1-E6-PU
ID248	est-not-ext	8.1	Fetal kidney	58-39-1-A12-PU
ID249	est-not-ext	8	Fetal kidney	58-46-1-C7-PU
ID250	est-not-ext	7.9	Dystrophic muscle	29-12-3-E10-PU
ID251	est-not-ext	7.9	Fetal kidney	58-17-2-D9-PU
ID252	est-not-ext	7.9	Fetal kidney	58-52-3-B7-PU
ID253	est-not-ext	7.6	Fetal kidney	58-24-3-E7-PU
ID254	est-not-ext	7.6	Heart	25-8-4-B12-PU
ID255	est-not-ext	7.6	Dystrophic muscle	29-4-4-D12-PU
ID256	est-not-ext	7.4	Muscle	27-1-2-B3-PU
ID257	est-not-ext	7.3	Fetal kidney	58-48-1-G3-PU
ID258	est-not-ext	7.3	Dystrophic muscle	29-2-3-F8-PU
ID259	est-not-ext	7.2	Fetal kidney	58-19-3-B3-PU
ID260	est-not-ext	7	Fetal kidney	58-14-2-C4-PU
ID261	est-not-ext	6.7	Fetal kidney	58-16-3-B6-PU
ID262	est-not-ext	6.6	Fetal kidney	58-9-4-F6-PU
ID263	est-not-ext	6.4	Fetal kidney	58-1-1-E3-PU
ID264	est-not-ext	6.4	Fetal kidney	58-33-3-B4-PU
ID265	est-not-ext	6.3	Dystrophic muscle	29-12-1-H1-PU
ID266	est-not-ext	6.3	Muscle	27-9-3-A5-PU
ID267	est-not-ext	6.2	Muscle	27-17-4-C12-PU
ID268	est-not-ext	6.2	Fetal kidney	58-33-1-F1-PU
ID269	est-not-ext	5.9	Fetal kidney	58-48-4-H2-PU
ID270	est-not-ext	5.9	Fetal kidney	58-42-1-A6-PU
ID271	est-not-ext	5.7	Fetal kidney	58-33-4-E1-PU
ID272	est-not-ext	5.7	Fetal kidney	58-26-2-E12-PU
ID273	est-not-ext	5.6	Fetal kidney	58-26-1-E12-PU
ID274	est-not-ext	5.5	Fetal kidney	58-54-1-D11-PU
ID275	est-not-ext	5.5	Muscle	27-9-2-F9-PU
ID276	est-not-ext	5.4	Fetal kidney	58-30-2-H10-PU
ID277	est-not-ext	5.3	Fetal kidney	58-29-1-H1-PU
ID278	est-not-ext	5.3	Kidney	21-1-4-F2-PU
ID279	est-not-ext	5.1	Fetal kidney	58-42-4-H7-PU
ID280	est-not-ext	5	Fetal kidney	58-34-3-H10-PU
ID281	est-not-ext	5	Kidney	21-7-3-B4-PU
ID282	est-not-ext	4.9	Fetal kidney	58-4-2-D12-PU
ID283	est-not-ext	4.8	Fetal kidney	58-31-2-C10-PU
ID284	est-not-ext	4.7	Fetal kidney	58-37-3-C10-PU
ID285	est-not-ext	4.7	Fetal kidney	58-1-1-D11-PU
ID286	est-not-ext	4.6	Fetal kidney	58-52-1-A11-PU
ID287	est-not-ext	4.3	Fetal kidney	58-4-3-E10-PU
ID288	est-not-ext	4.3	Heart	67-6-4-F2-PU
ID289	est-not-ext	4.2	Fetal kidney	58-49-3-G10-PU
ID290	est-not-ext	4.1	Dystrophic muscle	29-10-3-B11-PU

<u>SEQ. ID NO.</u>	<u>CATEGORY</u>	<u>VON HEIJNE SCORE</u>	<u>TISSUE SOURCE</u>	<u>INTERNAL DESIGNATION</u>
ID291	est-not-ext	4.1	Heart	25-5-4-A7-PU
ID292	est-not-ext	4.1	Fetal kidney	58-33-2-C6-PU
ID293	est-not-ext	4	Heart	25-7-3-D4-PU
ID294	est-not-ext	3.9	Heart	67-1-3-B11-PU
ID295	est-not-ext	3.9	Fetal kidney	58-23-1-G5-PU
ID296	est-not-ext	3.7	Fetal kidney	58-6-1-B6-PU
ID297	est-not-ext	3.7	Dystrophic muscle	29-6-2-H8-PU
ID298	est-not-ext	3.7	Fetal kidney	58-43-4-B8-PU
ID299	est-not-ext	3.6	Muscle	27-3-4-G9-PU
ID300	est-not-ext	3.6	Fetal kidney	58-38-1-F10-PU
ID301	est-not-ext	3.5	Heart	67-6-4-E7-PU
ID302	est-not-ext	3.5	Fetal kidney	58-54-1-E6-PU
ID303	est-not-ext	3.5	Heart	67-4-4-G7-PU
ID304	est-not-ext	3.5	Fetal kidney	58-23-4-F4-PU
ID305	ext-vrt-not-genomic	10.5	Fetal kidney	58-42-3-A12-PU

TABLE III

<u>SEQ. ID</u> <u>NO.</u>	<u>SIGNAL PEPTIDE</u>
ID38	MMWRPSVLLLLLLLRHGAQG
ID39	MERPLCSHLCSCLAMLALLSPLSLA
ID40	MIHLGHILFLLLLPVAAA
ID41	MAVKLGTTLLALALGLAQPASA
ID42	METLGALLVLEFLLSPVEA
ID43	MLLPLLLSSLLGGSQA
ID44	MLWLLFFLVTAIHA
ID45	MAGSPSRAAGRRQLPLLCFLQGATA
ID46	MKWPWTCLAILCPGPVLSPPCSGPXLALALLVLPLLWP
ID47	MPSWIGAVILPLLGLLLSLPAGA
ID48	MLLHWVRSQXXSDXKLWLSLLVPSCLCA
ID49	MKYLRHRRPNATLLAIGAFTLLLSLLVSPPTC
ID50	MPGPRVWGKYLWRSPHSGCPGAMWWLLWGVLQA
ID51	MCGPAMFPAGPPWPRVRVVQVLWALLAVLLASWRLWA
ID52	MHRRKLPLTNKRQLQKXLSKFIFDELFRNLFSLRTLRLMILSLLLLSTALNILA
ID53	MKLWVSALLMAWFGVLS
ID54	MQLPLALCLVCLLVHTAFR
ID55	MLCIHXXRIIQDSFIALKILLCSVAVXLSPS
ID56	MGGFFPPTREVVCANQGAAHNRDRLPFLSLFWPWAPG
ID57	MKLFYNQLVSETKHDF AHLWILLFSFCWM
ID58	MPSESPLLFFHILFHSCFS
ID59	MSSMWSEYTIGGVKIYFPYKAYPSQLAMMNSILRGLNSKQHCLLESPTGSGKSLALLCSA LAWQQSLS
ID60	MALFLELFLNSYSLLFVRFLGFVSCLQS
ID61	MNEDEKEMKEILMAGSSLSAGVSG
ID62	MGSFLLGGIPLIXXLSLCLC
ID63	MLQVATTNYLELAREVKPVCLLCSGCSCAWS
ID64	MFCLAPFFLALCFPKSTS
ID65	MSES RFQPQNQGSLQLPLQCLCCISPPVFC
ID66	MPKHCHSFITSSCLLGLLHLSSQ
ID67	MCLLFXFIXFPFLPFSSFS
ID68	MASERXPNRPXCLLVASGXAEGVSA
ID69	MFPDYKLGGSYLLAFQLVFLRATSG
ID70	MRRISLTSSPVRLLLXLXLLIALE
ID71	MTFLLLLFXNAGRS
ID72	MRTVVLTMKASVIEMFLVLLVTGVHS
ID73	MSSPLLVEQSSTKSPKSWWSFLAFSCISLLFIFFSIANS
ID74	MYLFCLFSVSKTIPLLLFFHLSFL
ID75	MTVCLLLKFLSPAET
ID76	MDKSIKSSHWLILCFLFILHTHT
ID77	MFFIFINGFTLLMLTAMKPRHPIDLLLLXXSNQ
ID78	MCPSLEEAPSVKGTLPSCGQQQPFPGASNIPLLLGRSRKVARGAPVLWPFLTWINPALS
ID79	MLQDLLSALWFCHPCCL
ID80	MMDLRPLLSLAAYLSGPHQ
ID81	MEMPPCLLPGLPLVRTSFS
ID82	MTVELWLRRLRGKGLAMLHVTRGVXG
ID83	MSIEDFVNRSILLLLCSSPPDRV
ID84	MRHYLLFALLFLFLVPVPG
ID85	MCLLTALVTQVIS

<u>SEQ. ID</u> <u>NO.</u>	<u>SIGNAL PEPTIDE</u>
ID86	MMGNPGLALVAGTPPSRS
ID87	MNHLMPLTVLHSVLEMLRTPRTPPWPCVSLWAPRXFA
ID88	MGHVVFQDIKNSLLXLRASQLSEG
ID89	MAGGRDYSQLFGRGPGRLSRARASVVRWSPRATACAPPSPDLKRQELVSRIECGRG PVGATADFFLSLLXSSETPG
ID90	MFWXGSLWCFHSFISFSL
ID91	MAWPNVFQXGSLLSQFXHHVVVFLLTFFSYSLLHA
ID92	MILRNLWILAVGLSLPSS
ID93	MLTVNDVRFYRNVRSNHFFVRLCGLLHLWLKVFS
ID94	MNLKPGLPCLNLCILAXPFS
ID95	MMQGEAHPASLIDRTIKMRKETEARVVLAWGLLNVSMA
ID96	MMNQTHPXXLLLAHITQS
ID97	MGLPERRGLVLLSLAEILF
ID98	MWGLEEDRSYQGLRPLCWALLYNCFSS
ID99	MLCRDGSACVPRSRRLPLPAAVRAHGPMADXXDSARGCVVFEDVFVYFSREEWELL DDAQRLLYHDVMLENFALLASLGIAFSRS
ID100	MLITRLQSGIDFAIQDESTDIGSCITLLVYVRYAWQDDFLEDFLCFLNLTSHLSG
ID101	MESQQLHCILNSNSVACSFAVGAGFLAFLSCLAFLVLD
ID102	MSNKYKPSMSPGNTDHLFLLFPRSCSS
ID103	MVELKQLGPRSFFFFLPPXP
ID104	MPYVTIPYIIVYSLIPALFFFLHC
ID105	MPPLAAVMGSLPLLCLMDLPHSVLS
ID106	MLQIPERREFLFLGFPSNSWP
ID107	MFFVHFLITLFCVVVVG
ID108	MACFGEKRHAKSCLHLRCLQLYWA
ID109	MVDRDENILLKQIYSPSLALQSSCCLC
ID110	MKVKPPFVSVSLCVCDCVRG
ID111	MISSCGVKYLFSHASLFFMVGSTGSLILLTSCFYTLVSS
ID112	MGGGIAESFLCNFLVSLSL
ID113	MDALERGLRNEQALVYAGLAYFLCCQGVIFG
ID114	MEYLFQQPGHSRGEARAAAASLETSSLWFLPLPTHVYT
ID115	MVSSMLITLSFIFA
ID116	MPLFTMNLVSALASSAXG
ID117	MICKHYCIKKNLDYLNRMVYSAQLKLILLHCSIRVFF
ID118	MKIPVWHKTCFLKSESFDPNLSVSLPCRPSQVPSQGGKSFLLQLIHEDKA
ID119	MGAAVFFGCTFVAFXPFA
ID120	MVGGLDPPGRRRFQKGFDRNLWSSCWLA PLADG
ID121	MSKMPVFASLLVSCFYQISG
ID122	MXVTQLLPFSSPDSA
ID123	MGKAWQEMRVEWGADKGNVRSSFHFLPWALGAMA
ID124	MKVMMRKRKKKDQCLPGICRSLKRRKSPRSPGMKVIRLSQFLKQWP
ID125	MTSFCCFFPGFKPLLFHYFLXSFSTLLWGLNC
ID126	MAGGMKVAVSPAVGPGPWGSGVGGGTVRLLLILSGCLVYG
ID127	MVEMTGVWQCQAEAVKGLPLLSCSCPPPLG
ID128	MQITPGSAAGLLPLLGNAPG
ID129	MILSTWLLTLQNSVFT
ID130	MAFSYWGKSLQSFKTFMRVCIVLALCHTSRP
ID131	MKLRFTLLPLVLHSQS
ID132	MMIILGFAFCPGHFRNFIPFLVIYSFVLS
ID133	MNRVPADSPNMCLICLLSYIALGAJHA
ID134	MDLFLNPLVIGTIP

<u>SEQ. ID</u> <u>NO.</u>	<u>SIGNAL PEPTIDE</u>
ID135	MXKNHRNKKSIHFPLCTIPSMXKSCTLP LQRTWDXXPSFVHWXQARLQSPXSHLVXLS VIRSTLVLSQCLC
ID136	MSFIALVYSSLSFQ
ID137	MVFDTLKSRIVLFLNSXFPIIC
ID138	MLEMETWLRLCDCSRWGMASAWGRGGKLLGAQVALHPRNCSKAKIFLFSILLMSLRT
ID139	MDDLMLFFLGALCRESG
ID140	MVLGALNLPSELPTLLLPVGAPG
ID141	MLVSKIQTFSVFLSIPVLG
ID142	MCNPVAHTFRGVHEHHAMLLSTGLNILGTQA
ID143	MQCWILLWEACTGRCQA
ID144	MTGYPWANSITTVLCILGCHGNLCC
ID145	MVSCDVXSYVIIFTALFLXLHVA
ID146	MKSFDKKLFAIFLMCLKSIG
ID147	MFGAGDEDDTDFLSPSGGARLASLFGLDQXAXG
ID148	MVLTGESPVLVGRRLSLSAADGXDX
ID149	MVIELTSVFQAMIWSQG
ID150	MESTLGAGIVIAEALQNQLAWLENVWLWXXLXXXIPXILFLFYFPAAYYA
ID151	MIIVSELGTPTGVLVGFLSTFLYC
ID152	MNWNVRGTRGFLLCPLVCGLRR
ID153	MLRCGGRGLLLGLAVAAAA
ID154	MILLMIVFSIFLL
ID155	MSLLFIFRSILISC
ID156	MPLISKVLIQLSQAFA
ID157	MDTSSVGGLELTDQTPVLLGSTAMATSLT
ID158	MDTGESFSPTSCRGHWRIILLTHVPPWILE
ID159	MPYLDPYITQPIIQUIERKLVLSSVLKEPVSR
ID160	MDTSSVGGLELTDQTPVLLGSTAMATSLT
ID161	MHVLFNIVTTNXXNHFGLLDFVQQCCDS
ID162	MPPQSCCSKTAYWLSFMSWAQS
ID163	MSCVFFHFLQGGLG
ID164	MSISLSSILLPIWINMAQI
ID165	MTALNLVAPFSDGDSGSVSLASFCAVVLSPVFQ
ID166	MWSRPVQVLGGLATCQH
ID167	MRYRLRIQITTSNLQILLFLLISC
ID168	MPFFSNQPTQVSLLFFCCSPLYSP
ID169	MRVKDPTKALPEKAKRSKRPTVPHDEDSSDDIAVGLTCQHVSIA
ID170	MVSLGYYLIFVLYLWLCFMQISEEKLIEHTGTYLTSSSPLCQL
ID171	MSLTSRXXIMXTIKIQNISITKVLCCLLIATPTFF
ID172	MXAEAAGVVSTSVAAAVA
ID173	MWIMSSCLALTYTNS
ID174	MPRGVYNSNALVLVTRGSSS
ID175	MIEPCEKMKHYDMNWFLCMYECFFHLETEFLPCVHPFSVIA
ID176	MAMWNRPCQXLPQQPLVAEPTAEGEPHPTGRELTEANRFAYAALCGISLSQXFP
ID177	MEQVCLLVSYAVDSAAG
ID178	MRKISHCLHCWPESGATLRCWASTPVSG
ID179	MCINDHIIKLLHPCGSITLTSS
ID180	MRCRVALQCGLTIPALX
ID181	MTVRYGKFLSLLKDGAENDLTWVLKHCERFLKQQQTSIKSSLLCLQGNYAGHDWFVSSLF MIMLGDKKETFQFLHQFSRLTSAFLWLPRLHI
ID182	MAFDVSCFFWVVLFSAGCKV
ID183	MLTRLVLSAHLSTTSPPWTHA

SEQ. ID NO.	SIGNAL PEPTIDE
ID184	MRYFQGSPSPYSEIEIELCDHVYSFQGLCVNLLLGFEFVIS
ID185	MXXKRTHXXSVFNGLVYAAGGRNAEGSLASLECYVPSTNQ
ID186	MFLKVQSQSFYXPYRDCLNFHKSTYLLFFHLLLNDDFT
ID187	MQPLKJIFYLSVSIWILIIYTFQCNS
ID188	MMRTTARVAACATAAPLQA
ID189	MEAATTLHPGPRPALPLGARARWASSCLHPSARS
ID190	MQGVRGPVSFSWSTTMLCPVIFPNSNCWK
ID191	MXXFSFXLLFXFXFFRQ
ID192	MLLLSEALSESVRLLFRFSVIMA
ID193	MALISLPCTTAFPLLSS
ID194	MSEEEAAQIPRSSVWEQDQQNVVQRVVALPLVRATCT
ID195	MAAAAAAGAASGLPGPVAQGLKEALVDTLTGILSPVQEVRAAAEEQIKVLEVTEEFVHIL AELTVDPQGALA
ID196	MNSGGGFGGLGLGGLTPTSVIQTNLSSAVTSEQMRTLFSFLGEIEELRLYPDPNAPLAF SSXVCYVKFRDPSSVGVAQHLTNTVFIDRLXSCSLCRRLVSRFXXXLYNFCPVCYC
ID197	MIEMLIFLDCVLS
ID198	MHPFLAAHGAFAHKGKYSTINIVDIYPMCHILGLKPHPNNGTFGHTKCLLVDQWCINL PEAIAIVIGSLLVLTMLTC
ID199	MIWPMSASVATLWS
ID200	MGIDIFYPSHIPDFHPIHLFIYLVFVECLLC
ID201	MKELNQKLTNKNKIEDLEQEIQKQKQETLQEEITSLQSSVQEYEEKNXKIKQLLVKT KKELADSKQAETDHLILQASLKGELEA
ID202	MGNTLKEMQDVQGALQCYTRAIQINPAFADAHSNLASIHKDSGNIPEAIASYRTALKLP DFPDAYCNLAHCLQIVCDWTDYDERMKKLVSIVADQLEKNRLLLCILIVCYI
ID203	MLILADTRRVQGGTLGLIPAVLNRVHVAYAIPIPSLFC
ID204	MLVGIYFCVFLFPLISNTSS
ID205	MFLAPSLITKLLTGSESPDGNPPALGRPLLQGACPLIFL
ID206	MDPSASKSCLFYLQKVSG
ID207	MSLTASGPRAAWEERVGGHTWGANIPTAPDSQRWLCLQAYLASFS
ID208	MKYQMVSQSAQLASPLLPATP
ID209	MNGTFPGTYVYLVAYGDLRIFGCFWGLMYXWLLLG
ID210	MGPSTPLLLFLLSWGPLQG
ID211	MKFISTSLLLMLLVSSLSPVQG
ID212	MNYQYGFNMVMSHPHAVNEIALSLNNKNPRTKALVLELLAAVCLVRG
ID213	MAQSIHMYAARVQWGLVMCFLSYFGTFA
ID214	MGSGYSHSLHLFHLIRPXQG
ID215	MARCFSLVLLTSIWT
ID216	MAMRYNRLTVLAGAMLALGLMTCLSVLFGYATS
ID217	MPQQPVEQGSPLLRLPLPPFSFP
ID218	MPSRSPFTWSHLCWRAGRCPRWRACLSSSSVRMCSPAAPSRFGALGXSARRWPRDA DTWCAPOQVMRASLLPMLLGSWA
ID219	MSHTEVKLKIPFGNKLLDAVCLVPNKSLTYGILTHGASG
ID220	MELGSCLEGGREAAEEEGEPEVKKRRLLCXEFXSVASDA
ID221	MGRTYIVEETVGQYLSNINLQGKAFVSGLLIGQCSS
ID222	MGRKCGGCLSCLLIPLALWS
ID223	MGRKCGGCLSCLLIPLALWS
ID224	MWWFQQGLSFLPSALVIWTS
ID225	MFNASTFTDWSSSIFVFTFKSKKSAGLPLIFSLWCSGVLL
ID226	MKMASSLAFLLLNFHVSLLLVQLLTPCSA
ID227	MHILQLLTTVDDGIQAIVHCPDTGKDIWNLLFDLVCFEFCQS
ID228	MSDQIKFIMDSLNKEPFRKNYNLITFXSLEPMQLLQVLSDVLA

<u>SEQ. ID NO.</u>	<u>SIGNAL PEPTIDE</u>
ID229	MATSSQXRQLSDYGPPSLGYTQGTGNSQXPQSKYAELLAIXELGKEIRPMYAGSKSAM ERLKRGIHAXGLVRECLA
ID230	MRLLGAAAVAALGRG
ID231	MAQRLLRRFLASVIS
ID232	MFRLNSLSALAEAVG
ID233	MSGNSGSKENSHNKARTSPYPGSKVERSQVPNEKVGWLVEWQDYKPVEYTAHSVLA GPRWA
ID234	MRTTLMFSLTAQWXTS
ID235	MSDLLLGLIGGLTLLLLLTLAFA
ID236	MEGTEMGARPGGHPXKWSFLWSLALWLPLALS
ID237	MXFLRKVXSILSLQVLLTTVTSTVFLYFESVRTFVXESPALILLFALGSLGLIFA
ID238	MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQG
ID239	MSSWMYLGYPVTSNTTCLKLISSEFPQLPFLFPFPVNA
ID240	MAPGVIIQLCLLLPSCSL
ID241	MRHGFIIQQFSLTAFSXXXIFTLXXLSQLLSSAAPKHTAAPTALPCLQGQQLNSLSLGT SELSCVLASSCLSTKTDPSGLSLSLGASAPVQC
ID242	MFQNIQKCLNVPFVRGYHVFYNLNAVILIIFLSFLPFINS
ID243	MSLSQRGFPVLALFLSGSLA
ID244	MAARWRFWCVSVTMVVALLIVCDVPSASA
ID245	MFAPAVMRAFRKNKTLGYGVPMLLLVGGSGF
ID246	MELPSGPGPERLFDSHRLPGDCFLLLVLLYAPVGFC
ID247	MAQSQGWVXRYXKAFCKGFFVAVPVAVTFLDRVACVARVEGASMQPSLNPGGXSXS DVVXXNHWKVRNFEVHRGDIVSLVLLTVTPSXRQ
ID248	MSSAAADHWAWLLVLSFVFGCNV
ID249	MNLFKTNHVFFLLLAHIA
ID250	MPALLPVASRLLLPRVLLTMASG
ID251	MIGSGLAGSGGAGGPSSTVTWCALFSNHVAATQASLLLSFVWMPALLPVASRLLLPRVL LTMASG
ID252	MPALLPVASRLLLPRVLLTMASG
ID253	MEASWGSFNAERGWYVSVOQPEEAEEELSPLLSNELHRQRSPGVSFGLSVFNLMAIMG SGILGLAYVMANTGVFGFSFLLTVALLASYS
ID254	MPSSFLLLRFFLRIDG
ID255	MKRTHLFIVGIYFLSSCRA
ID256	MGDKIWLFPVLLLAALPPVLLP
ID257	MPHSSLHPSIPCPRGHGAQKAALVLLSACLVTWGLG
ID258	MGAWGRGWPWEERQGHLLLLLLPAPTLK
ID259	MGQCGITSSKTVLVFLNLIWGAAGILCYVGAYVFITYDDYDHFEDVYTLIPAVVIAV RALLFIIGLIGCCAT
ID260	MPXAFSVSSFPVSIPAVLTQTDWTEPWLMGLATFHLCVLLTCLSSRSYRLQIGHFLCLV ILVYC
ID261	MLLSLFFPLRISL
ID262	METGERARLILVLQLLLRIR
ID263	MCGXXFSLPCLRLFLVVTCTYXLLLLHKEILGCSSVCQLCTG
ID264	MNPVTESPSCLFSPSESALASQLALSASCDQRAPFSLAGVXSXXPRLASRQVAPPFGR ACCFLSAFSPTLT
ID265	MSRSSKVVLGLSVLLTAATVA
ID266	MGIQTSPVLLASLGVGLVTLLGLAVG
ID267	MYPSYLLIXPPIPSQFLKQCPPTLSDPFLPLALRSLDVLLSSAXLVXXS
ID268	MEQKHXRELEQLKLTENKILLXTFTQWCLR
ID269	MMTAPVLAAQTLKFTLLQKSNA
ID270	MDSAACAAAATPVPALALAXAPDLAQA

<u>SEQ. ID</u> <u>NO.</u>	<u>SIGNAL PEPTIDE</u>
ID271	MASLGLQLVGYILGLLGTLVA
ID272	MASLGLQLVGYILGLLGTLVA
ID273	MLCSLLCECLLLVAGYA
ID274	MASRLCGGALWYVCPCPSGAWM
ID275	MTSALTQGLERIPDQLGYLVLSEGAVLA
ID276	MASPSRRLQTKPVITCFKSVLLIXTXIXWITGVILLAVGIWG
ID277	MADAASQVLLGSGLTLSQP
ID278	MSRNLRTALIFGGFISLIGA
ID279	MPHGLWCFHLVVLSLYS
ID280	MSLVAVFLSCGLIS
ID281	MMKRAAAAAGVGGALAVGAVPVVLS
ID282	MAVIVDKPWFDYDMKKVWEGYPIQSTIPSQYWYYMIELSFYWSLLFSIASDVKRKDFKEQI IHHVATILISFSWFANYIRA
ID283	MIISLFYIFLTCSNT
ID284	MAAELVEAKNMVMSFRVSDLQMLLGFVGRSKS
ID285	MTGLSMXGGGSXXGDVXPXYGKXGPLRXLPEPSGPLPPSSGLSQPVHALCPLSPLVTT
ID286	MQMYSRQLASXEWLTIQGGLLGXGLXXXSLT
ID287	MASLEVSRSPRRSRRELEVRSPRQNKYSVLLPTYNERENLPLIVWLLVKSFSSES
ID288	MDKDSQGLLDSSLMASGTAS
ID289	MGLLTFGYIEXXKTEHNPDDHHSCLAVSWEAAGCHG
ID290	MGLYAAVAGVLAGVES
ID291	MGLYAAAAGVLAGVESRQSGIKGLVYSSNFQNVKQLYALVCETQRYSAVLDAVIASA GLLRA
ID292	MGAQHTALLNTEVRWLSRGKVLVRLFELRRELLVFMDSAFRLSDCLTNSSWLLRLAYLA DIFT
ID293	MSLRNLWRDYKVLVVMVPLVGLIHL
ID294	MVLRSLVEYSQDVL AHPVSEEHLPDVSLIGFSDPAELGKLLQLVLGCAIS
ID295	MIHGFCLAPTTSA
ID296	MXCPRTWCLACVEASPG
ID297	MADVEDGEETCALASHSGSSG
ID298	MFKVAAPPMLIXXIIMFLLIIVCGSP
ID299	MDFWDPAVFXMCLWSLRNLFS
ID300	MSPAGKHNSKFTFFVALDGSVPLLSLSHSIGI
ID301	MHWALVCVGLHTEGPWG
ID302	MFGAAARSADLVLEKNLQAAHGYAQEDRERMHRXIVSLXQNLLNFMIGSILDLWQCF LWFIYGSSLNTRG
ID303	MAARWRFWCVSVTMVVALLIVCDVPSA
ID304	MVVLLQLPSMIQEVT
ID305	MLHLHXSCLCFRSWLPAMLA VLLSLAPSASS

Minimum signal peptide score	false positive rate	false negative rate	proba(0.1)	proba(0.2)
3.5	0.121	0.036	0.467	0.664
4	0.096	0.06	0.519	0.708
4.5	0.078	0.079	0.565	0.745
5	0.062	0.098	0.615	0.782
5.5	0.05	0.127	0.659	0.813
6	0.04	0.163	0.694	0.838
6.5	0.033	0.202	0.725	0.855
7	0.025	0.248	0.763	0.878
7.5	0.021	0.304	0.78	0.889
8	0.015	0.368	0.816	0.909
8.5	0.012	0.418	0.836	0.92
9	0.009	0.512	0.856	0.93
9.5	0.007	0.581	0.863	0.934
10	0.006	0.679	0.835	0.919

TABLE IV

Minimum signal peptide score	All ESTs	New ESTs	ESTs matching public EST closer than 40 bp from beginning	ESTs extending known mRNA more than 40 bp	ESTs extending public EST more than 40 bp
3.5	2674	947	599	23	150
4	2278	784	499	23	126
4.5	1943	647	425	22	112
5	1657	523	353	21	96
5.5	1417	419	307	19	80
6	1190	340	238	18	68
6.5	1035	280	186	18	60
7	893	219	161	15	48
7.5	753	173	132	12	38
8	636	133	101	11	29
8.5	543	104	83	8	26
9	456	81	63	6	24
9.5	364	57	48	6	18
10	303	47	35	6	15

TABLE V

Tissue	All ESTs	New ESTs	ESTs matching public EST closer than 40 bp from beginning	ESTs extending known mRNA more than 40 bp	ESTs extending public EST more than 40 bp
Brain	329	131	75	3	24
Cancerous prostate	134	40	37	1	6
Cerebellum	17	9	1	0	6
Colon	21	11	4	0	0
Dystrophic muscle	41	18	8	0	1
Fetal brain	70	37	16	0	1
Fetal kidney	227	116	46	1	19
Fetal liver	13	7	2	0	0
Heart	30	15	7	0	1
Hypertrophic prostate	88	23	22	2	2
Kidney	10	7	3	0	0
Large Intestine	21	8	4	0	1
Liver	23	9	6	0	0
Lung	24	12	4	0	1
Lung (cells)	57	38	6	0	4
Lymph ganglia	163	60	23	2	12
Lymphocytes	23	6	4	0	2
Muscle	33	16	6	0	4
Normal prostate	181	61	45	7	11
Ovary	90	57	12	1	2
Pancreas	48	11	6	0	1
Placenta	24	5	1	0	0
Prostate	34	16	4	0	2
Spleen	56	28	10	0	1
Substantia nigra	108	47	27	1	6
Surrenals	15	3	3	1	0
Testis	131	68	25	1	8
Thyroid	17	8	2	0	2
Umbilical cord	55	17	12	1	3
Uterus	28	15	3	0	2
Non tissue-specific	568	48	177	2	28
Total	2677	947	601	23	150

TABLE VI

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Description of Transcription Factor Binding Sites present on promoters isolated from SignalTag sequences

Promoter sequence P13H2 (546 bp):

Matrix	Position	Orientation	Score	Length	Sequence
CMYB_01	-502	+	0.983	8	TGTCAGTTG
MYOD_Q6	-501	-	0.981	10	CCCAACTGAC
S8_01	-444	-	0.960	11	AATAGAATTAG
S8_01	-425	+	0.966	11	AACTAAATTAG
DELTAEF1_01	-390	-	0.960	11	GCACACCTCAG
GATA_C	-364	-	0.964	11	AGATAAATCCA
CMYB_01	-349	+	0.958	8	CTTCAGTTG
GATA1_02	-343	+	0.959	14	TTGTAGATAGGACA
GATA_C	-339	+	0.953	11	AGATAGGACAT
TAL1ALPHA47_01	-235	+	0.973	16	CATAACAGATGGTAAG
TAL1BETA47_01	-235	+	0.983	16	CATAACAGATGGTAAG
TAL1BETA1TF2_01	-235	+	0.978	16	CATAACAGATGGTAAG
MYOD_Q6	-232	-	0.954	10	ACCATCTGTT
GATA1_04	-217	-	0.953	13	TCAAGATAAAGTA
IK1_01	-126	+	0.963	13	AGTTGGGAATTCC
IK2_01	-126	+	0.985	12	AGTTGGGAATTC
CREL_01	-123	+	0.962	10	TGGGAATTCC
GATA1_02	-96	+	0.950	14	TCAGTGATATGGCA
SRV_02	-41	-	0.951	12	TAAACAAAACA
E2F_02	-33	+	0.957	8	TTTAGCGC
MZF1_01	-5	-	0.975	8	TGAGGGGA

Promoter sequence P16B4 (881bp):

Matrix	Position	Orientation	Score	Length	Sequence
NFY_Q6	-748	-	0.956	11	GGACCAATCAT
MZF1_01	-738	+	0.962	8	CCTGGGGA
CMYB_01	-684	+	0.994	9	TGACCGTTG
VMYB_02	-682	-	0.985	9	TCCAACGGT
STAT_01	-673	+	0.968	9	TTCTTGGA
STAT_01	-673	-	0.951	9	TTCCAGGA
MZF1_01	-556	-	0.956	8	TTGGGGGA
IK2_01	-451	+	0.965	12	GAATGGGATTTC
MZF1_01	-424	+	0.986	8	AGAGGGGA
SRV_02	-398	-	0.955	12	GAAACAAAACA
MZF1_01	-216	+	0.960	8	GAAGGGGA
MYOD_Q6	-190	+	0.981	10	AGCATCTGCC
DELTAEF1_01	-176	+	0.958	11	TCCCACCTTC
S8_01	5	-	0.992	11	GAGGCAATTAT
MZF1_01	16	-	0.986	8	AGAGGGGA

Promoter sequence P29B6 (555 bp):

Matrix	Position	Orientation	Score	Length	Sequence
ARNT_01	-311	+	0.964	16	GGACTCACGTGCTGCT
NMYC_01	-309	+	0.965	12	ACTCACGTGCTG
USF_01	-309	+	0.985	12	ACTCACGTGCTG
USF_01	-309	-	0.985	12	CAGCACGTGAGT
NMYC_01	-309	-	0.956	12	CAGCACGTGAGT
MYC MAX_02	-309	-	0.972	12	CAGCACGTGAGT
USF_C	-307	+	0.997	8	TCACGTGC
USF_C	-307	-	0.991	8	GCACGTGA
MZF1_01	-292	-	0.968	8	CATGGGGA
ELK1_02	-105	+	0.963	14	CTCTCCGGAAGCCT
CETS1P54_01	-102	+	0.974	10	TCCGGAAGCC
AP1_Q4	-42	-	0.963	11	AGTGACTGAAC
AP1FJ_Q2	-42	-	0.961	11	AGTGACTGAAC
PADS_C	45	+	1.000	9	TGTGCTCTC

TABLE VII

CLAIMS

1. A purified or isolated nucleic acid comprising the sequence of one of SEQ ID NOs: 38-305 or comprising a sequence complementary thereto.
- 5 2. The nucleic acid of Claim 1, wherein said nucleic acid is recombinant.
3. A purified or isolated nucleic acid comprising at least 10 consecutive bases of the sequence of one of SEQ ID NOs: 38-305 or one of the sequences complementary thereto.
4. A purified or isolated nucleic acid comprising at least 15 consecutive bases of
10 one of the sequences of SEQ ID NOs: 38-305 or one of the sequences complementary thereto.
5. The nucleic acid of Claim 4, wherein said nucleic acid is recombinant.
6. A purified or isolated nucleic acid of at least 15 bases capable of hybridizing under stringent conditions to the sequence of one of SEQ ID NOs: 38-305 or one of the
15 sequences complementary to the sequences of SEQ ID NOs: 38-305.
7. The nucleic acid of Claim 6, wherein said nucleic acid is recombinant.
8. A purified or isolated nucleic acid encoding a human gene product, said human gene product having a sequence partially encoded by one of the sequences of SEQ ID NO: 38-305.
- 20 9. A purified or isolated nucleic acid having the sequence of one of SEQ ID NOs: 38-305 or having a sequence complementary thereto.
10. A purified or isolated nucleic acid comprising the nucleotides of one of SEQ ID NOs: 38-305 which encode a signal peptide.
11. A purified or isolated polypeptides comprising a signal peptide encoded by
25 one of the sequences of SEQ ID NOs: 38-305.
12. A vector encoding a fusion protein comprising a polypeptide and a signal peptide, said vector comprising a first nucleic acid encoding a signal peptide encoded by one of the sequences of SEQ ID NOs: 38-305 operably linked to a second nucleic acid encoding a polypeptide.
- 30 13. A method of directing the extracellular secretion of a polypeptide or the insertion of a polypeptide into the membrane comprising the steps of:

obtaining a vector according to Claim 12; and

introducing said vector into a host cell such that said fusion protein is secreted into the extracellular environment of said host cell or inserted into the membrane of said host cell.

14. A method of importing a polypeptide into a cell comprising contacting said
5 cell with a fusion protein comprising a signal peptide encoded by one of the sequences of SEQ ID NOs: 38-305 operably linked to said polypeptide.

15. A method of making a cDNA encoding a human secretory protein that is partially encoded by one of SEQ ID NOs 38-305, comprising the steps of:

obtaining a cDNA comprising one of the sequences of SEQ ID NOs: 38-305;

10 contacting said cDNA with a detectable probe comprising at least 15 consecutive nucleotides of said sequence of SEQ ID NO: 38-305 or a sequence complementary thereto under conditions which permit said probe to hybridize to said cDNA;

identifying a cDNA which hybridizes to said detectable probe; and

isolating said cDNA which hybridizes to said probe.

15 16. An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-305 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of Claim 15.

17. The cDNA of Claim 16 wherein said cDNA comprises the full protein coding
20 sequence partially included in one of the sequences of SEQ ID NOs: 38-305.

18. A method of making a cDNA comprising one of the sequences of SEQ ID NOs: 38-305, comprising the steps of:

contacting a collection of mRNA molecules from human cells with a first primer capable of hybridizing to the polyA tail of said mRNA;

25 hybridizing said first primer to said polyA tail;

reverse transcribing said mRNA to make a first cDNA strand;

making a second cDNA strand complementary to said first cDNA strand using at least one primer comprising at least 15 nucleotides of one of the sequences of SEQ ID NOs 38-305; and

30 isolating the resulting cDNA comprising said first cDNA strand and said second cDNA strand.

19. An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-305 or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of Claim 18.

5 20. The cDNA of Claim 19 wherein said cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-305.

21. The method of Claim 18, wherein the second cDNA strand is made by:
contacting said first cDNA strand with a first pair of primers, said first pair of primers comprising a second primer comprising at least 15 consecutive nucleotides of one of the
10 sequences of SEQ ID NOs 38-305 and a third primer having a sequence therein which is included within the sequence of said first primer;

performing a first polymerase chain reaction with said first pair of nested primers to generate a first PCR product;

contacting said first PCR product with a second pair of primers, said second pair of
15 primers comprising a fourth primer, said fourth primer comprising at least 15 consecutive nucleotides of said sequence of one of SEQ ID NO:s 38-305 , and a fifth primer, said fourth and fifth primers being capable of hybridizing to sequences within said first PCR product; and
performing a second polymerase chain reaction, thereby generating a second PCR product.

20 22. An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein encoded by one of SEQ ID NOs 38-305, or a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of Claim 21.

23. The cDNA of Claim 22 wherein said cDNA comprises the full protein coding
25 sequence partially included in one of the sequences of SEQ ID NOs: 38-305.

24. The method of Claim 18 wherein the second cDNA strand is made by:
contacting said first cDNA strand with a second primer comprising at least 15
consecutive nucleotides of the sequences of SEQ ID NOs: 38-305;
hybridizing said second primer to said first strand cDNA; and
30 extending said hybridized second primer to generate said second cDNA strand.

25. An isolated or purified cDNA encoding a human secretory protein, said human secretory protein comprising the protein partially encoded by one of SEQ ID NOs 38-305 or comprising a fragment thereof of at least 10 amino acids, said cDNA being obtainable by the method of Claim 24.

5 26. The cDNA of Claim 25, wherein said cDNA comprises the full protein coding sequence partially included in one of the sequences of SEQ ID NOs: 38-305.

27. A method of making a protein comprising one of the sequences of SEQ ID NO: 306-573, comprising the steps of:

obtaining a cDNA encoding the full protein sequence partially included in one of the
10 sequences of sequence of SEQ ID NO: 38-305;

inserting said cDNA in an expression vector such that said cDNA is operably linked to a promoter;

introducing said expression vector into a host cell whereby said host cell produces the protein encoded by said cDNA; and

15 isolating said protein.

28. An isolated protein obtainable by the method of Claim 27.

29. A method of obtaining a promoter DNA comprising the steps of:

obtaining DNAs located upstream of the nucleic acids of SEQ ID NO: 38-305 or the sequences complementary thereto;

20 screening said upstream DNAs to identify a promoter capable of directing transcription initiation; and

isolating said DNA comprising said identified promoter.

30. The method of Claim 29, wherein said obtaining step comprises chromosome walking from said nucleic acids of SEQ ID NO: 38-305 or sequences complementary thereto.

25 31. The method of Claim 30, wherein said screening step comprises inserting said upstream sequences into a promoter reporter vector.

32. The method of Claim 30, wherein said screening step comprises identifying motifs in said upstream DNAs which are transcription factor binding sites or transcription start sites.

30 33. An isolated promoter obtainable by the method of Claim 32.

34. An isolated or purified protein comprising one of the sequences of SEQ ID NO: 306-573.

35. In an array of discrete ESTs or fragments thereof of at least 15 nucleotides in length, the improvement comprising inclusion in said array of at least one of the sequences of
5 SEQ ID NOs: 38-305, or one of the sequences complementary to the sequences of SEQ ID NOs: 38-305, or a fragment thereof of at least 15 consecutive nucleotides.

36. The array of Claim 35 including therein at least two of the sequences of SEQ ID NOs: 38-305, the sequences complementary to the sequences of SEQ ID NOs: 38-305, or fragments thereof of at least 15 consecutive nucleotides.

10 37. The array of Claim 35 including therein at least five of the sequences of SEQ ID NOs: 38-305, the sequences complementary to the sequences of SEQ ID NOs: 38-305, or fragments thereof of at least 15 consecutive nucleotides.

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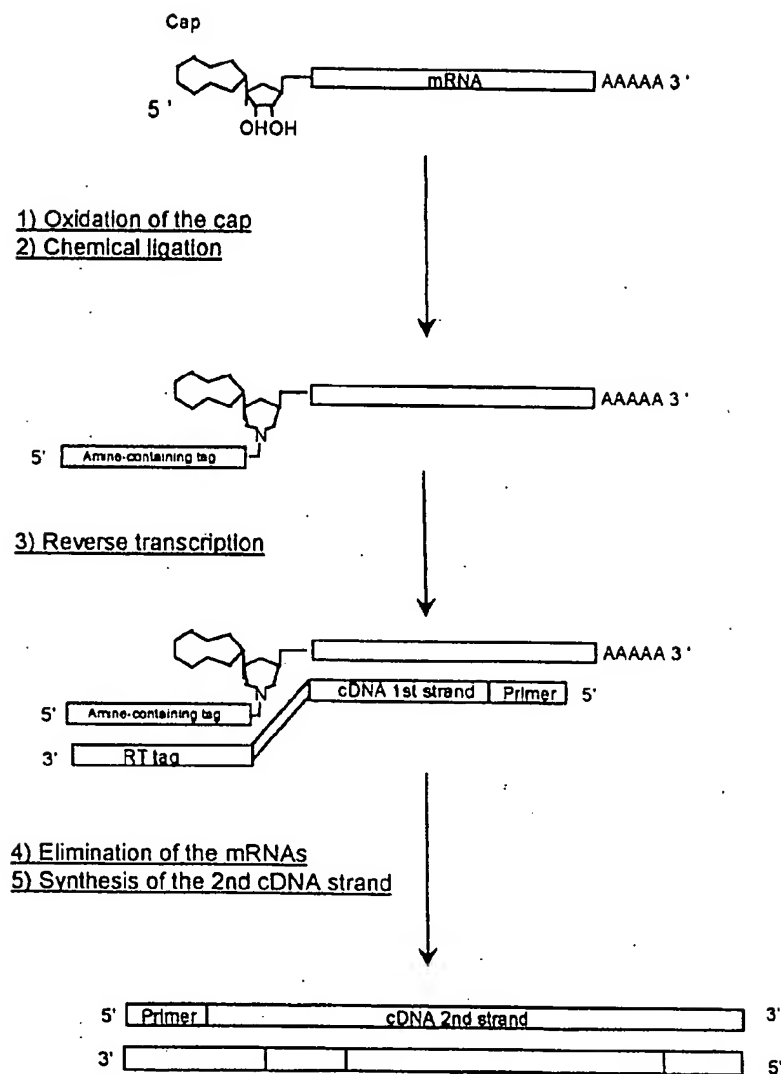


Figure 1

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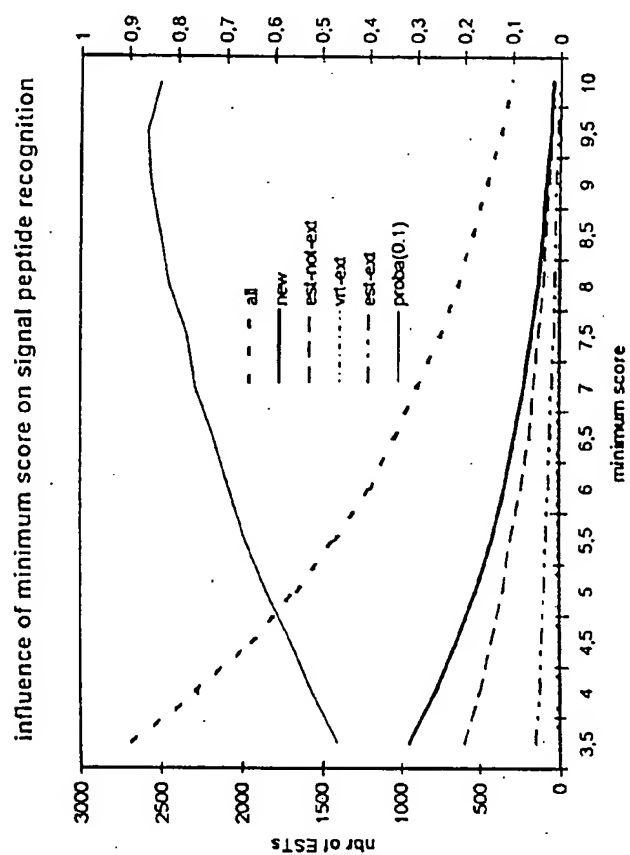


Figure 2

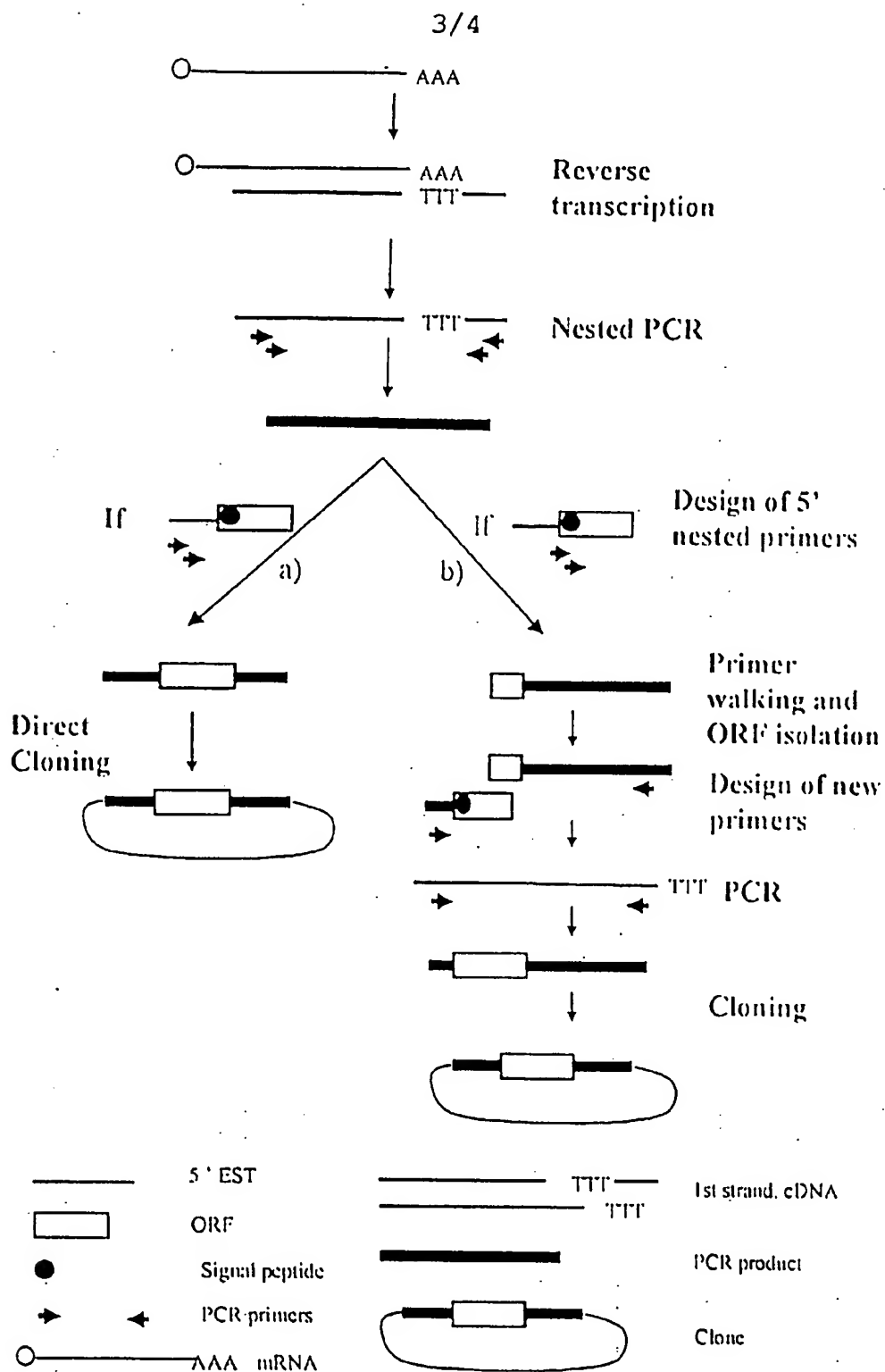
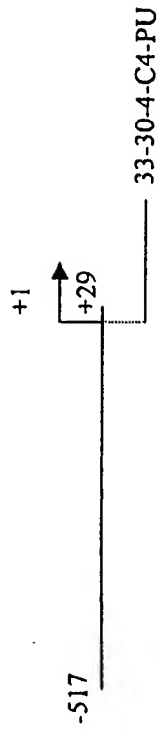
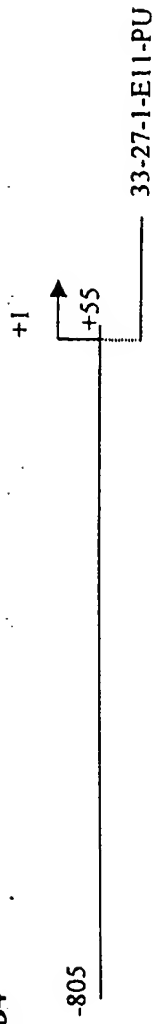


Figure 3

Promoter P13H2



Promoter P15B4



Promoter P29B6

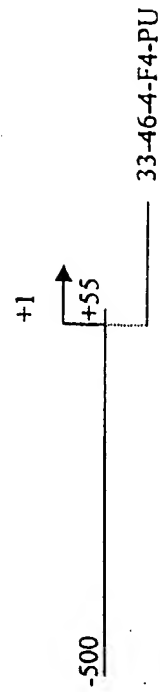


Figure 4

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME : GENSET SA
- (B) STREET :24, RUE ROYALE
- (C) CITY: PARIS
- (E) COUNTRY : FRANCE
- (F) POSTAL CODE (ZIP) : 75008

(ii) TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
EXPRESSED IN MUSCLE AND OTHER MESODERMAL TISSUES

(iii) NUMBER OF SEQUENCES: 573

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy Disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: Win95
- (D) SOFTWARE: Word

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(ix) FEATURE:

- (A) NAME/KEY: Cap
- (B) LOCATION: 1
- (C) OTHER INFORMATION: m7Gppp added to 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCAUCCUAC UCCCAUCCAA UCCACCCUA ACUCCUCCCA UCUCCAC

47

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GCAUCCUACU CCCAUCCAAU UCCACCCUAA CUCCUCCCAU CUCCAC

46

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATCAAGAATT CGCACGAGAC CATTA

25

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TAATGGTCTC GTGCGAATTC TTGAT

25

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCGACAAGAC CAACGTCAAG GCCGC

25

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TCACCAGCAG GCASTGGCTT AGGAG

25

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

AGTGATTCCT GCTACTTTGG ATGGC

25

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCTTGGTCTT GTTCTGGAGT TTAGA

25

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TCCAGAATGG GAGACAAGCC AATTT

25

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Other nucleic acid
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AGGGAGGAGG AAACAGCGTG AGTCC

25

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Other nucleic acid
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATGGGAAAGG AAAAGACTCA TATCA

25

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Other nucleic acid
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AGCAGCAACA ATCAGGACAG CACAG

25

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Other nucleic acid
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATCAAGAATT CGCAGGAGAC CATTA

25

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

ATCGTTGAGA CTCGTACCAG CAGAGTCACG AGAGAGACTA CACGGTACTG GTTTTTTTTT 60

TTTTTVN 67

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CCAGCAGAGT CACGAGAGAG ACTACACGG 29

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CACGAGAGAG ACTACACGGT ACTGG 25

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 526 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Lymph ganglia
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(261..376)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 166..281
 id N70479
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(380..486)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 54..160
 id N70479
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(110..145)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 403..438
 id N70479
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(196..229)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 315..348
 id N70479
 est
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 90..140
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8.2
 seq LLLITAILAVAVG/FP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AATATRARAC AGCTACAATA TTCCAGGGCC ARTCACTTGC CATTTCATCAT AACAGCGTCA 60
GAGAGAAAGA ACTGACTGAR ACGTTTGAG ATG AAG AAA GTT CTC CTC CTG ATC 113

Met Lys Lys Val Leu Leu Ile
-15 -10

ACA GCC ATC TTG GCA GTG GCT GTW GGT TTC CCA GTC TCT CAA GAC CAG 161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
-5 1 5

GAA CGA GAA AAA AGA AGT ATC AGT GAC AGC GAT GAA TTA GCT TCA GGR 209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
10 15 20

WTT TTT GTG TTC CCT TAC CCA TAT CCA TTT CGC CCA CTT CCA CCA ATT 257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
25 30 35

CCA TTT CCA AGA TTT CCA TGG TTT AGA CGT AAN TTT CCT ATT CCA ATA 305
Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Xaa Phe Pro Ile Pro Ile
40 45 50 55

CCT GAA TCT GCC CCT ACA ACT CCC CTT CCT AGC GAA AAG TAAACAARAA 354
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
60 65

GGAAAAGTCA CRATAAACCT GGTCACCTGA AATTGAAATT GAGCCACTTC CTTGAARAAT 414

CAAAATTCCT GTTAATAAAA RAAAAACAAA TGTAATTGAA ATAGCACACA GCATTCTCTA 474

GTCAATATCT TTAGTGATCT TCTTTAATAA ACATGAAAGC AAAAAAAAAA AA 526

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..17
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.2
seq LLLITAILAVAVG/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
1 5 10 15
Gly

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 822 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 260..464
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 96
region 153..357
id H57434
est
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 118..184
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98
region 98..164
id H57434
est
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 56..113
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98
region 35..92
id H57434
est
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 454..485
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 100
region 348..379
id H57434
est
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 118..545
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98
region 1..428
id N27248
est
- (ix) FEATURE:
 - (A) NAME/KEY: other

(B) LOCATION: 65..369
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 41..345
id H94779
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 61..399
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 6..344
id H09880
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 408..458
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 355..405
id H09880
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..399
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 56..395
id H29351
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 393..432
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 391..430
id H29351
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 346..408
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq SFLPSALVIWTS/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ACTCCTTTTA GCATAGGGGC TTCGGCGCCA GCGGCCAGCG CTAGTCGGTC TGGTAAGTGC	60
CTGATGCCGA GTTCCGTCTC TCGCGTCTTT TCCTGGTCCC AGGCAAAGCG GASGNAGATC	120
CTCAAACGGC CTAGTGCTTC GCGCTTCCGG AGAAAATCAG CCGTCTAATT AATTCCTCTG	180
GTTTGTGAA GCAGTTACCA AGAATCTTCA ACCCTTTCCC ACAAAGCTA ATTGAGTACA	240

```

CGTTCCTGTT GAGTACACGT TCCTGTIGAT TTACAAAAGG TGCAGGTATG AGCAGGTCTG      300
AAGACTAACA TTTTGTGAAG TTGTAAAACA GAAAACCTGT TAGAA ATG TGG TGG TTT      357
                                     Met Trp Trp Phe
                                     -20

CAG CAA GGC CTC AGT TTC CTT CCT TCA GCC CTT GTA ATT TGG ACA TCT      405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
      -15                      -10                      -5

GCT GCT TTC ATA TTT TCA TAC ATT ACT GCA GTA ACA CTC CAC CAT ATA      453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
      1                      5                      10                      15

GAC CCG GCT TTA CCT TAT ATC AGT GAC ACT GGT ACA GTA GCT CCA RAA      501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Xaa
      20                      25                      30

AAA TGC TTA TTT GGG GCA ATG CTA AAT ATT GCG GCA GTT TTA TGT CAA      549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln
      35                      40                      45

AAA TAGAAATCAG GAARATAATT CAACTTAAAG AAKTTCATTT CATGACCAA      602
Lys

CTCTTCARAA ACATGTCTTT ACAAGCATAT CTCTTGATT GCTTTCTACA CTGTGAATT      662
GTCTGGCAAT ATTTCTGCAG TGGAAAATTT GATTARMTA GTTCTTGACT GATAAATATG      722
GTAAGGTGGG CTTTTCCCCC TGTGTAATTG GCTACTATGT CTTACTGAGC CAAGTTGTAW      782
TTTGAAATAA AATGATATGA GAGTGACACA AAAAAAAAAA      822

```

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..21
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq SFLPSALVIWISA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```

Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
 1              5              10              15

```


Ile Trp Thr Ser Ala
20

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(103..398)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..296
id AA442893
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 185..295
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LSYASSALSPCLT/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

ATCACCTTCT TCTCCATCCT TSTCTGGGCC AGTCCCCARC CCAGTCCCTC TCCTGACCTG      60
CCCAGCCCCAA GTCAGCCTTC AGCAGCGGCT TTTCTGCACA CAGATATTCC AGGCCTACCT      120
GGCATTCCAG GACCTCCGMA ATGATGCTCC AGTCCCTTAC AAGCGCTTCC TGGATGAGGG      180
TGGC ATG GTG CTG ACC ACC CTC CCC TTG CCC TCT GCC AAC AGC CCT GTG      229
Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
      -35          -30          -25

AAC ATG CCC ACC ACT GGC CCC AAC AGC CTG AGT TAT GCT AGC TCT GCC      277
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
      -20          -15          -10

CTG TCC CCC TGT CTG ACC GCT CCA AAK TCC CCC CGG CTT GCT ATG ATG      325
Leu Ser Pro Cys Leu Thr Ala Pro Xaa Ser Pro Arg Leu Ala Met Met
      -5          1          5          10

CCT GAC AAC TAAATATCCT TATCCAAATC AATAAARWRA RAATCCTCCC TCCARAAGGG      384
Pro Asp Asn

TTTCTAAAAA CAAAAAAAAA A      405

```

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..37
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LSYASSALSPCLT/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```

Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val Asn
 1             5             10             15
Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu
          20             25             30
Ser Pro Cys Leu Thr
          35

```

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 149..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..183
id AA397994
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 328..485
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 179..336
 id AA397994
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(182..496)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 14..328
 id AA399680
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 196..240
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.5
 seq ILSTVTALTFAA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

AAAAAATTGG TCCCAGTTTT CACCCTGCCG CAGGGCTGGC TGGGGAGGGC AGCGGTTTAG	60
ATTAGCCGTG GCCTAGGCCG TTAAACGGGG TGACACGAGC NTGCAGGGCC GAGTCCAAGG	120
CCCGGAGATA GGACCAACCG TCAGGAATGC GAGGAATGTT TTTCTTCGGA CTCTATCGAG	180
GCACACAGAC AGACC ATG GGG ATT CTG TCT ACA GTG ACA GCC TTA ACA TTT	231
Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe	
-15 -10 -5	
GCC ARA GCC CTG GAC GGC TGC AGA AAT GGC ATT GCC CAC CCT GCA AGT	279
Ala Xaa Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser	
1 5 10	
GAG AAG CAC AGA CTC GAG AAA TGT AGG GAA CTC GAG ASC ASC CAC TCG	327
Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Xaa Xaa His Ser	
15 20 25	
GCC CCA GGA TCA ACC CAS CAC CGA AGA AAA ACA ACC AGA AGA AAT TAT	375
Ala Pro Gly Ser Thr Xaa His Arg Arg Lys Thr Thr Arg Arg Asn Tyr	
30 35 40 45	
TCT TCA GCC TGAAATGAAK CCGGGATCAA ATGGTTGCTG ATCARAGCCC ATATTTAAAT	434
Ser Ser Ala	
TGGAAAAGTC AAATTGASCA TTATTAAATA AAGCTTGTTT AATATGTCTC AAACAAAAAA	494
AA	496

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..15
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq ILSTVTALTFAXA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```
Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Xaa Ala
  1             5             10             15
```

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 49..96
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.1
seq LVLTLCTLPLAVA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```
AAAGATCCCT GCAGCCCGGC AGGAGAGAAG GCTGAGCCTT CTGGCGTC ATG GAG AGG      57
                                     Met Glu Arg
                                     -15

CTC GTC CTA ACC CTG TGC ACC CTC CCG CTG GCT GTG GCG TCT GCT GGC      105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
-10             -5             1

TGC GCC ACG ACG CCA GCT CGC AAC CTG AGC TGC TAC CAG TGC TTC AAG      153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
  5             10             15

GTC AGC AGC TGG ACG GAG TGC CCG CCC ACC TGG TGC AGC CCG CTG GAC      201
```

Val	Ser	Ser	Trp	Thr	Glu	Cys	Pro	Pro	Thr	Trp	Cys	Ser	Pro	Leu	Asp	
20					25					30					35	
CAA	GTC	TGC	ATC	TCC	AAC	GAG	GTG	GTC	GTC	TCT	TTT	AAA	TGG	AGT	GTA	249
Gln	Val	Cys	Ile	Ser	Asn	Glu	Val	Val	Val	Ser	Phe	Lys	Trp	Ser	Val	
				40					45					50		
CGC	GTC	CTG	CTC	AGC	AAA	CGC	TGT	GCT	CCC	AGA	TGT	CCC	AAC	GAC	AAC	297
Arg	Val	Leu	Leu	Ser	Lys	Arg	Cys	Ala	Pro	Arg	Cys	Pro	Asn	Asp	Asn	
			55					60					65			
ATG	AAK	TTC	GAA	TGG	TCG	CCG	GCC	CCC	ATG	GTG	CAA	GGC	GTG	ATC	ACC	345
Met	Xaa	Phe	Glu	Trp	Ser	Pro	Ala	Pro	Met	Val	Gln	Gly	Val	Ile	Thr	
	70						75					80				
AGG	CGC	TGC	TGT	TCC	TGG	GCT	CTC	TGC	AAC	AGG	GCA	CTG	ACC	CCA	CAG	393
Arg	Arg	Cys	Cys	Ser	Trp	Ala	Leu	Cys	Asn	Arg	Ala	Leu	Thr	Pro	Gln	
	85					90					95					
GAG	GGG	CGC	TGG	GCC	CTG	CRA	GGG	GGG	CTC	CTG	CTC	CAG	GAC	CCT	TCG	441
Glu	Gly	Arg	Trp	Ala	Leu	Xaa	Gly	Gly	Leu	Leu	Gln	Asp	Pro	Pro	Ser	
100					105				110						115	
AGG	GGC	ARA	AAA	ACC	TGG	GTG	CGG	CCA	CAG	CTG	GGG	CTC	CCA	CTC	TGC	489
Arg	Gly	Xaa	Lys	Thr	Trp	Val	Arg	Pro	Gln	Leu	Gly	Leu	Pro	Leu	Cys	
				120				125						130		
CTT	CCC	AWT	TCC	AAC	CCC	CTC	TGC	CCA	RGG	GAA	ACC	CAG	GAA	GGA		534
Leu	Pro	Xaa	Ser	Asn	Pro	Leu	Cys	Pro	Xaa	Glu	Thr	Gln	Glu	Gly		
			135					140					145			
TAACACTGTG	GGTGCCCCCA	CCTGTGCA	TT	GGGACCACRA	CTTCACCCTC	TTGGARACAA										594
TAAACTCTCA	TGCCCCCAAA	AAAAAAAAA														623

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..16
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.1
seq LVLTLCPLAVA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met	Glu	Arg	Leu	Val	Leu	Thr	Leu	Cys	Thr	Leu	Pro	Leu	Ala	Val	Ala
1				5				10						15	

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 32..73
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7
seq LWLLFFLVTAIHA/EL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

AACTTTGCCT TGTGTTTTCC ACCCTGAAAG A ATG TTG TGG CTG CTC TTT TTT CTG      55
                               Met Leu Trp Leu Leu Phe Phe Leu
                               -10

GTG ACT GCC ATT CAT GCT GAA CTC TGT CAA CCA GGT GCA GAA AAT GCT      103
Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn Ala
-5                               1                               5                               10

TTT AAA GTG AGA CTT AGT ATC AGA ACA GCT CTG GGA GAT AAA GCA TAT      151
Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala Tyr
                               15                               20                               25

GCC TGG GAT ACC AAT GAA GAA TAC CTC TTC AAA GCG ATG GTA GCT TTC      199
Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala Phe
                               30                               35                               40

TCC ATG AGA AAA GTT CCC AAC AGA GAA GCA ACA GAA ATT TCC CAT GTC      247
Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His Val
                               45                               50                               55

CTA CTT TGC AAT GTA ACC CAG AGG GTA TCA TTC TGG TTT GTG GTT ACA      295
Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val Thr
                               60                               65                               70

GAC CCT TCA AAA AAT CAC ACC CTT CCT GCT GTT GAG GTG CAA TCA GCC      343
Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser Ala
75                               80                               85                               90

ATA AGA ATG AAC AAG AAC CGG ATC AAC AAT GCC TTC TTT CTA AAT GAC      391
Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn Asp
                               95                               100                               105

CAA ACT CTG GAA TTT TTA AAA ATC CCT TCC ACA CTT GCA CCA CCC ATG      439

```

Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro Met	
110 115 120	
GAC CCA TCT GTG CCC ATC TGG ATT ATT ATA TTT GGT GTG ATA TTT TGC	487
Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe Cys	
125 130 135	
ATC ATC ATA GTT GCA ATT GCA CTA CTG ATT TTA TCA GGG ATC TGG CAA	535
Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp Gln	
140 145 150	
CGT ADA ARA AAG AAC AAA GAA CCA TCT GAA GTG GAT GAC GCT GAA RAT	583
Arg Xaa Xaa Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu Xaa	
155 160 165 170	
AAK TGT GAA AAC ATG ATC ACA ATT GAA AAT GGC ATC CCC TCT GAT CCC	631
Xaa Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp Pro	
175 180 185	
CTG GAC ATG AAG GGA GGG CAT ATT AAT GAT GCC TTC ATG ACA GAG GAT	679
Leu Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu Asp	
190 195 200	
GAG AGG CTC ACC CCT CTC TGAAGGCTG TTGTTCTGCT TCCTCAARAA	727
Glu Arg Leu Thr Pro Leu	
205	
ATTAAACATT TGTTTCTGTG TGA CTGCTGA GCATCCTGAA ATACCAAGAG CAGATCATAT	787
WTTTGTGTTT ACCATTCTTC TTTTGTAATA AATTTTGAAT GTGCTTGAAA AAAAAAAAAA	847
C	848

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..14
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7
seq LWLLFFLVTAIHA/EL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met	Leu	Trp	Leu	Leu	Phe	Phe	Leu	Val	Thr	Ala	Ile	His	Ala
1				5					10				

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GGGAAGATGG AGATAGTATT GCCTG

25

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CTGCCATGTA CATGATAGAG AGATTC

26

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 1..517

(ix) FEATURE:

- (A) NAME/KEY: transcription start site
- (B) LOCATION: 518.

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 17..25
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name CMYB_01
score 0.983
sequence TGTCAGTTG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(18..27)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name MYOD_Q6
score 0.961
sequence CCCAACTGAC

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(75..85)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name S8_01
score 0.960
sequence AATAGAATTAG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 94..104
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name S8_01
score 0.966
sequence AACTAAATTAG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(129..139)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name DELTAEF1_01
score 0.960
sequence GCACACCTCAG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(155..165)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name GATA_C
score 0.964
sequence AGATAAATCCA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 170..178
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name CMYB_01
score 0.958
sequence CTTCAGTTG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 176..189
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name GATA1_02
score 0.959
sequence TTGTAGATAGGACA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 180..190
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name GATA_C

score 0.953
sequence AGATAGGACAT

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 284..299
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name TAL1ALPHA47_01
score 0.973
sequence CATAACAGATGGTAAG

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 284..299
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name TAL1BETAE47_01
score 0.983
sequence CATAACAGATGGTAAG

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 284..299
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name TAL1BETAITF2_01
score 0.978
sequence CATAACAGATGGTAAG

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(287..296)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MYOD_Q6
score 0.954
sequence ACCATCTGTT

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(302..314)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name GATA1_04
score 0.953
sequence TCAAGATAAAGTA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 393..405
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name IK1_01
score 0.963
sequence AGTTGGGAATTCC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 393..404
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name IK2_01
score 0.985
sequence AGTTGGGAATTC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site

(B) LOCATION: 396..405
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name CREL_01
score 0.962
sequence TGGGAATTCC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 423..436
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name GATA1_02
score 0.950
sequence TCAGTGATATGGCA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(478..489)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name SRY_02
score 0.951
sequence TAAACAAAACA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 486..493
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name E2F_02
score 0.957
sequence TTAGCGC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(514..521)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MZF1_01
score 0.975
sequence TGAGGGGA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```
TGAGTGCAGT GTTACATGTC AGTTGGGTTA AGTTTGTTAA TGTCAATCAA ATCTTCTATG   60
TCTTGATTG CCTGCTAATT CTATTATTC TGGAACTAAA TTAGTTTGAT GGTTCIATTA  120
GTTATTGACT GAGGTGTGCT AATCTCCCAT TATGTGGATT TATCTATTC TTCAGTTGTA  180
GATAGGACAT TGATAGATAC ATAAGTACCA GGACAAAAGC AGGGAGATCT TTTTCCAAA  240
ATCAGGAGAA AAAAATGACA TCTGGAAAAC CTATAGGGAA AGGCATAACA GATGGTAAGG  300
ATACTTTATC TTGAGTAGGA GAGCCTTCCT GTGGCAACGT GGAGAAGGGA AGAGGTCGTA  360
GAATTGAGGA GTCAGCTCAG TTAGAAGCAG GGAGTTGGGA ATTCGGTTCA TGTGATTAG  420
CATCAGTGAT ATGGCAAATG TGGGACTAAG GGTAGTGATC AGAGGGTTAA AATTGTGTGT  480
TTTGTTTTAG CGCTGCTGGG GCATCGCCTT GGSTCCCCTC AAACAGATTC CCATGAATCT  540
CTTCAT                                     546
```

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GTACCAGGGA CTGTGACCAT TGC

23

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTGTGACCAT TGCTCCAAG AGAG

24

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 861 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 1..806

(ix) FEATURE:

- (A) NAME/KEY: transcription start site
- (B) LOCATION: 807

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(60..70)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name NFY_Q6
score 0.956
sequence GGACCAATCAT

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 70..77
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name MZF1_01
score 0.962
sequence CCTGGGGA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 124..132
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name CMYB_01
score 0.994
sequence TGACCGTTG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(126..134)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name VMYB_02
score 0.985
sequence TCCAACGCT

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 135..143
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name STAT_01
score 0.968
sequence TTCCTGGAA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(135..143)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name STAT_01
score 0.951
sequence TTCCAGGAA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(252..259)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name MZF1_01
score 0.956
sequence TTGGGGGA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 357..363
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name IK2_01
score 0.965
sequence GAATGGGATTTC

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 384..391
- (C) IDENTIFICATION METHOD: matinspector prediction

- (D) OTHER INFORMATION: name MZF1_01
score 0.986
sequence AGAGGGGA
- (ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(410..421)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name SRY_02
score 0.955
sequence GAAACAAAACA
- (ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 592..599
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MZF1_01
score 0.960
sequence GAAGGGGA
- (ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 618..627
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MYOD_Q6
score 0.981
sequence AGCATCTGCC
- (ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 632..642
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name DELTAEF1_01
score 0.958
sequence TCCCACCTTCC
- (ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(813..823)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name S8_01
score 0.992
sequence GAGGCAATTAT
- (ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(824..831)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MZF1_01
score 0.986
sequence AGAGGGGA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```
TACTATAGGG CACGCGTGGT CGACGGCCGG GCTGTTCTGG AGCAGAGGGC ATGTCAGTAA   60
TGATTGGTCC CTGGGGAAGG TCTGGCTGGC TCCAGCACAG TGAGGCATTT AGGTATCTCT   120
CGGTGACCGT TGGATTCCTG GAAGCAGTAG CTGTTCTGTT TGGATCTGGT AGGGACAGGG   180
```

CTCAGAGGGC TAGGCACGAG GGAAGGTCAG AGGAGAAGGS AGGSARGGCC CAGTGAGARG 240
 GGAGCATGCC TTCCCCAAC CCTGGCTTSC YCTTGGYMAM AGGGCGKTTY TGGGMACTTR 300
 AAYTCAGGGC CCAASCAGAA SCACAGGCCC AKTCNTGGCT SMAAGCACAA TAGCCTGAAT 360
 GGGATTTCAG GTTAGNCAGG GTGAGAGGGG AGGCTCTCTG GCTTAGTTTT GTTTTGT TTTT 420
 CCAAATCAAG GTAACCTGCT CCCTTCTGCT ACGGGCCTTG GTCITGGCTT GTCCTCACCC 480
 AGTCGGAACCT CCCTACCACT TTCAGGAGAG TGGTTTTAGG CCCGTGGGGC TGTCTGTTC 540
 CAAGCAGTGT GAGAACATGG CTGGTAGAGG CTCTAGCTGT GTGCGGGGCC TGAAGGGGAG 600
 TGGGTTCTCG CCCAAAGAGC ATCTGCCCAT TTCCACCTT CCCTTCTCCC ACCAGAAGCT 660
 TGCCTGAGCT GTTTGGACAA AAATCCAAAC CCCACTTGGC TACTCTGGCC TGGCTTCAGC 720
 TTGGAACCCA ATACCTAGGC TTACAGGCCA TCCTGAGCCA GGGGCCTCTG GAAATTCTCT 780
 TCCTGATGGT CCTTTAGGTT TGGGCACAAA ATATAATTGC CTCTCCCTC TCCCATTTTC 840
 TCTCTTGGGA GCAATGGTCA C 861

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CTGGGATGGA AGGCACGGTA

20

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GAGACCACAC AGCTAGACAA

20

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 555 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
 - (A) NAME/KEY: promoter
 - (B) LOCATION: 1..500
- (ix) FEATURE:
 - (A) NAME/KEY: transcription start site
 - (B) LOCATION: 501
- (ix) FEATURE:
 - (A) NAME/KEY: TF binding-site
 - (B) LOCATION: 191..206
 - (C) IDENTIFICATION METHOD: matinspector prediction
 - (D) OTHER INFORMATION: name ARNT_01
score 0.964
sequence GGACTCACGTGCTGCT
- (ix) FEATURE:
 - (A) NAME/KEY: TF binding-site
 - (B) LOCATION: 193..204
 - (C) IDENTIFICATION METHOD: matinspector prediction
 - (D) OTHER INFORMATION: name NMYC_01
score 0.965
sequence ACTCACGTGCTG
- (ix) FEATURE:
 - (A) NAME/KEY: TF binding-site
 - (B) LOCATION: 193..204
 - (C) IDENTIFICATION METHOD: matinspector prediction
 - (D) OTHER INFORMATION: name USF_01
score 0.985
sequence ACTCACGTGCTG
- (ix) FEATURE:
 - (A) NAME/KEY: TF binding-site
 - (B) LOCATION: complement(193..204)
 - (C) IDENTIFICATION METHOD: matinspector prediction
 - (D) OTHER INFORMATION: name USF_01
score 0.985
sequence CAGCACGTGAGT
- (ix) FEATURE:
 - (A) NAME/KEY: TF binding-site
 - (B) LOCATION: complement(193..204)
 - (C) IDENTIFICATION METHOD: matinspector prediction
 - (D) OTHER INFORMATION: name NMYC_01
score 0.956
sequence CAGCACGTGAGT
- (ix) FEATURE:
 - (A) NAME/KEY: TF binding-site
 - (B) LOCATION: complement(193..204)
 - (C) IDENTIFICATION METHOD: matinspector prediction

(D) OTHER INFORMATION: name MYCMAX_02
score 0.972
sequence CAGCACGTGAGT

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 195..202
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name USF_C
score 0.997
sequence TCACGTGC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(195..202)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name USF_C
score 0.991
sequence GCACGTGA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(210..217)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MZF1_01
score 0.963
sequence CATGGGGA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 397..410
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name ELK1_02
score 0.963
sequence CTCTCCGGAAGCCT

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 400..409
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name CETS1P54_01
score 0.974
sequence TCCGGAAGCC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(460..470)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name AP1_Q4
score 0.963
sequence AGTGACTGAAC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(460..470)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name AP1FJ_Q2
score 0.961
sequence AGTGACTGAAC

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 547..555
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name PADS_C
score 1.000
sequence TGIGGTCTC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```

CTATAGGGCA CGCKTGGTCG ACGGCCCCGGG CTGGTCTGGT CTGKTGTGGA GTCGGGTTGA    60
AGGACAGCAT TTGKACATC TGGTCTACTG CACCTTCCCT CTGCCGTGCA CTTGGCCTTT    120
KAWAAGCTCA GCACCGGTGC CCATCACAGG GCCGGCAGCA CACACATCCC ATTACTCAGA    180
AGGAAGTGAC GGAAGTACGT GCTGCTCCGT CCCCATGAGC TCAGTGGACC TGTCTATGTA    240
GAGCAGTCAG ACAGTGCCTG GGATAGAGTG AGAGTTCAGC CAGTAAATCC AAGTGATTGT    300
CATTCCTGTC TGCATTAGTA ACTCCCAACC TAGATGTGAA AACTTAGTTC TTTCTCATAG    360
GTTGCTCTGC CCATGGTCCC ACTGCAGACC CAGGCACTCT CCGGAAGCCT GGAAATCACC    420
CGTGTCTTCT GCCTGTCTCC GCTCACATCC CACACTTGTG TTCAGTCACT GAGTTACAGA    480
TTTTGCCTCC TCAATTTCTC TTGTCTTAGT CCCATCCTCT GTTCCCTGG CCAGTTTGTC    540
TAGCTGTGTG GTCTC                                         555

```

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 63..122
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 15.8
seq LLLLLLLRHGAQG/KP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

AACATTGGCG GGAACRSAGA GCGGANSNG NGACAGCGGA GGAVSTGGAT AACAGGGGAC    60
CG ATG ATG TGG CGA CCA TCA GTT CTG CTG CTT CTG TTG CTA CTG AGG    107
Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg
-20                      -15                      -10

```

CAC GGG GCC CAG GGG AAG CCA TCC CCA GAC GCA
 His Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala
 -5 1 5

140

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 285..359
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 14
seq LAMLALLSPLSLA/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

ACTAGTAAA AGTAAGTGGG AAAAGAGTAA ACGCGCGACT CCAGCGCGCG GCTACCTACG 60
 CTTGGTGCTT GCTTTCTCCA GCCATCGGAG ACCAGAGCCG CCCCTCTGC TCGAGAAAGG 120
 GGCTCAGCGG CGGCGGAAGC GGAGGGGGAC CACCGTGGAG AGCGCGGTCC CAGCCCGGCC 180
 ACTGCGGATC CCTGNAACCA AAAAGCTCCT GCTGCTTCTG TACCCCGCCT GTCCCTCCCA 240
 GCTGCGCAGG GCCCCTTCGT GGGATCATCA GCCCGAAGAC AGGG ATG GAG AGG CCT 296
 Met Glu Arg Pro
 -25
 CTG TGC TCC CAC CTC TGC AGC TGC CTG GCT ATG CTG GCC CTC CTG TCC 344
 Leu Cys Ser His Leu Cys Ser Cys Leu Ala Met Leu Ala Leu Leu Ser
 -20 -15 -10
 CCC CTG AGC CTG GCA CAG TAT GAC AGC TGG CCC CAD KAM CCC GAG TAC 392
 Pro Leu Ser Leu Ala Gln Tyr Asp Ser Trp Pro Xaa Xaa Pro Glu Tyr
 -5 1 5 10
 TTC CAG CAA CCG 404
 Phe Gln Gln Pro
 15

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 67..120
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 12.3
 seq HILFLLLLPVAAA/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```

AACAGTTCCT CTGGACTTCT CTGGACCACA GTCCTCTGCC AGACCCCTGC CAGACCCAG      60
TCCACC ATG ATC CAT CTG GGT CAC ATC CTC TTC CTG CTT TTG CTC CCA      108
Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro
          -15                      -10                      -5
GTG GCT GCA GCT CAG ACG ACT CCA GGA GAG AGA TCA TCA CTC CCT GCC      156
Val Ala Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala
          1                      5                      10
TTT TAC CCT GGC ACT TCA GGC TCT TGT TCC GGA TGT GGG TCC CTC TCT      204
Phe Tyr Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser
          15                      20                      25
CTG CCG CTC CTG GCA GGC CTC GTG GCT      231
Leu Pro Leu Leu Ala Gly Leu Val Ala
          30                      35

```

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 base pairs.
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 69..134
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 12.2

seq LALALGLAQPASA/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```

ATTCTCCAT CCTCAGTCTT TGCAAGGCCA CAGCTGTGCC AGCCGGGCTC TGGCAGGCTC   60
CTGGCAGC ATG GCA GTG AAG CTT GGG ACC CTC CTG CTG GCC CTT GCC CTG   110
      Met Ala Val Lys Leu Gly Thr Leu Leu Leu Ala Leu Ala Leu
        -20                -15                -10

GGC CTG GCC CAG CCA GCC TCT GCC CGC CGG AAG CTG CTG GTG TTT CTG   158
Gly Leu Ala Gln Pro Ala Ser Ala Arg Arg Lys Leu Leu Val Phe Leu
        -5                1                5

CTG                                     161
Leu

```

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 63..122
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.9
seq LVLEFLLSPVEA/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```

AAAAAACCTG TGGACGCCGA CCCGGGACCG CCGCTGGCTG GCTGCTGGCT CACTCGACCG   60
TC ATG GAG ACC CTG GGG GCC CTT CTG GTG CTG GAG TTT CTG CTC CTC   107
      Met Glu Thr Leu Gly Ala Leu Leu Val Leu Glu Phe Leu Leu Leu
        -20                -15                -10

TCC CCG GTG GAG GCC CAG CAG GCC ACG GAG CAT CGC CTG AAG CCG TGG   155
Ser Pro Val Glu Ala Gln Gln Ala Thr Glu His Arg Leu Lys Pro Trp
        -5                1                5                10

CTG GTG GGC CTG GCT GCG GTA GTC GGC TTC CTG TTC ATC GTC TAT TTG   203
Leu Val Gly Leu Ala Ala Val Val Gly Phe Leu Phe Ile Val Tyr Leu
        15                20                25

GTC TTC CTG GCC AAC CGC CTC TGG TGT TCC AAG GCC AGG GCT GAG GAC   251
Val Leu Leu Ala Asn Arg Leu Trp Cys Ser Lys Ala Arg Ala Glu Asp
        30                35                40

```

GAG GAG GAG ACC ACG TTC AGA ATG GAG TCC GGG
 Glu Glu Glu Thr Thr Phe Arg Met Glu Ser Gly
 45 50

284

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 63..110
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.3
seq PLLSSLLGGSQA/MD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

AACTCACAGC ACGACCAGAG AACAGGCCTG TCTCAGGCAG GCCCTGCGCC TCCTATGCGG	60
AG ATG CTA CTG CCA CTG CTG CTG TCM TCG CTG CTG GGC GGG TCC CAG	107
Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln	
-15 -10 -5	
GCT ATG GAT GGG AGA TTC TGG ATA CGA GTG CAG GAG TCA GTG ATG GTG	155
Ala Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val	
1 5 10 15	
CCG GAG GGC CTG TGC ATC TCT GTN KCC CTG CTC TTT CTC CTA CCC CCG	203
Pro Glu Gly Leu Cys Ile Ser Val Xaa Leu Leu Phe Leu Leu Pro Pro	
20 25 30	
ACA AGA CTG GAC AGG GTC TAC CCC AGC CGG	233
Thr Arg Leu Asp Arg Val Tyr Pro Ser Arg	
35 40	

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 32..73
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 10.7
 seq LWLLFFLVTAIHA/EL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

AACTTTGCCT TGTGTTTCC ACCCTGAAAG A ATG TTG TGG CTG CTC TTT TTT      52
                               Met Leu Trp Leu Leu Phe Phe
                               -10

CTG GTG ACT GCC ATT CAT GCT GAA CTC TGT CAA CCA GGT GCA GAA AAT      100
Leu Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn
      -5                      1                      5

GCT TTT AAA GTG AGA CTT AGT ATC AGA ACA GCT CTG GGA GAT AAA GCA      148
Ala Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala
      10                      15                      20                      25

TAT GCC TGG GAT ACC AAT GAA GAA TAC CTC TTC AAA GCG ATG GTA GCT      196
Tyr Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala
                      30                      35                      40

TTC TCC ATG AGA AAA GTT CCC AAC AGA GAA GCA ACA GAA ATT TCC CAT      244
Phe Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His
                      45                      50                      55

GTC CTA CTT TGC AAT GTA ACC CAG AGG GTA TCA TTC TGG TTT GTG GTT      292
Val Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val
                      60                      65                      70

ACA GAC CCT TCA AAA AAT CAC ACC CTT CCT GCT GTT GAG GTG CAA TCA      340
Thr Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser
                      75                      80                      85

GCC ATA AGA ATG AAC AAG AAC CGG ATC AAC AAT GCC TTC TTT CTA AAT      388
Ala Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn
                      90                      95                      100                      105

GAC CAA ACT CTG GAA TTT TTA AAA ATC CCT TCC ACA CTT GCA CCA ACC      436
Asp Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Thr
                      110                      115                      120

CGG                                                                439
Arg

```

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 base pairs

(B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 20..100
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 10.7
 seq LPLLCLFLQGATA/VL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

AGAGATCGCA GCCCAACCC ATG GCC GGG TCT CCT AGC CGC GCC GCG GGC CGG      52
           Met Ala Gly Ser Pro Ser Arg Ala Ala Gly Arg
                   -25                               -20

CGA CTG CAG CTT CCC CTG CTG TGC CTC TTC CTC CAG GGC GCC ACT GCC      100
Arg Leu Gln Leu Pro Leu Leu Cys Leu Phe Leu Gln Gly Ala Thr Ala
   -15                   -10                               -5

GTC CTC TTT GCT GTC TTT GTC CGC TAC AAC CAC AAA ACC GAC GCT GCC      148
Val Leu Phe Ala Val Phe Val Arg Tyr Asn His Lys Thr Asp Ala Ala
   1                   5                               10                               15

CTC TGG CAM CGG AAG CTT GGG
Leu Trp Xaa Arg Lys Leu Gly
                   20
  
```

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 40..156
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 10.6
 seq ALALLLVLP LLWP/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:


```

ACTGCCCTGC CCTGGCCTGA CCCAGGCCT ACTGAGTCC ATG AAA TGG CCC TGG      54
                               Met Lys Trp Pro Trp
                               -35

ACC TGC CTT GCC ATC CTC TGT CCT GGC CCT GTA TTG TCC CCA CCA TGC      102
Thr Cys Leu Ala Ile Leu Cys Pro Gly Pro Val Leu Ser Pro Pro Cys
                               -30                -25                -20

TCT GGT CCA RCG CTT GCC CTA GCC CTG TTG CTA GTC CTG CCA CTG CTA      150
Ser Gly Pro Xaa Leu Ala Leu Ala Leu Leu Leu Val Leu Pro Leu Leu
                               -15                -10                -5

TGG CCC TGC TCT GTT TTT GGC CAT GCC CTG TGC TAM CCT AGC CCT GCC      198
Trp Pro Cys Ser Val Phe Gly His Ala Leu Cys Xaa Pro Ser Pro Ala
                               1                5                10

CGA AGG                                                                204
Arg Arg
15

```

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 28..96
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10
seq PLLGLLLSLPAGA/DV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```

AACCGAGCTG GATTGTATG TTGCACC ATG CCT TCT TGG ATC GGG GCT GTG ATT      54
                               Met Pro Ser Trp Ile Gly Ala Val Ile
                               -20                -15

CTT CCC CTC TTG GGG CTG CTG CTC TCC CTC CCC GCC GGG GCG GAT GTG      102
Leu Pro Leu Leu Gly Leu Leu Leu Ser Leu Pro Ala Gly Ala Asp Val
                               -10                -5                1

AAG GCT CGG AGC TGC GGA GAG GTC CGC CAG GCG TAC GGT GCC AAG GGA      150
Lys Ala Arg Ser Cys Gly Glu Val Arg Gln Ala Tyr Gly Ala Lys Gly
                               5                10                15

```

[illegible]

CTT CTT CCT CCC AGC TTG CTG AGC TTG CTG
 Leu Leu Pro Pro Ser Leu Leu Ser Leu Leu
 15 20

242

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 122..223
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.6
seq LLLFSLLVSPPTC/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

AAAACTCTT TCTTCGGCTC GCGAGCTGAG AGGAGCAGGT AGAGGGGCAG AGGCGGGACT 60
 GTCGTCTGGG GGAGCCGCCC AGGAGGCTCC TCAGGCCGAC CCCAGACCCT GGCTGGCCAG 120
 G ATG AAG TAT CTC CGG CAC CGG CGG CCC AAT GCC ACC CTC ATT CTG GCC 169
 Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala
 -30 -25 -20
 ATC GGC GCT TTC ACC CTC CTC CTC TTC AGT CTG CTA GTG TCA CCA CCC 217
 Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro
 -15 -10 -5
 ACC TGC AAG GTC CAG GAG CAG CCA CCG GCG ATC CCC GAG GCC CTG GCC 265
 Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala
 1 5 10
 TGG CHC ACT CCA CCT ACC CGA TGG 289
 Trp Xaa Thr Pro Pro Thr Arg Trp
 15 20

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (E) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 26..130
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5
seq AMWWLLLWGVQLQA/WP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```

GCAGGTCCCA GATGTCCAGT TCCAG ATG CCT GGA CCC AGA GTG TGG GGG AAA      52
                               Met Pro Gly Pro Arg Val Trp Gly Lys
                               -35                               -30

TAT CTC TGG AGA AGC CCT CAC TCC AAA GGC TGT CCA GGC GCA ATG TGG      100
Tyr Leu Trp Arg Ser Pro His Ser Lys Gly Cys Pro Gly Ala Met Trp
-25                               -20                               -15

TGG CTG CTT CTC TGG GGA GTC CTC CAG GCT TGG CCA AMC CCG GGG CTC      148
Trp Leu Leu Leu Trp Gly Val Leu Gln Ala Trp Pro Xaa Pro Gly Leu
-10                               -5                               1                               5

CGT CCT CTT GGC CCA AGA GCT ACC CCA GCA GCT GAC ATC CCC CGG GTA      196
Arg Pro Leu Gly Pro Arg Ala Thr Pro Ala Ala Asp Ile Pro Arg Val
                               10                               15                               20

CCC AGA GCC GTA TGG CAA AGG CCA AGA GAG CAG CAC GGA CAT CAA GGC      244
Pro Arg Ala Val Trp Gln Arg Pro Arg Glu Gln His Gly His Gln Gly
                               25                               30                               35

TCC AGA GGG CTT TGC TGT GAG GCT CGT CTT CCA GGA CTT CGA CCT GGA      292
Ser Arg Gly Leu Cys Cys Glu Ala Arg Leu Pro Gly Leu Arg Pro Gly
                               40                               45                               50

GCC GTC CCA GGA CTG TGC AGG GGA CTC TRW BAC AAT CTC ATT CGT CGG      340
Ala Val Pro Gly Leu Cys Arg Gly Leu Xaa Xaa Asn Leu Ile Arg Arg
                               55                               60                               65                               70

TTC GGA TCC AAG CCA GTT CTG TGG TCA GCA AGG CTC CCC TCT GGG CAG      388
Phe Gly Ser Lys Pro Val Leu Trp Ser Ala Arg Leu Pro Ser Gly Gln
                               75                               80                               85

GCC CCC TGG TCA GAG GGA                                          406
Ala Pro Trp Ser Glu Gly
                               90

```

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 62..172

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.2
seq LLAVLLASWRLWA/IK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```

AACTGGTGCG GCCGAGTGAC AGTTGACCGG TTTTAACCAA GTGACTGGTT CTAGCCACGT    60
T ATG TGC GGC CCA GCC ATG TTC CCT GCC GGT CCT CCG TGG CCC AGA GTC    109
  Met Cys Gly Pro Ala Met Phe Pro Ala Gly Pro Pro Trp Pro Arg Val
    -35                -30                -25

CGA GTC GTG CAG GTG CTG TGG GCC CTG CTG GCA GTG CTC CTG GCG TCG    157
Arg Val Val Gln Val Leu Trp Ala Leu Leu Ala Val Leu Leu Ala Ser
  -20                -15                -10

TGG AGG CTG TGG GCG ATC AAG GAT TTC CAG GAA TGC ACC TGG CAG GTT    205
Trp Arg Leu Trp Ala Ile Lys Asp Phe Gln Glu Cys Thr Trp Gln Val
  -5                1                5                10

GTC CTG AAC GAG TTT AAG AGG GTA GGC GAG AGT GGT GTG AGC GAC AST    253
Val Leu Asn Glu Phe Lys Arg Val Gly Glu Ser Gly Val Ser Asp Xaa
    15                20                25

TCT TTG AGC AAG AGC CCG GGG    274
Ser Leu Ser Lys Ser Pro Gly
    30

```

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 71..235

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.2

seq SLLLLSTALNILA/CQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```

ACATATCTTT GCAATTGTGA ACATTCAATC ATTTTCAACA CACGTTTCATG GTTAATATTT   60
CTAGGAAACT ATG CAT AGA AGA AAA CTT CCT TTA ACC AAT AAA AGG CAA   109
      Met His Arg Arg Lys Leu Pro Leu Thr Asn Lys Arg Gln
      -55                -50                -45
CTT CAA AAA MCA TTG AGT AAA TTC ATA TTC AGT GAT GAA TTG TTT AGA   157
Leu Gln Lys Xaa Leu Ser Lys Phe Ile Phe Ser Asp Glu Leu Phe Arg
      -40                -35                -30
AAT ATT CTC TTT AGT TTA AGA ACA TTA AGG ATG ATA CTA TCA CTA CTT   205
Asn Ile Leu Phe Ser Leu Arg Thr Leu Arg Met Ile Leu Ser Leu Leu
      -25                -20                -15
CTG TTG AGC ACT GCA TTG AAT ATC TTA GCC TGC CAA ATA AAT GAA GAA   253
Leu Leu Ser Thr Ala Leu Asn Ile Leu Ala Cys Gln Ile Asn Glu Glu
      -10                -5                1                5
CTG GGG   259
Leu Gly

```

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 182..232
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3
seq VSALLMAWFGVLS/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```

AAAACGCCGG GAGCIGCGAG TGTCCAGCTG CGGAGACCCG TGATAATTCG TTAAC TAATT   60
CAACAAACGG GACCCCTCTG TGTGCCAGAA ACCGCAAGCA GTTGCTAACC CAGTGGGACA   120
GGCGGATTGG AAGAGCGGGA AGGTCCTGGC CCAGAGCAGT GTGACACTTC CCTCTGTGAC   180
C ATG AAA CTC TGG GTG TCT GCA TTG CTG ATG GCC TGG TTT GGT GTC CTC   229
  Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val Leu
      -15                -10                -5

```

AGC TGT GTG CAG GCC GAD HYG
 Ser Cys Val Gln Ala Xaa Xaa
 1 5

250

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 49..105
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.1
seq LCLVCLLVHTAFR/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

AAGAGCCTGT GCTACTGGAA GGTGGCGTGC CCTCCTCTGG CTGGTACC ATG CAG CTC	57
Met Gln Leu	
CCA CTG GCC CTG TGT CTC GTC TGC CTG CTG GTA CAC ACA GCC TTC CGT	105
Pro Leu Ala Leu Cys Leu Val Cys Leu Leu Val His Thr Ala Phe Arg	
-15 -10 -5	
GTA GTG GAG GGC CAG GGG TGG CAG GCG TTC AAG AAT GAT GCC ACG GAA	153
Val Val Glu Gly Gln Gly Trp Gln Ala Phe Lys Asn Asp Ala Thr Glu	
1 5 10 15	
ATC ATC CCC GAG CTC GGA GAG TAC CCC GAG CCT CCA CCG GAA CGG	198
Ile Ile Pro Glu Leu Gly Glu Tyr Pro Glu Pro Pro Pro Glu Arg	
20 25 30	

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 99..191
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8
 seq ILLCSVAVXLSPS/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

CATAGGGTTT CGAAAATTAT CCACACTTTC TATGGTAATA GAATCTGATA TGGTTCACCTC    60
TTGGTGTGTG ACATTCTGTG GGTCTGGGTA AATGTATA ATG TTA TGT ATC CAC CAN    116
                               Met Leu Cys Ile His Xaa
                               -30

KAT AGG ATC ATA CAG GAC AGT TTC ATT GCC CTA AAA ATT CTC TTA TGT    164
Xaa Arg Ile Ile Gln Asp Ser Phe Ile Ala Leu Lys Ile Leu Leu Cys
-25          -20          -15          -10

TCT GTC GCT GTA TSM CTG TCT CCC TCC GAG CCC CTG GCG CCG          206
Ser Val Ala Val Xaa Leu Ser Pro Ser Glu Pro Leu Ala Pro
          -5          1          5
  
```

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 8..121
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.9
 seq LPFLSLFWPWAPG/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

AAGGAGC ATG GGT GGT TTT TTT CCC CCT ACC GAG GTC CGT GAG GTG TGT    49
Met Gly Gly Phe Phe Pro Pro Thr Glu Val Arg Glu Val Cys
          -35          -30          -25

GCT AAC CAA GGG GCG GCT CAC AAC CGT GAC AGA CTG CCA TTC CTG AGT    97
Ala Asn Gln Gly Ala Ala His Asn Arg Asp Arg Leu Pro Phe Leu Ser
          -20          -15          -10
  
```


CTC TTC TGG CCA TGG GCC CCC GGA GCC GTG AGC GTC GGG CAG GCG CGG	145
Leu Phe Trp Pro Trp Ala Pro Gly Ala Val Ser Val Gly Gln Ala Arg	
-5 1 5	
TAC AGA ACA CCA ACG ACA KSA GCG CCC TCA GCA AGC GTT CCC TGG CCG	193
Tyr Arg Thr Pro Thr Thr Xaa Ala Pro Ser Ala Ser Val Pro Trp Pro	
10 15 20	
CGC GCG GGT ACG TGC AGG ACC CCT ACG	220
Arg Ala Gly Thr Cys Arg Thr Pro Thr	
25 30	

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 21..110
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9
seq HLWILLFSFCWM/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ACTTCCCTAT TATTCCTGAA ATG AAA TTA TTT TAC AAC CAG CTC GTT TCA GAA	53
Met Lys Leu Phe Tyr Asn Gln Leu Val Ser Glu	
-30 -25 -20	
ACA AAA CAT GAT TTT GCA CAT TTG TGG ATT TTG TTG TTA TTC TCA TTT	101
Thr Lys His Asp Phe Ala His Leu Trp Ile Leu Leu Leu Phe Ser Phe	
-15 -10 -5	
TGT TGG ATG TCT AGA AGC TTT TTT TTT TTT	131
Cys Trp Met Ser Arg Ser Phe Phe Phe Phe	
1 5	

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 111..170
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.9
seq LLFFHILFHSCFS/HL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

ACCTTTAAGA TTACCTGTAT AATAAATGTG TGCAGACACC ATCCAAAAG GTGTAAAAAA   60
TTGCAAAGGA AAAATAAATA CTGGCCAACA CAGTGTTCCT AAAAGTACCC ATG CCT   116
                                     Met Pro
                                     -20
AGT GAG TCC CCT CCC TTG CTG TTC TTT CAC ATT CTG TTC CAT AGC TGT   164
Ser Glu Ser Pro Pro Leu Leu Phe Phe His Ile Leu Phe His Ser Cys
      -15                      -10                      -5
TTC TCC CAC CTC TTG
Phe Ser His Leu Leu
      1

```

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 18..221
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.9
seq LLCSALAWQQSLG/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

ATAAACAGGA AAGCACT ATG TCT TCA AIG TGG TCT GAA TAT ACA ATT GGT   50
      Met Ser Ser Met Trp Ser Glu Tyr Thr Ile Gly
      -65                      -60
GGG GTG AAG ATT TAC TTT CCT TAT AAA GCT TAC CCG TCA CAG CTT GCT   98

```

Gly Val Lys Ile Tyr Phe Pro Tyr Lys Ala Tyr Pro Ser Gln Leu Ala	
-55 -50 -45	
ATG ATG AAT TCT ATT CTC AGA GGA TTA AAC AGC AAG CAA CAT TGT TTG	146
Met Met Asn Ser Ile Leu Arg Gly Leu Asn Ser Lys Gln His Cys Leu	
-40 -35 -30	
TTG GAG AGT CCC ACA GGA AGT GGA AAA AGC TTA GCC TTA CTT TGT TCT	194
Leu Glu Ser Pro Thr Gly Ser Gly Lys Ser Leu Ala Leu Leu Cys Ser	
-25 -20 -15 -10	
GCT TTA GCA TGG CAA CAA TCT CTT AGT GGG AAA CCA GCA GAT GAG GGC	242
Ala Leu Ala Trp Gln Gln Ser Leu Ser Gly Lys Pro Ala Asp Glu Gly	
-5 1 5	
GTA AGT GAA AAA GCT GAA GTA CAA TTG TCA TGT TGT TGT GCA TGC CAT	290
Val Ser Glu Lys Ala Glu Val Gln Leu Ser Cys Cys Cys Ala Cys His	
10 15 20	
TCA AAG GAT TTT ACA AAC AAT GAC ATG AAC CAA GGA ACT TCA CGT CAT	338
Ser Lys Asp Phe Thr Asn Asn Asp Met Asn Gln Gly Thr Ser Arg His	
25 30 35	
TTC AAC TAT CCA AGC ACA CCA CGG	362
Phe Asn Tyr Pro Ser Thr Pro Arg	
40 45	

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA :

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 19..102
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8
seq FVRFLGFVSLQS/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

TAGCTATTTT CAGCGCTT ATG GCT CTG TTC TTG GAG TTA TTT CTA AAT TCT	51
Met Ala Leu Phe Leu Glu Leu Phe Leu Asn Ser	
-25 -20	
TAT ICT CTT TTG TTT GTA AGG TTT CTT GGC TTT GTT TCC TGT TTG CAG	99
Tyr Ser Leu Leu Phe Val Arg Phe Leu Gly Phe Val Ser Cys Leu Gln	
-15 -10 -5	

TCT GAT CCC ATT TGC TCT TTT TTT TTT TTT
 Ser Asp Pro Ile Cys Ser Phe Phe Phe Phe
 1 5

129

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 114..185
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8
seq LMAGSSLSAGVSG/ED

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

ATACTTCAAA TCTTGAATTA AATGAAGAAA TTTATTTTAC TGATTCTCTT GAAATAAAGA	60
GAAATGAAAA TTTTCCAAAG GATTATGTGA AATTTTCAGA TGAAGAAGAA TTT ATG	116
	Met
AAT GAA GAT GAG AAG GAA ATG AAG GAA ATT CTA ATG GCA GGA AGT AGT	164
Asn Glu Asp Glu Lys Glu Met Lys Glu Ile Leu Met Ala Gly Ser Ser	
-20 -15 -10	
TTA TCA GCT GGA GTT AGT GGG GAA GAT AAA ACC GAG ATA TTG AAT CCC	212
Leu Ser Ala Gly Val Ser Gly Glu Asp Lys Thr Glu Ile Leu Asn Pro	
-5 1 5	
ACT CCA SCG ATG GCC AAA TCT CTG ACC ATA GAC TGT CTG GAA TTG GCA	260
Thr Pro Xaa Met Ala Lys Ser Leu Thr Ile Asp Cys Leu Glu Leu Ala	
10 15 20 25	
TTA CCC CCT GAA CTG GCT TTT CAA CTT AAT GAA TTA TTT GGT CCT GTT	308
Leu Pro Pro Glu Leu Ala Phe Gln Leu Asn Glu Leu Phe Gly Pro Val	
30 35 40	
GGT ATT GAT TCA GGG TCT CTA	329
Gly Ile Asp Ser Gly Ser Leu	
45	

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 167..229
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8
seq IIPLIXXLSLCLC/LW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```

CTATACGTGA TAAGTGAATA AAATGTGTCA GAGTGTACTA CTTAGAATTT TCATAGATTG   60
TAAAGATTTT CTATATATTT ATTTGAATTG GTAATTGGTT ATGAGCAGTT TGGTGTAGCT   120
GTTTTTAATT GTACAACAAT TAAGATATCA CCTATATTCT CGAAGA ATG GGA TCA       175
                                   Met Gly Ser
                                   -20
TTC CTT CTA GGA GGG ATT ATC CCT TTA ATA NNT TTN CTT TCT CTT TGT       223
Phe Leu Leu Gly Gly Ile Ile Pro Leu Ile Xaa Xaa Leu Ser Leu Cys
   -15                               -10                               -5
CTT TGT TTA TGG TGG AGA ATA ATT                                     247
Leu Cys Leu Trp Trp Arg Ile Ile
   1                               5

```

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 277..369
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8
seq VCLLCSGCSCAWS/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```

ACGAGTGTTA CAGAGGAGAT CTGGTTTCTG GAGGICTCCA GGATGGGGCT GTAGCCTAAA   60
AGGAAGACTA TGTGAGGCAG CAGGCAAGCA GCAGCAAGTG GAAAGGCTTG GAGATGTGGA   120
GGACGTTATA TGGTACTCAG AGAGCAGCAG TACATGGATG GCAAGTGTGG CGTTGTGCTG   180
CCACCCACTT CCCCATGCCA AAAGCATATA ACTGCTAATC AGTTACCGCA TTTTGTGCTG   240
CCGAATTCGT AAGCAGCCCC AAGAGTTCTC AACAGG ATG CTT CAG GTG GCC ACT   294
                                   Met Leu Gln Val Ala Thr
                                   -30

ACT AAT TAT TTG GAG TTG GCA CGT GAG GTT AAA CCT GTT TGT CTT CTT   342
Thr Asn Tyr Leu Glu Leu Ala Arg Glu Val Lys Pro Val Cys Leu Leu
-25                      -20                      -15                      -10

TGT AGT GGG TGT TCC TGT GCC TGG AGC GTA GGA TGT GTG TKG GAG TCG   390
Cys Ser Gly Cys Ser Cys Ala Trp Ser Val Gly Cys Val Xaa Glu Ser
                      -5                      1                      5

GAG TCA GAA   399
Glu Ser Glu
      10

```

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 175..228
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7
seq PFFLALCFPKSTS/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

```

ATTACTTTGT CTAGATCAGG AGATGCTAGI ATATTCTTAG CACTAAGACC CCTCTGAAAT   60
CTTGTC AAC ATTAGCCAC CCAGRAGT TG TKCTTTACTA CACCTTTGAG GGTTATGCCC   120
TGACATGTG CASCITAGGG GTTCAAGGAC AATCTCTTTA CACATTTT TG GGTT ATG   177
                                   Met

```

[illegible]

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 240..335
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..96
id AA270737
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 236..331
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.5
seq OCLLCISPPVFC/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TCCTCTTTGC	TGTTTTCATC	AAGATAGTAG	AGCACATCTT	CTTCTCACAG	ACTACAATA	60
TGTGGTTTCA	CACGAGGCAG	TAGAGGAAAG	TGCCTCGACT	GTGGGAGGCT	TGGSCAARAT	120
CCAAAGACTT	TCTCICCTTG	TTGCTGGAGT	CGCTAAAAGA	ACAGTTTAAT	AATGCCACAC	180
CCATCCCCAC	CCACAGITGT	CCCCTATCTC	CAGACCTCAT	TCGCAATGAA	GTAGA ATG	238
					Met	
TCT GAA AGC AGA TTT CAA CCA CAG AAT CAA GGA GGT TCT CTT CAA CTC						286
Ser Glu Ser Arg Phe Gln Pro Gln Asn Gln Gly Gly Ser Leu Gln Leu						
-30		-25		-20		
CCT CTT CAG TGC CTA CTA TGT TGC ATT TCT CCC CCT GTG TTT TGT GAA						334
Pro Leu Gln Cys Leu Leu Cys Cys Ile Ser Pro Pro Val Phe Cys Glu						
-15		-10		-5	1	

```

GGT AAC TGG TTA TCT TAC TTT TAT GTG CTT CCT GGA TTT GTG TGT GAA      382
Gly Asn Trp Leu Ser Tyr Phe Tyr Val Leu Pro Gly Phe Val Cys Glu
      5              10              15

TTA CAT AAA CTG GGT ATT TCT TGT TTA ATC CCC CTT TTC TCT GTC TCC      430
Leu His Lys Leu Gly Ile Ser Cys Leu Ile Pro Leu Phe Ser Val Ser
      20              25              30

CCT TTG GCA GCC TGG ATG GTG
Pro Leu Ala Ala Trp Met Val      451
      35              40

```

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (E) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 114..182
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3
seq SSCLLGLLHLSSQ/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

```

ATGGAGCAGA GGTCCAGCTG TGGTGAGGAT TGGCACAGTC GTGCTTGTGG GACTCCTCCT      60
TGGTCCAAC TAAATGGTCA ACCTACACCA TCACCCCTGT GCTTGCTCCT CTA ATG      116
Met
CCT AAG CAC TGT CAT TCC TTT ATC ACT AGT AGT TGC CTG TTG GGT TTG      164
Pro Lys His Cys His Ser Phe Ile Thr Ser Ser Cys Leu Leu Gly Leu
      -20              -15              -10

CTC CAT TTG TCC TCA CAG TTT AGC TGC CCT GGA AGG AAA CTC CAC CCT      212
Leu His Leu Ser Ser Gln Phe Ser Cys Pro Gly Arg Lys Leu His Pro
      -5              1              5              10

GCT CAG AGA CAC ACT GAG GCT GAG ACC CAA GGG AGG CCC CTC TCT GAC      260
Ala Gln Arg His Thr Glu Ala Glu Thr Gln Gly Arg Pro Leu Ser Asp
      15              20              25

AGG
Arg      263

```


(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 166..222
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq FIXFPFLPPFSFS/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```

AICTCTCCTT TTTCTGTGA ACTGTGCTGG TTTTGTGTTG GTCTTCCTCT CATACCCGTT   60
TCTGCATTC ATCTTTTCIT TCTATTGTGA CTTCAATTCA TTTTTTTTTT AACCTTATCT   120
TTTGTTCCTC TTGTTTATCC CATCCTTTTT GATAAAATCC ATCGC ATG TGT CTT CTT   177
                               Met Cys Leu Leu
TTT TYC TTT ATT TYC TTT CCT TTC CTT TTY CCT TTT TCT TTC TCC CAA   225
Phe Xaa Phe Ile Xaa Phe Pro Phe Leu Phe Pro Phe Ser Phe Ser Gln
-15                               -10                               -5                               1
ACT TTT TCC TTT TCA CAG CAT TGG AAC ACG GGA GGT AGT CAC CCA GAA   273
Thr Phe Ser Phe Ser Gln His Trp Asn Thr Gly Gly Ser His Pro Glu
                               5                               10                               15
GAA CTT GAG CGG CCT GGT GCC CAT CCG AGA CTT AAG GCT AGA CCC CAG   321
Glu Leu Glu Arg Pro Gly Ala His Pro Arg Leu Lys Ala Arg Pro Gln
                               20                               25                               30
CCT CCT CTG TTC CAT CCC TTT ATT AGC TCT                               351
Pro Pro Leu Phe His Pro Phe Ile Ser Ser
                               35                               40

```

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: 30..104
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.1
 seq LLVASGXAEGVSA/QS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

```

ACGCGCAGAC CCAGCGCCGA GCGCGAGCC ATG GCG TCC GAG CGG MTC CCT AAY      53
                Met Ala Ser Glu Arg Xaa Pro Asn
                -25                      -20

AGG CCC GGC TGT CTG CTC GTR GCC AGC GGC GMC GCC GAR GGT GTG TCG      101
Arg Pro Xaa Cys Leu Leu Val Ala Ser Gly Xaa Ala Glu Gly Val Ser
      -15                      -10                      -5

GCC CAG TCC TTC CTC CAS TGT TTC ACG ATG GCC AGC ACC GSC TTC AAC      149
Ala Gln Ser Phe Leu Xaa Cys Phe Thr Met Ala Ser Thr Xaa Phe Asn
      1                      5                      10                      15

CTG CAG GTG GCC AYC CCT GGG GGG AAA GCC ATG GAA TTT GTS GAT GTG      197
Leu Gln Val Ala Xaa Pro Gly Gly Lys Ala Met Glu Phe Val Asp Val
                20                      25                      30

ACT GAS AGC AAT GCA CGC TGG GTG CAA GAC      227
Thr Xaa Ser Asn Ala Arg Trp Val Gln Asp
                35                      40

```

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: 160..234
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.1
 seq LAFQLVFLRATSG/SC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```

AATTTCAAGT TGTCTAAAA GTTCAGACAA CCATCACTGG ACCTACAGAT TGAGTGATTA      60

```

TTATAGTGGG GATGTCCTTG GGTTAGTAAG CCTAAAGGAA GTAATTTCTG TTAAAGGAGA 120

TGTTAGTGGC CATTGTCATC TTAATGTCAA TCTTATCAG ATG TTC CCA GAC TAC 174
Met Phe Pro Asp Tyr
-25

AAA CTG GGT GGG TCA TAT CTC TTA GCA TTT CAA CTG GTA TTT CTC AGA 222
Lys Leu Gly Gly Ser Tyr Leu Leu Ala Phe Gln Leu Val Phe Leu Arg
-20 -15 -10 -5

GCA ACT AGT GGC TCA TGT TCC AAA TAT AGA AGG CAT TTG CAT AAC ATC 270
Ala Thr Ser Gly Ser Cys Ser Lys Tyr Arg Arg His Leu His Asn Ile
1 5 10

AAT GTT AGA CCT GGG CTT GTT AGA CTC TTG GGC TCA TGT ATA CAA AAG 318
Asn Val Arg Pro Gly Leu Val Arg Leu Leu Gly Ser Cys Ile Gln Lys
15 20 25

CAA CCT GGG 327
Gln Pro Gly
30

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 44..118
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq LLLXLXLLLIALE/IM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

AAATGTGTAC ACGCCCAGCT TCCTGCCTGT TACTCTCCAC AGT ATG CGA AGA ATA 55
Met Arg Arg Ile
-25

TCC CTG ACT TCT AGC CCT GTG CGC CTT CTT TTG TDT CTG CWG TTR CTA 103
Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Leu Xaa Leu Xaa Leu Leu
-20 -15 -10

CTA ATA GCC TTG GAG ATC ATG GTT GGT GGT CAC TCT CTT TGC TTC AAC 151
Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser Leu Cys Phe Asn
-5 1 5 10

TTC ACT ATA AAA TCA TTG TCC AGA CCT GGA CAG CCC TGG TGT GAA GCG	199
Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro Trp Cys Glu Ala	
15 20 25	
CAT GTC TTC TTG AAT AAA AAT CTT TTC CTT CAG TAC AAC AGT GAC AAC	247
His Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr Asn Ser Asp Asn	
30 35 40	
AAC ATG GTC AAA CCT CTG GGC CTC CTG GGG AAG AAG GTA TAT GCC ACC	295
Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys Val Tyr Ala Thr	
45 50 55	
AGC ACT TGG GGA GAA TTG ACC CAA ACG CTG GGA GAA GTG GGG CGA GAC	343
Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu Gly Glu Val Gly Arg Asp	
60 65 70 75	
CTC AGG ATG CTC CTT TGT GAC ATC AAA	370
Leu Arg Met Leu Leu Cys Asp Ile Lys	
30	

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 193..234
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq TFLLLLFxNAGRS/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

AAAATATTTT ATATTAGGGA GAGCTCTGTG CTGCCCTTTC CCAAAGCTTT GGTTATTTGA	60
TGGGAGGGGA AGTCTTCTCG AACCTATGTC MGAATATKCC GCTTTGRAAG AGGAGGGTTT	120
TTCTTGAGGC TAGTTTTGTA CCTGCTGTWT CTTTtagAAA TGATTGCTTT ATGGATTTAA	180
AAGGTGACCC AA ATG ACT TTT TTA TTA TTA TTA TTT KTT AAT GCT GGG AGG	231
Met Thr Phe Leu Leu Leu Leu Phe Xaa Asn Ala Gly Arg	
-10 -5	
AGT TTG CGT ATG TGT	246
Ser Leu Arg Met Cys	

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 215..292
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq EMFLVLLVTGVHS/NK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

```

AAAAAGTACT GAGAGGTTGA TGGGACTGTT CGATTAGCTC CTCTGAGAAG AAGAGAAAAG   60
GTTCTTGGAC CTCTCCCTGT TTCTTCCTTA GAATAATTG GATGGGATTT GTGATGCAGA  120
AAAGCCTAAG GGAAAAAGAA TATTCATTCT GTGTGGTGAA AATTTTTTGA AAAAAAATT  180
GCCTTCTTCA AACAAGGGTG TCATTCTGAT ATTT ATG AGG ACT GTT GTT CTC ACT  235
                               Met Arg Thr Val Val Leu Thr
                               -25                      -20

ATG AAG GCA TCT GTT ATT GAA ATG TTC CTT GTT TTG CTG GTG ACT GGA   283
Met Lys Ala Ser Val Ile Glu Met Phe Leu Val Leu Leu Val Thr Gly
          -15                      -10                      -5

GTA CAT TCA AAC AAA GAA ACG GCA AAG AAG ATT AAA AGG CCC GGG   328
Val His Ser Asn Lys Glu Thr Ala Lys Lys Ile Lys Arg Pro Gly
          1                      5                      10

```

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 150..269
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq ISLLFIFFSIANS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```

ATTCTTTCCT TCTCATATCT ACAATTGCTC CTTTCTAGTT CAGTTCCTA GTACAGCTGG   60
AGTGATTATT KSKSKTTAAA AAATGCAAGC ATAAAAAGA AATAACAAA TAGTTAAATC  120
ATGTTATTCT TTTGTTTACA CTGTAATGA ATG TCT TCC CCA TTG CTT GTA GAA   173
                               Met Ser Ser Pro Leu Leu Val Glu
                               -40                               -35
CAA AGT TCT ACA AAG TCT CCC AAA AGC TGG TCC TGG TCC TTT CTA GCT   221
Gln Ser Ser Thr Lys Ser Pro Lys Ser Trp Ser Trp Ser Phe Leu Ala
      -30                               -25                               -20
TTC TCT TGC ATA AGT CTT CTT TTT ATT TTT TTC AGC ATT GCA AAT TCT   269
Phe Ser Cys Ile Ser Leu Leu Phe Ile Phe Phe Ser Ile Ala Asn Ser
      -15                               -10                               -5
TCC CCC TGC GGG                                           231
Ser Pro Cys Gly
1

```

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 96..170
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq IPLLLFFHLSFL/NS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

```

AGAACAAAGT TTAGAATGAT ATGTTTATGC CTGTGACAT TTATCTTGTT AGATTATGCT   60
CACTAAGCCA TTGGGGTGTT TGGGGAATTT GATCA ATG TAT CTT TTC TGT CTC   113

```

Met Tyr Leu Phe Cys Leu
-25 -20

TTT TCA GTT TCG AAA ACT ATC CCT CTG CTG CTG CTT TTC TTC CAC TTG 161
Phe Ser Val Ser Lys Thr Ile Pro Leu Leu Leu Leu Phe Phe His Leu
-15 -10 -5

TCT TTT CTC AAT AGC TTG 179
Ser Phe Leu Asn Ser Leu
1

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 170..217
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq CLLILKFLSPAET/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

ACAGAGTTCA CTTCTAGGAT ATTCCTTCCC AATCTTCACA GTCACCTCAT AGTCACTATG 60
AGGATTACAT GAGTKAATAT TTGTA AAAAG CGITCAGGAG AGTGCTTGCT TCACATCAAA 120
TACTATATAT ACTTGTTAAA TAAATAGATC TCATTACCCC CACGAAACA ATG ATC GTT 178
Met Ile Val
-15
TGT CTC CTG ATT CTC AAG TTT TTG TCT CCA GCA GAG ACB TCT ATT CTG 226
Cys Leu Leu Ile Leu Lys Phe Leu Ser Pro Ala Glu Thr Ser Ile Leu
-10 -5 1
AGC TCC ATA GCT ACA TAT GGG GCT TTT TAT TTC ATA GTT CCA CTG GAG 274
Ser Ser Ile Ala Thr Tyr Gly Ala Phe Tyr Phe Ile Val Pro Leu Glu
5 10 15
GTT TCA CAA ATC CTT CAA ACT CAG 298
Val Ser Gln Ile Leu Gln Thr Gln
20 25

(2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 180..254
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.7
seq LILCFLFILHTHT/HT
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

```

ACAACTGGT TACCCTGCCA CATGTATACC CCCTTCTCCC CATTCTCACT TCCTCGTTAG   60
ACGAAATGAT CATCCAGTGA AGCCATAGAT TATATTGGCC ATCTAATATC AAACCATATT  120
GGTCTCATTT GAAATCTTT CATGATGCTT TGTGGTATTC ACAGTGAAGT TTAGATTCC   179
ATG GAT AAG AGC ATC AAG TCC TCT ATA ATC TGG TCT CTG ATT CTC TGT   227
Met Asp Lys Ser Ile Lys Ser Ser Ile Ile Trp Ser Leu Ile Leu Cys
-25          -20          -15          -10
TTT CTT TTT ATC CTG CAC ACA CAC ACA CAC ACA CAC ACA CAC ACA CAC   275
Phe Leu Phe Ile Leu His Thr His Thr His Thr His Thr His Thr His
          -5              1              5

```

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 405 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 283..390
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 6.7
seq IFDLLLLLXXSNQ/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

```

ACAGACCTCT TTGAAATCT AATGAGAGCC ATAGACTTCA CCCTAAAAAA ATATATATGC   60
ATAAAAAGTT TAAATATAGT TTGGAGAGTA ACGCACCTTC CCCTAAAGCA ATTCCTAAAC   120
CTCATTTAAA GGATCTATAT TCTATAGTTC AGTTCTGCAT TTTTAATGTC TTCTATATTG   180
TCTCATGCTA GAATAGTCAT TATATCTTCA TATGTAATAT TTAAAGTGTG AATTATCATC   240
TAACACTTCC TGTCTTCTGT CCCCCAATC TATACTTCTC CC ATG TTC TTT ATT   294
                                   Met Phe Phe Ile
                                   -35

TTC ATT AAT GGC TTT ACW CTC CTT CTA ATG ACC CTA GCC ATG AAA CCC   342
Phe Ile Asn Gly Phe Thr Leu Leu Leu Met Thr Leu Ala Met Lys Pro
      -30                      -25                      -20

AGG CAT CCT ATT TTT GAC CTC TTG CTA TTG CTK RAB HTA TCT AAT CAA   390
Arg His Pro Ile Phe Asp Leu Leu Leu Leu Xaa Xaa Ser Asn Gln
      -15                      -10                      -5

TTG CCA GTT ACG GGG   405
Leu Pro Val Thr Gly
  1                      5

```

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 3..182
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq LWPFLTWINPALS/IC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

```

AC ATG TGC CCT AGT CTG GAA GAG GCT CCC AGT GTC AAG GGG ACT CTG   47
Met Cys Pro Ser Leu Glu Glu Ala Pro Ser Val Lys Gly Thr Leu
      -60                      -55                      -50

CCC TGC TCA GGA CAA CAG CAG CCT TTC CCG TTT GGA GCC TCA AAC ATC   95
Pro Cys Ser Gly Gln Gln Gln Pro Phe Pro Phe Gly Ala Ser Asn Ile

```

-45	-40	-35	-30	
CCA CTA CTC CTG GGC AGG AGC AGA AAG GTG GCT CGA GGT GCA CCG GTC	143			
Pro Leu Leu Leu Gly Arg Ser Arg Lys Val Ala Arg Gly Ala Pro Val				
-25	-20	-15		
CTG TGG CCA TTT CTC ACT TGG ATA AAC CCT GCA CTG TCC ATC TGT GAC	191			
Leu Trp Pro Phe Leu Thr Trp Ile Asn Pro Ala Leu Ser Ile Cys Asp				
-10	-5	1		
CCC TTA GGA TCC TGC GGA TGG CAG	215			
Pro Leu Gly Ser Cys Gly Trp Gln				
5	10			

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 287..337
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq LLSALWFCHPCCL/CC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

AAGCTCCAAG GCAGGAAGAG AATTGGGCAT CGGGTACGAA CCTGGCAGCT CAGGAGTCGG	60
GGCTCCACTC ACCCCACACA AAAAGATGAA AAAAGCGCAW AGAGCTCAAT GCATTGATTG	120
GTTTGGCTGG GGACAGCCGG AGAAAGAAGC CCAAGAAAGG CCCAAGCAGT CACCGCCTGC	180
TTCGCACTGA GCCTCCCGAC TCATACTCTG AGTCCAGCTC CGAAGAGGAA GAGGAATTGG	240
GTGTGGTTGG AAATCGCTCT CGCTTTGCCA AGGGAGACTA TTTACG ATG CTG CAA	295
Met Leu Gln	
-15	
GAT CTG TTA TCC GCT CTG TGG TTT TGT CAT CCT TGC TGC CTG TGT TGT	343
Asp Leu Leu Ser Ala Leu Trp Phe Cys His Pro Cys Cys Leu Cys Cys	
-10	-5
1	
GGC CTG TGT TGG CTT GGT GTG GAT GCA GGT TGC TCT CAA GGA GGA TCT	391
Gly Leu Cys Trp Leu Gly Val Asp Ala Gly Cys Ser Gln Gly Gly Ser	
5	10
15	

GGA TGC CCG
Gly Cys Pro
20

400

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 167..223
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq LLSLAAYLSGPHQ/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

```

AAAATGTCCT CCACAGCTTT GCCCAGTGGG ACACATGGCT CCTGACATAC GTAACCCAGG    60
ATGGGATGCC TTGTTGGAGT CTCTCAGATA TGGAGCAAAA TGGGCCATGT GCAGTCAAGA   120
CGCCATCTAM CCTGGGCAGC TTGCCTAAGC CTCGAGGGAC CTGCCA ATG ATG GAT      175
                               Met Met Asp
CTG AGA CCT CTT CTG TCC CTG GCT GCC TAT CTG TCT GGT CCT CAT CAA      223
Leu Arg Pro Leu Leu Ser Leu Ala Ala Tyr Leu Ser Gly Pro His Gln
  -15                      -10                      -5
GAA CCC AGT GTT CCC ACC CGA GAT GGA GAC GTG AAT AAT CTT CCT AAG      271
Glu Pro Ser Val Pro Thr Arg Asp Gly Asp Val Asn Asn Leu Pro Lys
   1                      5                      10                      15
CCT AAT CCT GCC AGA AGC GTG AAG CAA GGG GGA ATH TGG AAG GCG GAA      319
Pro Asn Pro Ala Arg Ser Val Lys Gln Gly Gly Ile Trp Lys Ala Glu
          20                      25                      30
CAG GAA AGA GTG GAA GTG GAG
Gln Glu Arg Val Glu Val Glu
          35

```

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: NUCLEIC ACID

- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 147..203
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq LLPGLPLVRTSFS/HF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

```
AGCGGTCAGA GGATGCCCTC TTCGCCCTGT GAGCAGCTCT GTGGTTTGCC TCCCCAGATG    60
GCGGGTCCCC GCTTGCACCC CGTGGACACC GGGCACTGGC CACTCCTACA TCCCCAGCTC   120
CACACGGCCT GCACACCTGT GTTTC ATG GAA ATG CCA CCG TGT CTG CTC CCA    173
                               Met Glu Met Pro Pro Cys Leu Leu Pro
                               -15
GGC CTC CCA CTA GTC AGG ACC AGC TTC AGC CAC TTC TTT TCT CTG AGT    221
Gly Leu Pro Leu Val Arg Thr Ser Phe Ser His Phe Phe Ser Leu Ser
-10                      -5                      1                      5
GGT GGG ACA ACT ACA GCC AGA GGG                                245
Gly Gly Thr Thr Thr Ala Arg Gly
                               10
```

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 19..93
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.5
seq GLAMLHVTRGVXG/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

```

ACATGCGCAG GAGGCTCA ATG ACA GTC GAG CTT TGG CTA AGG CTC CGG GGA      51
      Met Thr Val Glu Leu Trp Leu Arg Leu Arg Gly
      -25                      -20                      -15

AAG GGT CTA GCC ATG CTG CAT GTG ACC CGG GGG GTC TRG GGG TCC AGG      99
Lys Gly Leu Ala Met Leu His Val Thr Arg Gly Val Xaa Gly Ser Arg
      -10                      -5                      1

GTC CGA GTA TRG YCA MTG TTG CCC GCG CTC CTC GGG MCC CCC MGG GCC      147
Val Arg Val Xaa Xaa Xaa Leu Pro Ala Leu Leu Gly Xaa Pro Arg Ala
      5                      10                      15

CTC TCA TCG MTG GCA GCC AAA ATG GGG GAK TAT CGC AAS ATG TGG      192
Leu Ser Ser Xaa Ala Ala Lys Met Gly Xaa Tyr Arg Xaa Met Trp
      20                      25                      30

```

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 7..78
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4
seq LLILLCSSFPDRV/SY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

```

ACAAAC ATG TCT ATA GAA GAT TTT GTG AAT AGA AGC ATA CTT CTG ATC      48
      Met Ser Ile Glu Asp Phe Val Asn Arg Ser Ile Leu Leu Ile
      -20                      -15

TTG CTC TGT TCT TCC CCA CCT GAT AGG GTC AGC TAC AGA GCC AAG GTT      96
Leu Leu Cys Ser Ser Pro Pro Asp Arg Val Ser Tyr Arg Ala Lys Val
      -10                      -5                      1                      5

TTA CAC TCA TTG CTT CAA TTG CCC GCC CAG      126
Leu His Ser Leu Leu Gln Leu Pro Ala Gln
      10                      15

```

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: NUCLEIC ACID

- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 32..91
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4
seq FALLFLFLVPVPG/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

```

AAGTCTCAGC GTGGGGTGAA GCCTAGCAGC T ATG AGG ATC CAT TAT CTT CTG      52
               Met Arg Ile His Tyr Leu Leu
               -20                      -15

TTT GCT TTG CTC TTC CTG TTT TTG GTG CCT GTT CCA GGT CAT GGA GGA      100
Phe Ala Leu Leu Phe Leu Phe Leu Val Pro Val Pro Gly His Gly Gly
               -10                      -5                      1

ATC ATA AAC ACA TTA CAG AAA TAT TAW TTG CAG AGT CAG AGG CGG CCG      148
Ile Ile Asn Thr Leu Gln Lys Tyr Xaa Leu Gln Ser Gln Arg Arg Pro
               5                      10                      15

GTG TGC TGT GCT CAG CTG CCT TCC AAA GGA GAA AGG      184
Val Cys Cys Ala Gln Leu Pro Ser Lys Gly Glu Arg
               20                      25                      30

```

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 217..255
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4
seq MCLLTALVTQVIS/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

```

AATGCCAGTG TCAGCTTCTC TCCGAAACT GGGTAATACG AAATGGTCTT TATTGGTTGT   60
GAACACTCGA GCTGAGAAAC ATTTTAGGAT CTTTGTGTCT TTTGTGATGA TTTTGTCTTCT  120
GRAAGRWGGA AASCTGTCTA AAAATATTCA AGTGTGCAAC CAAGGATTTA GATGAAGCCA  180
GCAAACAAAG GAATCATGTA ATCAGGACCT GAGCGA ATG TGC TTA CTC ACG GCG   234
                               Met Cys Leu Leu Thr Ala
                               -10
TTA GTT ACA CAG GTG ATT TCC TTA AGA AAA AAT GCA GAG AGA ACT TGT   282
Leu Val Thr Gln Val Ile Ser Leu Arg Lys Asn Ala Glu Arg Thr Cys
      -5                      1                      5
TTA TGC AAG AGG AGA TGG CCC TGG NGC CCC TCG CCC CGG ATC TAC TGC   330
Leu Cys Lys Arg Arg Trp Pro Trp Xaa Pro Ser Pro Arg Ile Tyr Cys
  10                      15                      20                      25
TCA TCC ACC CCA TGC GAT TCC AAA TTC CCC ACC GTC TAC TCC AGT   375
Ser Ser Thr Pro Cys Asp Ser Lys Phe Pro Thr Val Tyr Ser Ser
      30                      35                      40

```

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 76..129
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq GLALVAGTPPSRS/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```

ATCTGGCGCG TGGTCTTGCA TTTCCTACTT GGTCTGTTC GTGGCGCCGC GCCTCCGGGT   60
GTTGGGGAGT CCGGG ATG ATG GGG AAT CCG GGG CTC GCC CTA GTC GCG GGG   111
      Met Met Gly Asn Pro Gly Leu Ala Leu Val Ala Gly
      -15                      -10
ACA CCG CCT TCC AGG AGC TGT CCC CAG GCA AAC TCA CAG ACG CGG   156
Thr Pro Pro Ser Arg Ser Cys Pro Gln Ala Asn Ser Gln Thr Arg
      -5                      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 186..299
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq PCVSLWAPRXFA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

```

ATAACCCATA TAGTAGTTAA GCCATTGTGG TGAGGGTGTT TGAAACCCAG CTATCCTATG   60
TAATGCTATT TCCAGGGGAA AAATATTCCC AATTCCAGGT AAAAGATCAG AACAGATAT   120
CACCTGSAWT TTGTCCACC TTCACCCAG GCTTCAGCTA TACTTAGGTA TACTCTCTG   180
GTCCC ATG AAC CAT CTC ATG CCT TIG ACT GTG CTG CAC TCA GTG CTT GAA   230
Met Asn His Leu Met Pro Leu Thr Val Leu His Ser Val Leu Glu
      -35                -30                -25

ATG CTC CGC ACA CCC CGC ACA CCT CCC TGG CCC TGT GTA TCC CTT CTA   278
Met Leu Arg Thr Pro Arg Thr Pro Pro Trp Pro Cys Val Ser Leu Leu
      -20                -15                -10

TGG GCG CCC AGA GSA TTT GCT TCC TCT TGC TCT CAA GCA ITT ACC ACT   326
Trp Ala Pro Arg Xaa Phe Ala Ser Ser Cys Ser Gln Ala Phe Thr Thr
      -5                1                5

CTG CAN KGC AAT TGC TTG CTT ACT AAT CCA TCT CCC ACA CTA GAT TGT   374
Leu Xaa Xaa Asn Cys Leu Leu Thr Asn Pro Ser Pro Thr Leu Asp Cys
      10                15                20                25

GAC CTC CCT GAG GGC TCA GAA ATA TTA AAT TCT TCT CTG TAT CCT CAT   422
Asp Leu Pro Glu Gly Ser Glu Ile Leu Asn Ser Ser Leu Tyr Pro His
      30                35                40

TGC CTA CTC AGT GCT TGG AAC ACA CGA CAC TCA ACA   458
Cys Leu Leu Ser Ala Trp Asn Thr Arg His Ser Thr
      45                50

```

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 13..84
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq SLLXLRASQLSEG/DT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

```
ATTATTATTT TT ATG GGA CAT GTT GTG TTT GGG GAT ATA AAA AAT AGT TTA    51
      Met Gly His Val Val Phe Gly Asp Ile Lys Asn Ser Leu
                -20                      -15

TTA KGT TTA AGG GCT TCG CAG CTT AGT GAG GGA GAC ACA TGR VTG AAM    99
Leu Xaa Leu Arg Ala Ser Gln Leu Ser Glu Gly Asp Thr Xaa Xaa Xaa
-10                -5                      1                      5

TVA TGT CCA BRT ATG RTG AGA GGT AAA CAC ATA TCC TAT    138
Xaa Cys Pro Xaa Met Xaa Arg Gly Lys His Ile Ser Tyr
      10                      15
```

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 48..290
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq FLSLLXSVSETPG/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```
ACTTCTTCCC CGGGTCTCCG AAGCCGCTAG GGAAGCGCAA GTGGGCC ATG GCT GGC    56
                        Met Ala Gly
```

-80

GGG AGG CGG GAT TAC AGC CAG CTC TTT GGC CGC GGC CCC GGT CGG CTC	104
Gly Arg Arg Asp Tyr Ser Gln Leu Phe Gly Arg Gly Pro Gly Arg Leu	
-75 -70 -65	
TCG CGA GCG CGA GCC TCT GTT GTG CGT TGG TCT CCC CGG GCA ACT GCT	152
Ser Arg Ala Arg Ala Ser Val Val Arg Trp Ser Pro Arg Ala Thr Ala	
-60 -55 -50	
TGC CCT GCG CCA CCG AGC CTC CCG GAT TTA AAG CGG CAG GAG CTG GTT	200
Cys Pro Ala Pro Pro Ser Leu Pro Asp Leu Lys Arg Gln Glu Leu Val	
-45 -40 -35	
AGC CGG ATA GAA TGT GGG TGC CGA GGG CCG GTG GGG GCC ACC GCA GAC	248
Ser Arg Ile Glu Cys Gly Cys Arg Gly Pro Val Gly Ala Thr Ala Asp	
-30 -25 -20 -15	
TTC TTT CTG TCC CTG CTC TDC AGC GTC TCT GAA ACC CCT GGC AGC CTG	296
Phe Phe Leu Ser Leu Leu Xaa Ser Val Ser Glu Thr Pro Gly Ser Leu	
-10 -5 1	
CGG RGA AAC GAT CTT TTC TTC GTC TCT CAG CTT ATT TGG GGC CGG	341
Arg Xaa Asn Asp Leu Phe Phe Val Ser Gln Leu Ile Trp Gly Arg	
5 10 15	

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 207..263
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq LWCFHSFISFSLSS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

ATCCTCCATA GCTATATCCA TTTCCTGGGA CATGGGTGG CCCAAGAGGG AATGAGAAGG	60
ACCTGCGATT GCACAGGAAA TTCTGGGGCA CATTTAACGT TAAATCATTA AGCTTCTGCC	120
AATAAATCCA TTA CTGTAA TTACTGAG ATGGCCAACG ATCTGCTGAC AATATTCCTT	180
CATTGATTTT CATTCTCAGT GAATCG ATG TTC TGG CNT GGC TCT CTT TGG TGT	233
Met Phe Trp Xaa Gly Ser Leu Trp Cys	

-15

TTT CAT TCT TTC ATT TCT TTC TCC CTG TCC TCA TCA CGG 272
 Phe His Ser Phe Ile Ser Phe Ser Leu Ser Ser Ser Arg
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 118..225
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6
seq FLLTFFSYLLHA/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

AGGCNNNCGG ASCSGGGCTG GAGAGCGGCS NCCACTGCGG ATCTCGGAAG GAAGAAATGA 60
 TGTAATCAC TCATSSAVAC TTAAAGGTCTN NNGTGAGAM GGAAGGTCAG GMAGAAC 117
 ATG GCC TGG CCA AAT GTT TTT CAA ABA GGG TCT CTG CTG TCC CAG TTC 165
 Met Ala Trp Pro Asn Val Phe Gln Xaa Gly Ser Leu Leu Ser Gln Phe
 -35 -30 -25
 AKN BAT CAT CAT GTT GTA GTG TTC CTG CTC ACT TTC TTC AGT TAT TCG 213
 Xaa Xaa His His Val Val Val Phe Leu Leu Thr Phe Phe Ser Tyr Ser
 -20 -15 -10 -5
 TTG CTC CAT GCT TCA CGA AAA ACA TTT RGC AAT GTC AAA GTC AGT ATC 261
 Leu Leu His Ala Ser Arg Lys Thr Phe Xaa Asn Val Lys Val Ser Ile
 1 5 10
 TCT GAG CAG TGG ACC CCA AGT GCT TTT AAC ACG TCA GTT GAG CTG CCT 309
 Ser Glu Gln Trp Thr Pro Ser Ala Phe Asn Thr Ser Val Glu Leu Pro
 15 20 25
 GTG GAG ATC TGG AGC AGC RAC CAT TTG TTC CCC AGT GCA GAG 351
 Val Glu Ile Trp Ser Ser Xaa His Leu Phe Pro Ser Ala Glu
 30 35 40

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 466 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 380..436
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6
 seq WILAVGLSLPSSS/XI
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```

ACTCTCTTCT ACTGGAATGG TACCCTTGTT GACTGACTCA TGTATAGCTG CTTGGCTTAA   60
GGTAGACCA GATATTCAGG TCCTCTGAGA CAGGCCCTG ATGACTTTTG CAACTACATC  120
TTTCAMCACA GCCTGCCTTG CATTTTGGAC TCTAGCAACA CTGAAATACA TGTCATTTC   180
CAAGGCATGT TAAGCTGTTT CTATTCTCTA GGCTCTCCCT TTTTCCTAGA ATGCCCTTTT  240
CCTCTAGGCT AATGTCTTTC TCCTTTAAAT TAGTCATCTT CAACAAAGGC TACCTTGACC  300
TTCTCTTGAC TTTGCCACAT TCCTGCTGCT GCCTTCCTTC CATGGCCTTT GTCACGCTAT  360
ATGGTAATTG ACAGGTTC ATG ATC TTG AGG AAC TTA TGG ATT TTA GCA GTG   412
           Met Ile Leu Arg Asn Leu Trp Ile Leu Ala Val
           -15                               -10

GGT CTT AGC TTG CCA TCT TCT TCA MCC ATC AAG TTT CAT TTC TCT CTT   460
Gly Leu Ser Leu Pro Ser Ser Ser Xaa Ile Lys Phe His Phe Ser Leu
      -5                               1                               5'

TAC TCA                               466
Tyr Ser
      10

```

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 389 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 267..371
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.9
seq LCGLLHLWLKVFS/LK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

ACAATCAGTT TGCCAATACC TCAGAAACAA ATACCTCGGA CAAATCTTTC TCTAAAGACC   60
TCAGTCAGAT ACTAGTCAAT ATCAAATCAT GTAGATGGCG GCATTTTAGG CCTCGGACAC   120
CATCCCTACA TGACAGTGAC AATGATGAAC TCTCCTGTAG AAAATTATAT AGGAGTATAA   180
ACCGAACAGG AACAGCACAA CCTGGGACCC AGACATGCAG TACCTCTACG CAAAGTAAAA   240
GTAGCAGTGG TTCAGCACAC TTTGGT AIG TTG ACT GTT AAT GAT GTA CGT TTC   293
                               Met Leu Thr Val Asn Asp Val Arg Phe
                               -35                               -30

TAT AGA AAT GTC AGG TCC AAC CAT TTC CCA TTT GTT CGA CTA TGT GGT   341
Tyr Arg Asn Val Arg Ser Asn His Phe Pro Phe Val Arg Leu Cys Gly
   -25                               -20                               -15

CTG TTA CAT TTA IGG CTT AAA GTC TTT TCT CTT AAA CAG TTA AAA AAA   389
Leu Leu His Leu Trp Leu Lys Val Phe Ser Leu Lys Gln Leu Lys Lys
  -10                               -5                               1                               5

```

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 111..179
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.9
seq LFLNLCILAXPFS/KQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```

ATTAATTTTA ATTTTCATTG TCAATATTTT GAGCTTAGAA CATTTATGGT ATAAAAATTT   60

```

```

AAACTAATCA AAGTTGIGTG ATGATTCCG GGAATTATTA TTGAAAGCCT ATG AAT      116
                                   Met Asn

TTA AAA CCA GGT TTA CCA TGT AAT TTG TTT TTA AAT TTA TGT ATA CTA      164
Leu Lys Pro Gly Leu Pro Cys Asn Leu Phe Leu Asn Leu Cys Ile Leu
-20                               -15                -10

GCC TGV CCT TTC TCC AAG CAA ATT ATT GAA CTA TTA GAA TAT GTT AGT      212
Ala Xaa Pro Phe Ser Lys Gln Ile Ile Glu Leu Leu Glu Tyr Val Ser
-5                               1                   5                10

TAT CAT CCT TGT GTC TTA GTA TAT AGT GAA TAC AGM AAC ATC AGC ATT      260
Tyr His Pro Cys Val Leu Val Tyr Ser Glu Tyr Xaa Asn Ile Ser Ile
15                               20                25

GTA TAC ACT CTT                                                         272
Val Tyr Thr Leu
30

```

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 43..162
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq VVLAWGLLNVSMA/GM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

```

ACCAGAGAGA GTGGCGCGAG CTGCGTTTTC CGGCCAGAGG AC ATG ATG CAG GGG      54
                                   Met Met Gln Gly
                                   -40

GAG GCA CAC CCT AGT GCT TCC CTT ATT GAC AGA ACC ATC AAG ATG AGA      102
Glu Ala His Pro Ser Ala Ser Leu Ile Asp Arg Thr Ile Lys Met Arg
-35                               -30                -25

AAA GAA ACA GAG GCT AGG AAA GTG GTC TTA GCC TGG GGA CTC CTA AAT      150
Lys Glu Thr Glu Ala Arg Lys Val Val Leu Ala Trp Gly Leu Leu Asn
-20                               -15                -10                -5

GTA TCT ATG GCT GGA ATG ATA TAT ACT GAA ATG ACT GGA AAA TTG ATT      198
Val Ser Met Ala Gly Met Ile Tyr Thr Glu Met Thr Gly Lys Leu Ile

```

	1	5	10	
AGT TCA TAC TAC AAT GTG ACA TAC TGG CCC CTC TGG TAT ADY GAG CTT				246
Ser Ser Tyr Tyr Asn Val Thr Tyr Trp Pro Leu Trp Tyr Xaa Glu Leu				
	15	20	25	
GCC CTT GCA TCT CTC TTC AGC CTT AAT GCC TTA TTT GAT TTT TGG AGA				294
Ala Leu Ala Ser Leu Phe Ser Leu Asn Ala Leu Phe Asp Phe Trp Arg				
	30	35	40	
TAT TTC AAA TAT ACT GTG GCA CCA ACA AGT CTG GTT GTT AGT CCT GGA				342
Tyr Phe Lys Tyr Thr Val Ala Pro Thr Ser Leu Val Val Ser Pro Gly				
	45	50	55	60
CGG				345
Arg				

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 274..330
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq PXXLLILAHITQS/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

AGTATTTGTT AAATGCTACA AGAGTGACTG GGATCATAAG TGTTACGGGA GTTTGGCAAA	60
GAAGCAGGAG GTAGTTAGTG TAACTGTAA TGTGATTATA AGACTAATAC ATTTTGTKGG	120
RAGATAACTT ACCAAGTTTG GTTTGTGGAA AATTGGATT GAGAAGGAAA TTGTATGTTT	180
CCGTTAGAAG TAGAACAACA ACAACAAAT ATCTCCCATC ATTTGTTTGG TACTATCTGG	240
CCTCCCCAGT GCTGCTTGGG AGAATCATGA AAC ATG ATG AAT CAA ACA CAT CCT	294
	Met Met Asn Gln Thr His Pro
	-15
TRM RTG TTG CTC ATC CTG GCA CAT ATT ACA CAG AGT TGC CCA TGG GCC	342
Xaa Xaa Leu Leu Ile Leu Ala His Ile Thr Gln Ser Cys Pro Trp Ala	
	-10 -5 1
CAT GTA GGA GCA GCT CCA TCT GCC CTT CTA ATA CAT AGG TGG GAR CTG	390

```

His Val Gly Ala Ala Pro Ser Ala Leu Leu Ile His Arg Trp Glu Leu
 5              10              15              20
AGG GGG TGC TCG TAT TTG AAA CTG TTT TTG GTT ATG GTG CTC ATA TTT 438
Arg Gly Cys Ser Tyr Leu Lys Leu Phe Leu Val Met Val Leu Ile Phe
          25              30              35

GAA ATG CTT 447
Glu Met Leu

```

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 35..94
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq GLVLLLSLAEIF/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

```

AGTCCTAGTC AGAGTTTTCT GTGAAGGCAA GGGC ATG GGG TTG CCG GAG AGA.AGA 55
                               Met Gly Leu Pro Glu Arg Arg
                               -20              -15

GGA TTG GTC CTG CTT TTA AGC CTA GCT GAA ATT CTT TTC AAG ATC ATG 103
Gly Leu Val Leu Leu Leu Ser Leu Ala Glu Ile Leu Phe Lys Ile Met
          -10              -5              1

ATT CTG GAA GGA GGT GGT GTA ATG AAT CTC AAC CCC GGC AAC AAC CTC 151
Ile Leu Glu Gly Gly Gly Val Met Asn Leu Asn Pro Gly Asn Asn Leu
          5              10              15

CTT CAC CAG CCG CCA GCC TGG ACA GAC AGC TAC TCC ACG TGC AAT GTT 199
Leu His Gln Pro Pro Ala Trp Thr Asp Ser Tyr Ser Thr Cys Asn Val
          20              25              30              35

TCC AGT GGG TTT TTT GGA GGC CAG TGG CAT GAA ATT CAT CCT CAG TAC 247
Ser Ser Gly Phe Phe Gly Gly Gln Trp His Glu Ile His Pro Gln Tyr
          40              45              50

TGG ACC AAG TAC CAG GTG TGG GAG TGG CTC CAG CAC CTC CTG GAC ACC 295
Trp Thr Lys Tyr Gln Val Trp Glu Trp Leu Gln His Leu Leu Asp Thr
          55              60              65

```


AAC CAG CTG GAT GCC AAT TGT ATC CCT TTC CAA GAG TTC GAC ATC AAC 343
 Asn Gln Leu Asp Ala Asn Cys Ile Pro Phe Gln Glu Phe Asp Ile Asn
 70 75 80

GGC GAG CAM CGG 355
 Gly Glu Xaa Arg
 85

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 305..388
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq LCWALLYNCFSSS/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

ATCAGTCTGT GGAGACAGGT GAGCACGAAC TTCTGAGACA GGTGTGGGTG CGAGGGTCGG 60
 GAGGGTCATG GGATTGGGAC CGAGGTGTGA GGAGGGAATC TGCAATTCCT TGCTACACAG 120
 AGCGCTGGCA ACTTCTGACA GGCTGTTTCT GGGGTATGGG CTGCCTCGGG TTGTTGCTGT 180
 TACAAGGAAA GAAAAGAGTT CCCCTGCCCA CCGCTCCCA GCCACTGGGC TACCTCCTGG 240
 CAGGAAATTT GCAAACCTGAG TTTAACAAGT TAGGATCAGC AGAGGCTAGA GGAGGGCCTG 300
 GCAG ATG TGG GGT CTA GAA GAG GAC AGG AGT TAT CAG GGS CTC CGG CCA 349
 Met Trp Gly Leu Glu Glu Asp Arg Ser Tyr Gln Gly Leu Arg Pro
 -25 -20 -15

TTG TGC TGG GCT ITG CTG TAC AAT TGT TTC TCA AGC AGT TGT GTY CCT 397
 Leu Cys Trp Ala Leu Leu Tyr Asn Cys Phe Ser Ser Ser Cys Val Pro
 -10 -5 1

GTG GCT TTG GTG 409
 Val Ala Leu Val
 5

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(v²) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 129..383
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq ALLASLGIAFSRS/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

AGTAGCGGAC	ATTTTGTTC	TGTCAGGCTG	TCCCTGGCCG	GGGTTCIGTA	ACGCTTGTGT	50		
GGGCCGCAAG	TGGAGGTGTT	GGGAAAGCGC	GGAGGAGATG	TTGTCCCCAG	TGTCCCGAGA	120		
CGCGTCTG	ATG CTC	TGC AGG	GAC GGA	AGT GCC	TGC GTC	CCC CGA	TCG AGA	170
	Met Leu	Cys Arg	Asp Gly	Ser Ala	Cys Val	Pro Arg	Ser Arg	
	-85		-80		-75			
CGC CTG	CCG CTC	CCG GCA	GCT GTC	CGC GCC	CAC GGT	CCT ATG	GCG GAC	218
Arg Leu	Pro Leu	Pro Ala	Ala Val	Arg Ala	His Gly	Pro Met	Ala Asp	
	-70		-65		-60			
TGN NCG	GAC TCC	GCG CGG	GGC TGT	GTG GTC	TTT GAG	GAT GTG	TTT GTA	266
Xaa Xaa	Asp Ser	Ala Arg	Gly Cys	Val Val	Phe Glu	Asp Val	Phe Val	
	-55		-50		-45		-40	
TAC TTC	TCT CGG	GAA GAA	TGG GAG	CTT CTT	GAT GAT	GCT CAG	AGA CTT	314
Tyr Phe	Ser Arg	Glu Glu	Trp Glu	Leu Leu	Asp Asp	Ala Gln	Arg Leu	
		-35		-30			-25	
TTG TAC	CAT GAT	GTG ATG	CTG GAG	AAC TTT	GCA CTT	TTA GCC	TCA CTG	362
Leu Tyr	His Asp	Val Met	Leu Glu	Asn Phe	Ala Leu	Leu Ala	Ser Leu	
	-20		-15		-10			
GGA ATT	GCA TTT	TCC AGA	TCA CGT	GCA GTC	ATG AAA	CTA		401
Gly Ile	Ala Phe	Ser Arg	Ser Arg	Ala Val	Met Lys	Leu		
	-5		1		5			

(2) INFORMATION FOR SEQ ID NO: 100:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 61..228
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq FLCFLNLTSHLSG/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```

ATACCTAATG ATAACACAGT ATCTCTTCGA ATTTGTACTA TTGCAGAACA TTTAGAAACA    60
ATG CTT ATT ACT CGK TTA CAG TCT GGT ATA GAT TTT GCA ATC CAG CTT    108
Met Leu Ile Thr Arg Leu Gln Ser Gly Ile Asp Phe Ala Ile Gln Leu
-55                      -50                      -45

GAT GAA AGC ACT GAT ATT GGA AGC TGC ACA ACA CTT TTA GTT TAT GTC    156
Asp Glu Ser Thr Asp Ile Gly Ser Cys Thr Thr Leu Leu Val Tyr Val
-40                      -35                      -30                      -25

AGA TAT GCG TGG CAA GAT GAT TTT TTG GAG GAT TTT TTG TGT TTT TTA    204
Arg Tyr Ala Trp Gln Asp Asp Phe Leu Glu Asp Phe Leu Cys Phe Leu
-20                      -15                      -10

AAT TTA ACC TCA CAC CTA AGT GGA TTA GAT ATT TTT ACA GAA TTA GAA    252
Asn Leu Thr Ser His Leu Ser Gly Leu Asp Ile Phe Thr Glu Leu Glu
-5                      1                      5

AGG CGC GGG                                261
Arg Arg Gly
10

```

(2). INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 191..304
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7

seq LAFLSCLAFLVLD/TQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

AACTCTGCAG GGCCTCCAAG GCCAGGCTTC AGGGCTGGGA CTCAGTCCTG AGGCACTGGG    60
GAGCCATGAG GGGCTGTGGC AGGGAGGGGC AGGGTGTGGA AAGACTCCCC TGGGGCCATG    120
GTGGAGATGT GCTGAGGTCT TCTCCCTGAT CGTCTTCTCC TCCCTGCTGA CCGACGGCTA    180
CCAGAACKAG ATG GAG TCT CCG CAG CTC CAC TGC ATT CTC AAC AGC AAC    229
          Met Glu Ser Pro Gln Leu His Cys Ile Leu Asn Ser Asn
                -35                      -30

AGC GTG GCC TGC AGC TTT GCC GTG GGA GCC GGC TTC CTG GCC TTC CTC    277
Ser Val Ala Cys Ser Phe Ala Val Gly Ala Gly Phe Leu Ala Phe Leu
-25                -20                      -15                      -10

AGC TGC CTG GCC TTC CTC GTC CTG GAC ACA CAG GAG ACC CGC ATT GCC    325
Ser Cys Leu Ala Phe Leu Val Leu Asp Thr Gln Glu Thr Arg Ile Ala
                -5                      1                      5

GGC ACC CGC TTC AAG ACA GCC TTC CAG CTC CTG GAC HKC ATC CTG GCT    373
Gly Thr Arg Phe Lys Thr Ala Phe Gln Leu Leu Asp Xaa Ile Leu Ala
                10                      15                      20

GTT CTC TGG    382
Val Leu Trp
                25

```

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 190..273
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq DHLFLLFPRSCSS/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```

CICITGTAA CCTGTCTTTT GCTATAGGAG TGTCAGACCC TTATGAGGGG AGAGGAGAGA    60
TATCATACTT TTTCTACCTC TACACTTTTA ATATCATTA TTTTCTAACA ATGCCCAAT    120

```

```

CTTCAGTACA CCTCTCTCTC CTGAACCCTA TACTTGTACA GCAACTTTCT ATGTGACATT 180
TCTTCTTAA ATG TCT AAT AAG TAT ATC AAA CCT AGC ATG TCC CCA GGA AAC 231
      Met Ser Asn Lys Tyr Ile Lys Pro Ser Met Ser Pro Gly Asn
                -25                      -20                      -15

ACT GAT CAT CTT TTC CTA CTC TTC CCC CGA AGT TGT TCC TCC CTC GTC 279
Thr Asp His Leu Phe Leu Leu Phe Pro Arg Ser Cys Ser Ser Leu Val
      -10                      -5                      1

```

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 263..334
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq FFFFLFLLPPXPP/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

ATATGTGTAA TGTCTTTATT CCTTAGACTA TGGTCTCCGT GGAAGATTAC TGATACTCCC 60
ACTAGTATTA ATAACAATGT TAGGTAACAT TACTGAATGT TTACTGAGTG CCAGGTAATG 120
TTCTAATTGC TTTACATGTA TTAGGCTATG TATTCCTCAC ATGAACCATA TGAAAGAGAT 180
ACTCTTATTG TTGTCATTTT AGAAGTGAAG AACTGAGGC ACAGAAAAC TAAAGTAATTA 240
GTCCAATTCA TACAGGTAGT AT ATG GTA GAA CTG AAG CAG TTG GGC CCC AGG 292
      Met Val Glu Leu Lys Gln Leu Gly Pro Arg
                -20                      -15

TCT TTT TTT TTC TTT CTT TTT CTT CTG CCG CCG RCT CCT CCA ACC GGG 340
Ser Phe Phe Phe Phe Leu Phe Leu Leu Pro Pro Xaa Pro Pro Thr Gly
      -10                      -5                      1

```

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 17..94

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5
seq LILPALFFFPLHC/TF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```

AARACCTTC TCAGTG ATG CCT TAC GTC ACC ATC CCA TAT ATA ATA GTG TAC   52
      Met Pro Tyr Val Thr Ile Pro Tyr Ile Ile Val Tyr
      -25                      -20                      -15

TCA CTC ATT CTA CCT GCC CTC TTT TTT TTC CCT CTC CAC TGT ACT TTT   100
Ser Leu Ile Leu Pro Ala Leu Phe Phe Phe Pro Leu His Cys Thr Phe
      -10                      -5                      1

CAC GGT CTA ACA TAC TAT ATA TCA TGT GTT TGT TCA TTA TCT CTA CCC   148
His Gly Leu Thr Tyr Tyr Ile Ser Cys Val Cys Ser Leu Ser Leu Pro
      5                      10                      15

ACG
Thr                                     151
```

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 247..321

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5
seq LLLCMDLPHSVLS/NW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```

AATTATTTTA TAAACTTCT GGCTGGATTT AAATACTAGG CAGTATTCCA AGGGATGATA   60
```

```

AAATGTTTTT ACAAACTTAA TTAGACCCAT TTTTGTAAAT AAACTTTATT ATACATGTGC 120
TATGAGGATT AAACTTTGCC TCATAAAAGT ATTCTGACAG GTGCTTTGCA CAGAGTAAGT 180
CCGCCAAAGT GGACGTTCTC ATATGTAATT CTGAGCTTAC TCATACTGGC CAGGAAGGAC 240
GTGCAC ATG CCA CCT TTG GCA GCT GTG ATG GGG AGC CTG CCT CTG CTC 288
      Met Pro Pro Leu Ala Ala Val Met Gly Ser Leu Pro Leu Leu
      -25                -20                -15

TTG TGC ATG GAC CTT CCA CAT TCT GTC CTG TCC AAC TGG 327
Leu Cys Met Asp Leu Pro His Ser Val Leu Ser Asn Trp
      -10                -5                1

```

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 186..248
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq EFLFLGFPSNSW2/HR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

```

ACAGCTAGAA TATGTTGGAT TCAGGAGCTT GTCCATTATT TGTAGGTAAA AAAAGCTGCA 60
CGTAGATTTG ACTTCAACTC CGTAAAAAAG ACAGCTGTAT TTTCCGTCCA ACTGGAATTG 120
TTGAATCACA CTGCATAGCT GCCCAAAAGA GASTGTTTGG TCTTGAACCT TCTATACTTT 180
TATAA ATG TTA CAA ATT CCC GAA AGA AGG GAA TTT CTT TTT CTG GGG TTT 230
      Met Leu Gln Ile Pro Glu Arg Arg Glu Phe Leu Phe Leu Gly Phe
      -20                -15                -10

CCT TCA AAC TCT TGG CCC CAC AGG 254
Pro Ser Asn Ser Trp Pro His Arg
      -5                1

```

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 49..102
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq FLITLFCCCVVVG/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

```

ACATGTATCT GTTGGCTATT TGTATATCAT CTTTGCATCT TTGGATAA ATG TTC TTT      57
                                   Met Phe Phe
GTC CAT TTT TTA ATC ACT TTA TTT TGT TGT TGT GTT GTA GTG GGG TTT      105
Val His Phe Leu Ile Thr Leu Phe Cys Cys Cys Val Val Val Gly Phe
-15          -10          -5          1
TTT GGC CAT GAT CAT TCA TTT ATC TCA CAG TTC ATT CTT GTT ACT TGG      153
Phe Gly His Asp His Ser Phe Ile Ser Gln Phe Ile Leu Val Thr Trp
          5          10          15
GCC AGG GCA GGG                                  165
Ala Arg Ala Gly
          20

```

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 83..157
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq CLLHLRCLQLYWA/AR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

ATCAGTGTAT TTTTTTTATA GATTAAAAAT ATACCTGAAA ACTTTTCTAG GAAGAATAAT	60
TATTCATGGA AAGAGCATTG TA ATG GCA TGT TTT GGG GAG AAA AGA CAT GCC	112
Met Ala Cys Phe Gly Glu Lys Arg His Ala	
-25 -20	
AAG TCT TGT TTA CTA CAT TTA AGA TGT TTA CAA CTA TAC TGG GCT GCT	160
Lys Ser Cys Leu Leu His Leu Arg Cys Leu Gln Leu Tyr Trp Ala Ala	
-15 -10 -5 1	
CGG	163
Arg	

(2) INFORMATION FOR SEO ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 279..362
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq PLSLALQSSCCCLC/LT

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 109:

AATAAACCTT	ACTTTAACAG	AATTTAACAG	ATATCTCTTT	AAAAAACTGC	TTTAATGTTT	60
TTACCTTCTA	TCTTCTTTTT	CTCCAGCTTT	ATCCTGACAG	RGAAGTTAGC	ACTAATTAAT	120
CTATTTTCTC	TTCCCCCTCT	TTTTTCCCTT	GTGTGTGTCT	TTTCTGCCTT	CATCTACCCC	180
AGTGAATTTG	TTCAGCATTT	TGGCTCACTC	ATTTCTTCAG	CTAACTACAG	CTTACTACTA	240
CAGCCACCAC	TACTAGAGCC	ACTCCTGTCT	CATCCTGG	ATG GTT GAC AGA GAT GAA		296
				Met Val Asp Arg Asp Glu		
				-25		
AAC ATC TTG CTA AAG CAA ATA TAC AGY CCC CTT TCA CTG GCT CTC CAG						344
Asn Ile Leu Leu Lys Gln Ile Tyr Ser Pro Leu Ser Leu Ala Leu Gln						
-20		-15		-10		
TCC TCC TGC TGT CTT TGC TTG ACC TCC TGC						374
Ser Ser Cys Cys Leu Cys Leu Thr Ser Cys						
-5		1				

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 115..174
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq VSVSLCVCDCVRG/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

```

ATAAAATTTA CAGAAAAGTT GCAAAGAAGA TAGAATTCTT GCTTAGCTTT TGCCCCAATT   60
TCCCCTTGTC CACCCTTCCC TCTTTGTGTT TGTATCTTTT TTTTCTGAG CCAC ATG   117
                                         Met
                                         -20

AAA GTA AAG CCG CCT TTT GTG TCT GTG TCA CTC TGT GTG TGT GAC TGT   165
Lys Val Lys Pro Pro Phe Val Ser Val Ser Leu Cys Val Cys Asp Cys
          -15          -10          -5

GTA AGG GGT AGC ACA CTT ACA TGG AAC AGG TTA CTG CGT GTG GGA GGG   213
Val Arg Gly Ser Thr Leu Thr Trp Asn Arg Leu Leu Arg Val Gly Gly
          1          5          10

```

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 68..184

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.4
 seq ILLTSCFYTLVSS/TF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

ATGGCTAACA TATTCTTTTT TTTTCTCTG TAGTAGTTTT TTGAAAGAAG AAATAGGCTA   60
TTCTAGC ATG ATC TCA TCC TGT GGA GTT AAA TAC .TTG TTT TCA CAT GCC   109
      Met Ile Ser Ser Cys Gly Val Lys Tyr Leu Phe Ser His Ala
                    -35                      -30

TCC TTA TTT TTT ATG GTA GGG AGT ACA GGA AGT TTA ATA CTC TTA ACT   157
Ser Leu Phe Phe Met Val Gly Ser Thr Gly Ser Leu Ile Leu Leu Thr
-25                      -20                      -15                      -10

TCT TGT TTC TAT ACC CTT GTT TCA TCA ACC TTT CTT CAA AAA CTC TCT   205
Ser Cys Phe Tyr Thr Leu Val Ser Ser Thr Phe Leu Gln Lys Leu Ser
                    -5                      1                      5

TCT TTG CTC TTG ATA TTA TTT ACC GAA ACA AGT GTY CTT ATG TTA AAA   253
Ser Leu Leu Leu Ile Leu Phe Thr Glu Thr Ser Val Leu Met Leu Lys
      10                      15                      20

ACA TTT GTA GCT AAT TCT TGC TGT WAA TTG TGG TCT CAC AAT TGT ATT   301
Thr Phe Val Ala Asn Ser Cys Cys Xaa Leu Trp Ser His Asn Cys Ile
      25                      30                      35

AAT TTC TTC AAA AAG GTC CKG CCT TCT TAT TGC KGC AGC AGT CTA CTC   349
Asn Phe Phe Lys Lys Val Xaa Pro Ser Tyr Cys Xaa Ser Ser Leu Leu
      40                      45                      50                      55

TTC CTG GCC GTA CCT AGG   367
Phe Leu Ala Val Pro Arg
                    60
  
```

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 174..233
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq SFLCNFLVSLSL/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```

AGAAGGGGGT GAAAGGAGTA ACTGCTATAT TTAGAAGGAG GTTAAGGATA GCAATTGATT    60
TTAAGGGTGG GGCTAGGGAA CTTGTCTTTA AAATCCTGCA TTTGCACAGC AAGCACAGTT    120
CGTATTGAGA TTTTGCTATT TGGAAGTGTG AGGGAGGTAT AGGATGCTGC CTA ATG      176
                                   Met
                                   -20
GGA GGT GGG ATH GCA GAG AGT TTT CTA TGT AAT TTC TTG GTA TCA CTT      224
Gly Gly Gly Ile Ala Glu Ser Phe Leu Cys Asn Phe Leu Val Ser Leu
               -15                      -10                      -5
TCC CTC TCT TTC CTC CAT GGC CGG
Ser Leu Ser Phe Leu His Gly Arg
               1                      5

```

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 265..363
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq LAYFLCCQGVIFG/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

```

CTATTTCTCA TTGTCTGTCT GGTTTCCAT CCCCCTCACA TGTGGTGACC AGCACCTGGC    60
CCGCCACGGC AGCCAGGAGG CATTTGTTAA GCGAATAATC GAGACAGGGA AGAGGAGTGG    120
AGTTGGCTGC TCCAGACTCT GCTTAGTTTT CCTTTCTCAA AGTTCTCCCT CCTGTGTCCT    180
AGCCGGGGAA TTAGCTAAAA TGGAATTTTC TTTGGTGATC AGGTATCCTT CTGATGAAGA    240
GAAGAAAGGC CTAAACTCCC AGGC ATG GAT GCA TTA GAA AGA GGT AGT CTT      291
                                   Met Asp Ala Leu Glu Arg Gly Ser Leu
                                   -30                      -25
AGA AAT GAG CAG GCG TTG GTT ATT TAT GCA GGA CTG GCA TAC TTT CTG      339
Arg Asn Glu Gln Ala Leu Val Ile Tyr Ala Gly Leu Ala Tyr Phe Leu
               -20                      -15                      -10

```

TGC TGC CAA GGG GTG ATT TTT GGA AGT CTC CCC TCT AAT GCT GGT GCT 387
 Cys Cys Gln Gly Val Ile Phe Gly Ser Leu Pro Ser Asn Ala Gly Ala
 -5 1 5

GGG CCT TTG GGA TGG TCT AGC 408
 Gly Pro Leu Gly Trp Ser Ser
 10 15

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 78..194
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq SLWFLPLPTHVYT/HT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

TTGCTTGAAC CTAAGTGTCT TGTTTTTGTC TTCCTGTGAG TTCAAGGACA GGAGCAGTGC 60

TTAACACACA GTAGGTA ATG GAA TAT TTG TTC CAG CAG CCT GGA CAC TCA 110
 Met Glu Tyr Leu Phe Gln Gln Pro Gly His Ser
 -35 -30

AGG GGA GAA GCC AGG GCT GCT GCT GCC TCT CTG GAA ACC CTG TCT TCC 158
 Arg Gly Glu Ala Arg Ala Ala Ala Ala Ser Leu Glu Thr Leu Ser Ser
 -25 -20 -15

CTT TGG TTT CTG CCT CTC CCA ACC CAC GTG TAC ACA CAT ACA CAT GCC 206
 Leu Trp Phe Leu Pro Leu Pro Thr His Val Tyr Thr His Thr His Ala
 -10 -5 1

AAC 209
 Asn
 5

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 283..327
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq SSMLITILSFIFA/LG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```

ACCACAGTCA CTGTCACATT ATTCTGTTTT GTATTTTATT TACAGCTCTT ATAATTATCC    60
GAACTTACAA ATTTATTTTC TTGTGTTTTC TCCGCCTGCT CCTCCACTTC ATTCTGTAAT   120
ACTATAGTTC ACTATAATAC TTCTAGTTCC TAGGACTGGA ATTATGTGTC TGGCACATAG   180
TAGACAGTAG ATGTTCAITG AATGAATGAA TGATTCAAAT GAGATTTAAA TAGCAACAGT   240
CCTGACAGAA TGGTAAATTT CCACACTTAA GATGGTCTGT TA ATG GTA TCA TCA      294
                               Met Val Ser Ser
                               -15-

ATG TTG ATA ACT ATT CTA TCG TTT ATT TTT GCC TTA GGG TAC CAC ACA      342
Met Leu Ile Thr Ile Leu Ser Phe Ile Phe Ala Leu Gly Tyr His Thr
-10          -5          1          5

GCT TCT TAT CCA GTC TCC CTT CAT CCA CTC TCC TTT TTC CTA CAC          387
Ala Ser Tyr Pro Val Ser Leu His Pro Leu Ser Phe Phe Leu His
      10          15          20

```

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 316..359
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq MNLVSALASSAXG/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

```

ACAGTACTTG GAGGTATTCT AAAGGCAGAC ATACTTTATC TGAGCAGGTG CTTTGGCGT   60
GGTCCTGCCA AGAAAGAAAC AATGGCTTAG ATGACGTCTA TTCTAAGGCC TCAAGGCTTG   120
CACCCCTGCC ATGCTAAATA CAGATGCGCT CCTCCACCAA GAGAATCCCC TCTGCCCTCT   180
GCCATCTCAG CCCCAGCCA GCTCAGCTGC CCATGACCTG TGTGCAAAGC AGGGGGCGGG   240
ACAAACAGCT ATCGCCTTTG GCCTTCCCTT TGCTCCTGAC AGCGGTCTCA AACCTGGAGG   300
AGTCAAAGGT CCAAG ATG CCT TTG TTC ACT ATG AAC CTG GTG TCA GCT CTA   351
          Met Pro Leu Phe Thr Met Asn Leu Val Ser Ala Leu
                -15                      -10

GCG TCC TCA GCA RCA GGG CAG CGT GGA GCA GGG CCA GCC CTC TGG CAC   399
Ala Ser Ser Ala Xaa Gly Gln Arg Gly Ala Gly Pro Ala Leu Trp His
    -5              1              5              10

TTG TGT                                     405
Leu Cys

```

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 110..226
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq LILLHCSIRVFF/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

```

CTTGCTTGTA AACATAAGCA TGTATTATTA CCTAGGCTTT GAATTTCAAA ATACGGTGTA   60
AACTACTCAT GGTAATATAG ATCTTGTTAG ACAAACGTTT ATGTAAAAA ATG ATC TGC   118
          Met Ile Cys

AAG CAT TAC TGT ATA AAG AAA AAT AAC CTG GAT TAC TTG AAT AGA ATG   166
Lys His Tyr Cys Ile Lys Lys Asn Asn Leu Asp Tyr Leu Asn Arg Met
    -35          -30          -25

GTT TAC AGT GCT CAG TTA AAG TTG ATA CTT CTT CTA CAT TGC AGT ATT   214

```

Val Tyr Ser Ala Gln Leu Lys Leu Ile Leu Leu Leu His Cys Ser Ile
 -20 -15 -10 -5

AGG GTT TTT TTT TTT TTT
 Arg Val Phe Phe Phe Phe

232

1

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 232..390
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq SFLLLQLIHEDKA/IQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

AATTTGAGAA GTGCCCTCCT ATACTTAGAG AAAAGGAATA TCCATATCTC TGAAGACACA 60
 GGGACACAGA GAGAATCTGA ACACACAGCC TTGGTAGGAT TCCTTCCGTT TATCATCATT 120
 AGATCATAAC CCCYTTTGTC MAGTCCTATT TCTCCARGAC TGCCTCCTTC TTCATTAAAC 180
 CTTGCATAAA AACTCACAAA TTTAACCATT TATTTGGATT CTTATTTCTT T ATG AAA 237
 Met Lys
 ATT CCT GTG TGG CAT AAA ACG TGC TTT TTA AAA TCT GAA AGT TTT TCT 285
 Ile Pro Val Trp His Lys Thr Cys Phe Leu Lys Ser Glu Ser Phe Ser
 -50 -45 -40
 CCT GAT AAT TTA TCT GTT AGT TTG CCT TGT AGA CCT AGC CAG GTA CCC 333
 Pro Asp Asn Leu Ser Val Ser Leu Pro Cys Arg Pro Ser Gln Val Pro
 -35 -30 -25 -20
 TCA CAG GGG CAA GGA AAA TCT TTT CTC CTC CTA CAA CTT ATA CAT GAG 381
 Ser Gln Gly Gln Gly Lys Ser Phe Leu Leu Leu Gln Leu Ile His Glu
 -15 -10 -5
 GAT AAA GCC ATC CAG AAT GAA GCT ATT TTC CAG CCT TCT CTG CAG CTG 429
 Asp Lys Ala Ile Gln Asn Glu Ala Ile Phe Gln Pro Ser Leu Gln Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 133..189
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq FGCTFVAFXPFAFA/LS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

```

AGTCTGGGGG TGACATTGCA CCGCGCCCCT CGTGGGGTCG CGTTGCCACC CCACGCGGAC   60
TCCCCAGCTG GCGCGCCCCT CCCATTGCC TGTCTGGTC AGGCCCCCAC CCCCTTCCC   120
ACCTGACCAG CC ATG GGG GCT GCG GTG TTT TTC GGC TGC ACT TTC GTC GCG   171
      Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala
                -15                      -10

TTC DGC CCG GCC TTC GCG CTT TCH TTG ATC ACT GTG GCT GGG GAC CGT   219
Phe Xaa Pro Ala Phe Ala Leu Ser Leu Ile Thr Val Ala Gly Asp Arg
-5                      1                      5                      10

GGG
Gly
222

```

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 80..181
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.2
seq LWSSCWLA^{PL}ADG/ML

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

```

AAGATGAAGA GGAGCGDGTG GCAGTGGTGG AAGAAGAGGC GCGGCGGCGG GGGTAGGGAG    60
CCTGGAAACG CGAGCGGGG ATG GTA GGT GGT TTG GAC CCG CCG GGC CGC CGT    112
      Met Val Gly Gly Leu Asp Pro Pro Gly Arg Arg
                        -30                        -25
CGT TTC CAG AAA GGG TTT GAC TGG AGG AAC CTC TGG AGC AGC TGT TGG    160
Arg Phe Gln Lys Gly Phe Asp Trp Arg Asn Leu Trp Ser Ser Cys Trp
      -20                        -15                        -10
CTG GCT CCT CTG GCT GAT GGC ATG TTG AGG TAC ATG GGC CAG CVG CAG    208
Leu Ala Pro Leu Ala Asp Gly Met Leu Arg Tyr Met Gly Gln Xaa Gln
      -5                        1                        5
CGA NGG GCA TCC AAT CCA GAG GGG TCC ACT CTA GAG GCC AGG CCA CCA    256
Arg Xaa Ala Ser Asn Pro Glu Gly Ser Thr Leu Glu Ala Arg Pro Pro
      10                        15                        20                        25
GCA CCA TRG GCC AGT GTG TCA CCA AGT GTA AKH MTC CCT CAT CGA CCC    304
Ala Pro Xaa Ala Ser Val Ser Pro Ser Val Xaa Xaa Pro His Arg Pro
      30                        35                        40
TGG GCA GCA AAA ATG GAG ACC GTG AGC CCA GCA ACA AGT CRC ATA GCA    352
Trp Ala Ala Lys Met Glu Thr Val Ser Pro Ala Thr Ser Xaa Ile Ala
      45                        50                        55
GGC GGG
Gly Gly

```

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 110..172
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq SLLVVSCFYQISG/RW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

```

ATAGAACTAC TGC GGAACCT CAAAATCAGT AGATTGGAA GTGATTCAAA GCTAAACTTT    60
TTCCTTGGCC CTCCKTGTGT TCTAATTGCT TTGCAAGTGT AAKACTAGG ATG TCC AAG    118
                                   Met Ser Lys
                                   -20

ATG CCA GTT TTT GCT TCT TTG TTA GTT GTC AGC TGC TTT TAT CAA ATT    166
Met Pro Val Phe Ala Ser Leu Leu Val Val Ser Cys Phe Tyr Gln Ile
      -15                      -10                      -5

TCA GGC CGC TGG                                                    178
Ser Gly Arg Trp
      1

```

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 136..180
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq VTQLLPFSSPDSA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```

AACAAAGAGA CACAGACAGG GGACTGTCAG CYGGYACCGG AGGMGCGGAC AACGAGTTAT    60
CAGCAACTSA AAGCACCTGA BGGGCCGCAC ATTCCANCCC CAGCCCAGTC CTCGTCCTCC    120
ACGCCAGCNC CAAGC ATG TSA GTA ACC CAA CTT CTC CCT TTC TCC TCC CCA    171
      Met Xaa Val Thr Gln Leu Leu Pro Phe Ser Ser Pro
      -15                      -10                      -5

GAC TCT GCG GGT CCT TTT CTG TCC CCT TTC TCT                        204
Asp Ser Ala Gly Pro Phe Leu Ser Pro Phe Ser
      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..102
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq SFHFLPWALGAMA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 2..142
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq VIRLSQFLLKCWP/RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

```

A ATG AAA GTG ATG ATG AGG AAG AGG AAG AAA AAG GAC CAG TGT CTC CCA   49
  Met Lys Val Met Met Arg Lys Arg Lys Lys Lys Asp Gln Cys Leu Pro
    -45                      -40                      -35

GGA ATC TGC AGG AGT CTG AAG AGG AGG AAG TCC CCC AGG AGT CCT GGG   97
  Gly Ile Cys Arg Ser Leu Lys Arg Arg Lys Ser Pro Arg Ser Pro Gly
    -30                      -25                      -20

ATG AAG GTT ATT CGA CTC TCT CAA TTC CTC CTG AAA TGT TGG CCT CGT  145
  Met Lys Val Ile Arg Leu Ser Gln Phe Leu Leu Lys Cys Trp Pro Arg
    -15                      -10                      -5                      1

ACA AGT CTT ACA GCA GCT ACG   166
  Thr Ser Leu Thr Ala Ala Thr
                5

```

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 254..361
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq SFSIXTLLWGLNC/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

```

ACTGTTTTAG TGTITGAAT ATCTTCTTCC AGAGTTTGAT GTATAGTAT CTGGAGGTA   60

TATGTATTTC TAATTATATA AATATTGAC CCTCTTGCC TARTTGTTT TATCACTTC  120

AACTTGACC CTTTATACTT CTTTAAAT TTCACCTTCT TATGGTTGTT TTTCTACTTT  180

TCCTCAATGC CCTTTGTAAA ATTTTCATTT GAATCTATTA TTCTCCCTTG GACGTCTTAA  240

TTCCTTCTCT ACT ATG ACT TTT TCT TIC TTT TGT TTC TTT CCT GGG TTC   289
  Met Thr Phe Ser Phe Phe Cys Phe Phe Pro Gly Phe
    -35                      -30                      -25

AAG CCA CTC CTG TTT CAT TAC TTT CTT TTT WNK TCC TTT TCT ATT TKD  337
  Lys Pro Leu Leu Phe His Tyr Phe Leu Phe Xaa Ser Phe Ser Ile Xaa

```

	-20		-15		-10	
ACT CTK CTT TGG GGC TTG AAC TGT AAG AGG TCC TGG AAC ATA AAT TTG						385
Thr Leu Leu Trp Gly Leu Asn Cys Lys Arg Ser Trp Asn Ile Asn Leu						
	-5		1		5	
AGA ATT GTT GSA TCA TAC AGT AGT GGT TAC						415
Arg Ile Val Xaa Ser Tyr Ser Ser Gly Tyr						
	10		15			

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 11..133
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq RLLLILSGCLVYG/TA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

AGAGGCAACC ATG GCG GGA GGA ATG AAA GTG GCG GTC TCG CCG GCA GTT		49
Met Ala Gly Gly Met Lys Val Ala Val Ser Pro Ala Val		
	-40	-35
		-30
GGT CCC GGG CCC TGG GGC TCG GGA GTC GGG GGC GGT GGG ACA GTG CGG		97
Gly Pro Gly Pro Trp Gly Ser Gly Val Gly Gly Gly Gly Thr Val Arg		
	-25	-20
		-15
CTA CTC TTG ATC CTC TCC GGC TGC TTG GTC TAC GGC ACA GCT GAA ACT		145
Leu Leu Leu Ile Leu Ser Gly Cys Leu Val Tyr Gly Thr Ala Glu Thr		
	-10	-5
		1
GAT GTA AAT GTG GTC ATG CTT CAG GAA TCC CAA GTT TGT GAA AAG CGT		193
Asp Val Asn Val Val Met Leu Gln Glu Ser Gln Val Cys Glu Lys Arg		
	5	10
		15
		20
GCC AGC CTC GGG		205
Ala Ser Leu Gly		

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 58..153
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq PLLSCSCPPPLLG/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```

ACTTCCACGG GACCCACCAG CTAAATGCC GGCAGCCCTG GGACTTCTGG CCTCACA      57
ATG GTT GAG ATG ACT GGG GTG TGG CAG TGC CAA GCC GAG GCT GTG AAA      105
Met Val Glu Met Thr Gly Val Trp Gln Cys Gln Ala Glu Ala Val Lys
      -30                      -25                      -20

GGC CTT CCA CCT TTA CTC TCG TGC TCG TGC CCT CCC CCA TTG TTA GGA      153
Gly Leu Pro Pro Leu Leu Ser Cys Ser Cys Pro Pro Pro Leu Leu Gly
      -15                      -10                      -5

GAA GGG CAT GCT CAG GCC AGC CCA TTA GCC CAG GAG GAG GAC AAG AAA      201
Glu Gly His Ala Gln Ala Ser Pro Leu Ala Gln Glu Glu Asp Lys Lys
      1                      5                      10                      15

CAC ACG GAG CAG ACA CAA GCC ACC TCA CCA ACC CAG CCT      240
His Thr Glu Gln Thr Gln Ala Thr Ser Pro Thr Gln Pro
      20                      25

```

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 59..121
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5

seq AGLLP LLLGNAPG/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

```

AATTTGCTCA CACCCAGCAG GCAGAGAAGG CAGCAGCAGG CAGGACCGCC ACCCTCCC      58
ATG CAA ATC ACC CCC GGG AGT GCA GCT GGG CTC CTC CCG CTC CTC CTA      106
Met Gln Ile Thr Pro Gly Ser Ala Ala Gly Leu Leu Pro Leu Leu Leu
  -20                -15                -10
GGC AAT GCT CCT GGG GAG TCT GTT GGG GGA AGA TGC SAT CCA GGG TGC      154
Gly Asn Ala Pro Gly Glu Ser Val Gly Gly Arg Cys Xaa Pro Gly Cys
  -5                1                5                10
TGG
Trp

```

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 152..202
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq TWLLLTQNSVFT/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

```

AGAATTTTGC TGGGAATTAA TATTAAATAC TCACTGGAAT TTATCTTTAC CAACTTTAGT      60
GGAATTCAGC CTATCTACAG CTCTCCTTTC CACTTTGTTT CTCAGAAATT CTCAGCAATG      120
GTTTCATGAA CCACTGGGAG GTCATTTGCC T ATG ATT TTG TCC ACC TGG CTC      172
                               Met Ile Leu Ser Thr Trp Leu
                               -15
TTA CTT ACC CTT CAA AAC TCA GAA TTT ACA TCT TTC AGG ATA TCT CCC      220
Leu Leu Thr Leu Gln Asn Ser Val Phe Thr Ser Phe Arg Ile Ser Pro
-10                -5                1                5
AAC AGA ATA CAA AGT ATG CTA CCT CCC ATG
Asn Arg Ile Gln Ser Met Leu Pro Met
  10                15

```


(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 33..128
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq VCIVLALCHTSRP/MS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

```

AAATCTCTTC TAATCCTCCT TAATGCATTT TG ATG GCT TTT CAT AGC TAT TGG      53
                               Met Ala Phe His Ser Tyr Trp
                               -30

GGA AAA AGT TTA CAA TCC TTT AAG ACG TTC ATG AGA GTC TGC ATT GTC      101
Gly Lys Ser Leu Gln Ser Phe Lys Thr Phe Met Arg Val Cys Ile Val
-25                -20                -15                -10

TTG GCC CTT TGC CAC ACA TCC AGA CCC ATG TCT TAC CAT GTT CCC CTG      149
Leu Ala Leu Cys His Thr Ser Arg Pro Met Ser Tyr His Val Pro Leu
                -5                1                5

GCT GCT GGC TCC CCA CTC ATG CAC TGG TCT CCT TGT AGT CCT GTG CCC      197
Ala Ala Gly Ser Pro Leu Met His Trp Ser Pro Cys Ser Pro Val Pro
                10                15                20

TTC ATT GGG                                206
Phe Ile Gly
25

```

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: 113..160
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.9
 seq RFTLLPLVLHSQS/SC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

```

ATTCTCGTA AATGATGAGA TGGGGTTAAA TGGTTTTGCA GAAATATGTG AGAGGTAATG   60
TGAAATAAGT TACTTTAAGA AGGCCTGGCC CTGGTAATGT CGTTACCAGC TG ATG AAG   118
                                     Met Lys
                                     -15

TTG CGG TTT ACC TTG CTG CCC CTG GTG CTA CAT TCA CAA AGC AGC TGT   166
Leu Arg Phe Thr Leu Leu Pro Leu Val Leu His Ser Gln Ser Ser Cys
          -10                -5                1

GTC TTT TGG AAA GCC GGG   184
Val Phe Trp Lys Ala Gly
          5

```

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
 (E) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: 4..93
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.9
 seq FIFPLVIYSFVLS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

```

ACC ATG ATG ATC ATT CTG GGG TTT GCT TTT TGC CCT GST CAC TTT AGG   48
Met Met Ile Ile Leu Gly Phe Ala Phe Cys Pro Gly His Phe Arg
-30                -25                -20

TTT AAT TTT ATT CCA TTC CTG GTC ATT TAC AGT TTT GTT CTG TCA TCT   96
Phe Asn Phe Ile Pro Phe Leu Val Ile Tyr Ser Phe Val Leu Ser Ser
-15                -10                -5                1

CCC CAT ACC CAT CGA GAA CCC TAT TCT CCT GTG GCA GAC TTT AAT GAA   144
Pro His Thr His Arg Glu Pro Tyr Ser Pro Val Ala Asp Phe Asn Glu
          5                10                15

```

TGT AAC CGC AGT
Cys Asn Arg Ser
20

156

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 198..278
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq CLLSYIALGAIHA/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

```

AACTTTGCCT GGGTGTCTTG CGTTCTGCAC ATTCCGGAGG ACCAGCTTCC CCATCAGAAG   60
TCTGACTCCA TGGAAACCAG ATGGGGCAAC GGGGTGGTTC TAGTGCAGAC TGTAGCTGCA  120
GCTCCTCTCC ACCTCTAGCC TGCTCATTTT CAGCTCAGAA ATTCTACTAA TGGCGTTTTT  180
TCTTCCTGAA AAAGGAA ATG AAC AGG GTC CCT GCT GAT TCT CCA AAT ATG   230
          Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met
          -25                      -20

TGT CTA ATC TGT TTA CTG AGT TAC ATA GCA CTT GGA GCC ATC CAT GCA   278
Cys Leu Ile Cys Leu Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala
  -15                      -10                      -5

AAA ATC TGT AGA AGA GCA TTC CAG GAA GAG GGA AGA GCA RRT GCA AAG   326
Lys Ile Cys Arg Arg Ala Phe Gln Glu Glu Gly Arg Ala Xaa Ala Lys
   1           5           10           15

ACG GGC GTG                                     335
Thr Gly Val

```

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 195..239
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LFLNLPLVIGTIP/LH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

```

AATATGTAAA TGTACTATAC AGAATTATAC ATAAAAGAGA AACTTTTCAT GTATGTAAGT   60
TAAAAAATGA AGTAAATGGG GGTTCAAAT AACATTARAA TTGGTTATGA GTTTTGTAAA  120
AGGAAATCAT ACTTGGCATT CTAAACTTAA TATTTCTTTG CAATGTTTAG GTATATGTGG  180
ATATTCCTGG AGCT ATG GAT TTA TTT CTT AAT TTG CCA CTT GTC ATC GGT   230
      Met Asp Leu Phe Leu Asn Leu Pro Leu Val Ile Gly
      -15                      -10                      -5
ACC ATT CCT CTA CAT CCA TTT GGT AGC AGA ACC TCA AGT GTA AGC AGT   278
Thr Ile Pro Leu His Pro Phe Gly Ser Arg Thr Ser Ser Val Ser Ser
      1                      5                      10
CAG TGT AGC ATG AAT ATG AAC TGG CTC AGT TTA TCA CTT CCT GAA   323
Gln Cys Ser Met Asn Met Asn Trp Leu Ser Leu Ser Leu Pro Glu
      15                      20                      25

```

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 11..229
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq VIRSTLVLSQCLC/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

AAAAATATTAA ATG GMA AAA AAT CAC AGA AAT AAA AAA TCC ATA CAT TTT	49
Met Xaa Lys Asn His Arg Asn Lys Lys Ser Ile His Phe	
-70 -65	
CCA CTG TGC ACC ATT CCA AGT AGM ATG MTG AAA TCT TGT ACT CTC CCA	97
Pro Leu Cys Thr Ile Pro Ser Xaa Met Xaa Lys Ser Cys Thr Leu Pro	
-60 -55 -50 -45	
CTT CAG CGC ACC TGG GAC ATS MAT CCT TCC TTT GTC CAT TGG AWC CAA	145
Leu Gln Arg Thr Trp Asp Xaa Xaa Pro Ser Phe Val His Trp Xaa Gln	
-40 -35 -30	
GCC CGY CTA CAA ICC CCA CCG YCT AGT CAC TTA GTA SCC CTC TCG GTG	193
Ala Arg Leu Gln Ser Pro Pro Xaa Ser His Leu Val Xaa Leu Ser Val	
-25 -20 -15	
ATC AGA TCG ACT CTC GTG CTA TCC CAG TGC TTG TGT TCA AGG MAC CCT	241
Ile Arg Ser Thr Leu Val Leu Ser Gln Cys Leu Cys Ser Arg Xaa Pro	
-10 -5 1	
TAT TTT AGT GCA ATG ATG ACC CCA AAG TGC AAG AGT ATT GMT GCT GGC	289
Tyr Phe Ser Ala Met Met Thr Pro Lys Cys Lys Ser Ile Xaa Ala Gly	
5 10 15 20	
AAT TCA GGT ATG CCA AAG AGA AAC TGT AAA GTG CTT CCT TCA AGT GAA	337
Asn Ser Gly Met Pro Lys Arg Asn Cys Lys Val Leu Pro Ser Ser Glu	
25 30 35	
AAG ATG MAA GTT CAC	352
Lys Met Xaa Val His	
40	

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 317..358
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq SFIALVYSSLSFQ/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

```

AGAGCAAAGC AGACAGAAAT TCCTCTGGTT CTGTAGAGCT GACAATTCAT TAATGTGAGG   60
TAGTCAATAA CAAATATATT TTATGTCAAG TGGTGRATGG DTYCDATTGA AGAAAAATGA   120
CTCAATAAGA GGAGAGAAAA TGATGGTATG TGTATGGTGG GTAGGTGTGC GTGATGCTGT   180
TTTGGATAGC GAGGCCTCCG ATTAGATGCT ACGTGAGCAG GGACCCAAAA GAGCCATGTG   240
TTTCATCTAC CTGGGGGAGA AGCCTGCTGG CAGATCCTGT TGAACACTCG TTACCTAAAT   300
CTCTTGCAAT GGCTCC ATG TCA TTT ATT GCT CTA GTG TAT TCT TCA CTA TCT   352
          Met Ser Phe Ile Ala Leu Val Tyr Ser Ser Leu Ser
                    -10                               -5

TTT CAG AAA GTG CCA GGG
Phe Gln Lys Val Pro Gly
          1

```

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 93..158
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq IVLFLNSXFPIIC/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```

ATATATAGA TCTTTAATTT CTCTCAGCAA TGATTATAGT TCACAATGTG GAGGATTTAC   60
ATGTCTTTCA TTAAATTTAT CCAAAGTACT TT ATG GTT TTT GAT ACT TTA AAA   113
          Met Val Phe Asp Thr Leu Lys
                    -20

AGT AGA ATT GTT CTT TTT TTA AAT TCG RWT TTC CCA ATC ATT TGC AGC   161
Ser Arg Ile Val Leu Phe Leu Asn Ser Xaa Phe Pro Ile Ile Cys Ser
-15          -10          -5          1

CGG
Arg

```

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 68..244
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq IFLEFSILLMSLRT/FH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

```

AAAGCACAGA TGGCAGTCCA TTCATTGAAG ATGGTTTTTT TCAAGGTGAG TGTTGGTCTT    60
TTGCACA ATG CTT GAG ATG GAA ATG ACT TGG CTG AGA CTA TGT GAT GAG    109
      Met Leu Glu Met Glu Met Thr Trp Leu Arg Leu Cys Asp Glu
                        -55                      -50

TGC TCC AGA TGG GGC ATG GCA TCG GCA TGG GGT AGG GGT GGA AAG CTT    157
Cys Ser Arg Trp Gly Met Ala Ser Ala Trp Gly Arg Gly Gly Lys Leu
-45                      -40                      -35                      -30

CTT GGA GCT CAA GTA GCC CTT CAT CCT AGA AAC TGC AGC AAA GCT AAG    205
Leu Gly Ala Gln Val Ala Leu His Pro Arg Asn Cys Ser Lys Ala Lys
                        -25                      -20                      -15

ATC TTC CTG TTC AGT ATT TTA TTA ATG TCT TTA AGA ACT TTT CAC TGT    253
Ile Phe Leu Phe Ser Ile Leu Leu Met Ser Leu Arg Thr Phe His Cys
                        -10                      -5                      1

AAT TAT TTC AGA GGC AAT GGG                                274
Asn Tyr Phe Arg Gly Asn Gly
      5                      10

```

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 104..154
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq MLFFLGALCRESG/V?

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

```

AACAAAGGAG GGAAGGGTTA GAGTGAGGTA CTCACCCAGA GAAGAGCTGT CCCGGCCTGG      60
GGGTCCCAIT CGTCCCTTCT CTTTCTTGCC AAAGAGACGG CCT ATG GAT GAC TTG      115
                                     Met Asp Asp Leu
                                     -15

ATG CTC TTC TTC TTG GGG GCT TTG TGC AGA GAA TCT GGG GTG CCC TCA      163
Met Leu Phe Phe Leu Gly Ala Leu Cys Arg Glu Ser Gly Val Pro Ser
      -10                      -5                      1

CTG GGA AAG CAG GAG AGA ATG AGA GCA TAT GCT GCT GAG ATG CCC CCT      211
Leu Gly Lys Gln Glu Arg Met Arg Ala Tyr Ala Ala Glu Met Pro Pro
      5                      10                      15

CTC CTC CCA AGT CCT TGT CCA CCC CCT TCT CAT CTT CCC AAG CCA GCT      259
Leu Leu Pro Ser Pro Cys Pro Pro Pro Ser His Leu Pro Lys Pro Ala
      20                      25                      30                      35

TCT CCC TGT CCC TAT CCC TTG NNC CTG CTG ACC TTC CCC GTG GGG GTC      307
Ser Pro Cys Pro Tyr Pro Leu Xaa Leu Leu Thr Phe Pro Val Gly Val
      40                      45                      50

CCC CAT CTT CCA GGG ACC CGC CTG CAG TGC CAA GGC CTG GGT CAT TCT      355
Pro His Leu Pro Gly Thr Arg Leu Gln Cys Gln Gly Leu Gly His Ser
      55                      60                      65

CTC ARA CGG GCA GAG CGG GGA GTG GGT GGT GGG GTG TCT CCT GGG      400
Leu Xaa Arg Ala Glu Arg Gly Val Gly Gly Gly Val Ser Pro Gly
      70                      75                      80

```

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: 13..87
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: . score 4.6
 seq LPTLLLLPVGAPG/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

```

ATCGAATGCA GA ATG GTT TTG GGA GCC CTG AAC CTT CCC TCC CAG GAA CTC   51
      Met Val Leu Gly Ala Leu Asn Leu Pro Ser Gln Glu Leu
      -25                      -20                      -15

CCC ACT CTC CTG CTC CTC CCA GTG GGG GCA CCT GGR AAG AAA AAA GGC   99
Pro Thr Leu Leu Leu Leu Pro Val Gly Ala Pro Gly Lys Lys Lys Gly
      -10                      -5                      1

ATG GAA GGC AAA ACT CCC TTG GAC CTG TTT GCT CAT TTT GGC CCT GAG   147
Met Glu Gly Lys Thr Pro Leu Asp Leu Phe Ala His Phe Gly Pro Glu
      5                      10                      15                      20

CCA GGG GAC CAC TCA GAT CCG CTG CCT CCC TCT GCA CCC TCT CCC ACT   195
Pro Gly Asp His Ser Asp Pro Leu Pro Pro Ser Ala Pro Ser Pro Thr
      25                      30                      35

CGG GAG GGG GCT CTG ACC CCG CCC CCA GGG   225
Arg Glu Gly Ala Leu Thr Pro Pro Pro Gly
      40                      45
  
```

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 207..263
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq QTFVSFLSIPVLG/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

```

ATACACCTCC ATTTTAAATG TGCTGCAATA TGAATGAAGT GACCTGTGTT TCATCACTTG   60
TTCAATGAT TCTTATCCAT GTTTTGTAC TTAGTAAGGG CCATACGTAG TGGGATTAA   120
TATTTGTGCC CTTGCTTTGA AAACAAAACT GAAAGTGAAT GACACATAAG GGCAGGGATT   180
  
```

TCAGAACAGA TTTTCTTGA ATAAAA ATG CTT GTG TCA AAA ATT CAA ACA TTT 233
 Met Leu Val Ser Lys Ile Gln Thr Phe
 -15

GTC TCT TTC CTT TCC ATT CCA GTT CTA GGT CTC GTT CCA GAT CAT ATT 281
 Val Ser Phe Leu Ser Ile Pro Val Leu Gly Leu Val Pro Asp His Ile
 -10 -5 1 5

CTC CAG CTC ATA ACA GAG AAA GAA ACC 308
 Leu Gln Leu Ile Thr Glu Lys Glu Thr
 10 15

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 188..280
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq LLSTGLNILGTQA/FR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

ATCATAGTCA CTTTCCAAGT TTATGACCCA GAGCAATCTG ACCTTGGTAG CTTGTCTCCC 60

TCATTAAATT CTCTGACTTC ATAATCAGCT CACATTCCTT TCCTCTCTTT CCCTCTCTTT 120

TTAAATATCT GTAAACATT CAAATTGATC CACGTAGATT TATCTTGCTT TTAGGCCACA 180

CTCTGAG ATG TGT AAT CCG GTT GCT CAC ACA TTT AGA GGA GTC CAT GAG 229
 Met Cys Asn Pro Val Ala His Thr Phe Arg Gly Val His Glu
 -30 -25 -20

CAT CAC GCC ATG CTA CTC TCC ACT GGT TTG AAC ATC TTA GGC ACT CAG 277
 His His Ala Met Leu Leu Ser Thr Gly Leu Asn Ile Leu Gly Thr Gln
 -15 -10 -5

GCA TTC CGT TAC GAA GAT GGG CAG CTG 304
 Ala Phe Arg Tyr Glu Asp Gly Gln Leu
 1 5

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 410 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 126..176
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq ILLWEACTGRCQA/SL
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

```

TATTCAGTTG GGGGCAAGCC AGCCATGATG TGGACCTTTC ATTGGGTAGG GCAAGTCCCC   60
AAAGTTGGAA AAATGGAAAG TGGGAGCTGT GAGGCACGTG TTACACCCAC ACTTTCCTCC  120
TACAG ATG CAG TGT TGG ATT TTG TTG TGG GAG GCA TGC ACA GGT AGG TGC   170
    Met Gln Cys Trp Ile Leu Leu Trp Glu Ala Cys Thr Gly Arg Cys
        -15                -10                -5

CAG GCC TCC CTA CTC TCT CCC TGG CCC AGA GGT GGC AGG GGC AAG TTA   218
Gln Ala Ser Leu Leu Ser Pro Trp Pro Arg Gly Gly Arg Gly Lys Leu
        1                5                10

GTG GCA GTG GTG GCT GCA AAA TGG TTG GCA GCA ATC TGT GGG ATT TGG   266
Val Ala Val Val Ala Ala Lys Trp Leu Ala Ala Ile Cys Gly Ile Trp
    15                20                25                30

GCT ATC AAA GAA ATG CCA AGC CAT GGC CAC AGT CTT CAA GCA GGG GCA   314
Ala Ile Lys Glu Met Pro Ser His Gly His Ser Leu Gln Ala Gly Ala
        35                40                45

GGG GAA GGT GCA CTG GTG ACC TGG AGC CTG CAA ACC TCA TTT GGT GTG   362
Gly Glu Gly Ala Leu Val Thr Trp Ser Leu Gln Thr Ser Phe Gly Val
        50                55                60

AAG CAG TAT AAG TGG GGA GTT GTG TGG CAT GAA GCA AAC CTG TTG CTT   410
Lys Gln Tyr Lys Trp Gly Val Val Trp His Glu Ala Asn Leu Leu Leu
        65                70                75

```

(2) INFORMATION FOR SEQ ID NO: 144:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 247 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 149..223
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq VLCILGCHGNLCC/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

```
ATTTTAGAAA GTAAGGAAAT AAAACTTTAA TTGAAGCTGG AATAAACTCA GTTCTGAGCA    60
TTCCATTCTA CTCTGCAGTT GTCATTTATA GACAGCTGTG GATCATAATA CCTATAGACT    120
AGATATCGTT ATCTACTTAT TTATATTA ATG ACA GGA TAT CCC TGG GCA AAC    172
                        Met Thr Gly Tyr Pro Trp Ala Asn
                        -25                      -20
AGC ATC ACC ACT GTA CTG TGT ATT CTT GGT TGT CAT GGG AAC CTT TGC    220
Ser Ile Thr Thr Val Leu Cys Ile Leu Gly Cys His Gly Asn Leu Cys
      -15              -10              -5
TGT GAA CCA GCA GTG AGA GCA CTC GGG    247
Cys Glu Pro Ala Val Arg Ala Leu Gly
  1              5
```

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 475..546
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq IFTALFLXLHSAV/IN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```
AAATTATGGA TGCCTACCAT CTACCAGGTA CTGTTCTAGC TACAAGGAAT AACTAAAAAT    60
```

```

AGGTAAACAA AACAGATGAA AACTTAGAA ATTTATACTG ATGTTATCAG AGTAATGTTT 120
AATTTTTCAG ATAATTGTTA TGTCTAAATT AGCATTGAT TTTCAATTA AGAATTTTTA 180
AATTATCCAA TATTGCAAGC ATATATAGAA ACATGGAAAA CAACAAATT CTCATGCATA 240
TACTTCAAAC ACAGAGCTAA CAGATGTTAT TATTTTTTAT TTCTTTCACA ACCCAACTTT 300
CGGGAAACAA AATAGGCACA GCAAACTGG GATCTCCTCA TCCCCTTCTC CTTTCTTATA 360
TAAAAGTAAT CCTGCTCTTG GTACAGCTAT GTATCATACT CATCCAGGTT TTAATTTTTC 420
TTATATAACG GAACATATAT GGTGTTATTT TACGGATTTT AAAGCTTTAC ATAA ATG 477
                                         Met
GTG TCA TGT GAT GTW CVN TCT TAT GTG ATC ATT TTT ACT GCA CTC TTT 525
Val Ser Cys Asp Val Xaa Ser Tyr Val Ile Ile Phe Thr Ala Leu Phe
      -20              -15              -10
TTA WTG CTG CAT AGT GTG GCA ATA AAT GAA GAG TTT 561
Leu Xaa Leu His Ser Val Ala Ile Asn Glu Glu Phe
      -5              1              5

```

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 80..139
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq LFAIFLMCLKSIG/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

```

ATGATAAGGG CTTATTCACA TTATTCATTC TTGAATGAAT TTGATAGTG TCTGTCTTTC 60
AGGAACCTTG TCCTAAGTA ATG AAA TCC TTT GAT AAA AAG TTG TTT GCA ATA 112
      Met Lys Ser Phe Asp Lys Lys Leu Phe Ala Ile
      -20              -15              -10
TTT CTT ATG TGT TTA AAG TCT ATA GGT TCT GTG GTG ATG CCC CAG CCG 160
Phe Leu Met Cys Leu Lys Ser Ile Gly Ser Val Val Met Pro Gln Pro
      -5              1              5

```

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 36..134
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq LASLFGLDQXAXG/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

```

ATTTCCTCC CCGCAACCTG GTGAAAGCCA AYKCA ATG TTC GGT GCG GGG GAC      53
                               Met Phe Gly Ala Gly Asp
                               -30

GAG GAC GAC ACC GAT TTC CTC TCG CCG AGC GGC GGT GCC AGA TTG GCC      101
Glu Asp Asp Thr Asp Phe Leu Ser Pro Ser Gly Gly Ala Arg Leu Ala
-25                               -20                               -15

TCA CTT TTT GGA CTG GAT CAG GYA GCY SST GGC CAT GGA AAT GAA TTT      149
Ser Leu Phe Gly Leu Asp Gln Xaa Ala Xaa Gly His Gly Asn Glu Phe
-10                               -5                               1                               5

TTC CAG TAC ACA GCC CCA AAA CAG CCT AAG AAA GGC CAG GGA ACG GCA      197
Phe Gln Tyr Thr Ala Pro Lys Gln Pro Lys Lys Gly Gln Gly Thr Ala
10                               15                               20

GCA ACA GGA AAT CAG GCA RCA CCA AAA ACA GCA CCA GCC RSC ATG AGC      245
Ala Thr Gly Asn Gln Ala Xaa Pro Lys Thr Ala Pro Ala Xaa Met Ser
25                               30                               35

ACT CCC ACA ATA CTG GTC GCA ACA GCA GTC CAT GCA TAT CGA TAC ACA      293
Thr Pro Thr Ile Leu Val Ala Thr Ala Val His Ala Tyr Arg Tyr Thr
40                               45                               50

RAT GGT CRA TAT GTA AAG CAG GSR AAT TTG GTG CTG CAG TTC TGG      338
Xaa Gly Xaa Tyr Val Lys Gln Xaa Asn Leu Val Leu Gln Phe Trp
55                               60                               65

```

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 107..190
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq RFLSLSAADGXDX/SX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

```

AAAGTCAGCG CTGGAGTCGG CTAGGCGGCT GGAAACGGCG GCTGCCGCCG GTGACTCAGG    60
GAGGCGGGGAG GCCGMSGGMG GAGCTCTTCC TGCAGGCGTG GARACC ATG GTG CTC    115
                               Met Val Leu
ACG CTC GGA GAA AGT TGG CCG GTA TTG GTG GGG AGG AGG TTT CTC AGT    163
Thr Leu Gly Glu Ser Trp Pro Val Leu Val Gly Arg Arg Phe Leu Ser
-25                -20                -15                -10
CTG TCC GCA GCC GAC GGC ASC GAT GSC AGC CAM GAC AGC TGG GAC GTG    211
Leu Ser Ala Ala Asp Gly Xaa Asp Xaa Ser Xaa Asp Ser Trp Asp Val
                -5                1                5
GAG CGC GTC GCC GAG TGG CCC TGG CTC TCC GGG ACC ATT CGA GCT GTT    259
Glu Arg Val Ala Glu Trp Pro Trp Leu Ser Gly Thr Ile Arg Ala Val
                10                15                20
TCC CAC ACC GAC GTT ACC AAG AAG GAT CTG AAG    292
Ser His Thr Asp Val Thr Lys Lys Asp Leu Lys
                25                30

```

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 361..411

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq LTSVFQAMIWSQG/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```

ATGAAAACAG TTTTCTTTGT GATTGTGCAA TTGATGTTTA AACAGTGTTC ATCCTTCCAG   60
GTAGTATGAT GATGTATTTG TTGGAGACAA ARTATTTGCC CTAGCCTTTT TACTAATATT  120
TCAGATGAGA TTCTGTGGAG GAGAAGCATC TCCCCAAATG TCCTTGTTTT ATAGTAAATA  180
ATTCTACCAC GAGGATCCTT ATCCATAAAT CTATATTCAT GTTTATTTTG TGCTAGATAC  240
AGATCTTGCA ATATTCATGA AGCTTTAAGA AGAGCACTTT GAATCTTAAA AGAGATTCTC  300
TGAGCAGGGG TTGGCAGTGG TGAGGTCCAG GTAGTTATAA TAGCCATAAG AGCAGGGATT  360
ATG GTT ATT GAG CTC ACC AGT GTG TTT CAA GCC ATG ATC TGG AGT CAA   408
Met Val Ile Glu Leu Thr Ser Val Phe Gln Ala Met Ile Trp Ser Gln
      -15                      -10                      -5

GGT GTT AGT GAT TCC TCT AAG                               429
Gly Val Ser Asp Ser Ser Lys
      1                      5
  
```

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 47..196
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq ILFLFYFPAAYYA/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

```

ATDCCGCCCT GGAGCAAGCC GGGGCCTGGT CGGCARCTGG GCCGCC ATG GAG TCC   55
                                   Met Glu Ser
                                   -50

ACG CTG GGC GCG GGC ATC GTG ATA GCC GAG GCG CTA CAG AAC CAG CTA   103
Thr Leu Gly Ala Gly Ile Val Ile Ala Glu Ala Leu Gln Asn Gln Leu
      -45                      -40                      -35
  
```


(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 80..145
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq GFLLCPLVCGLRR/WT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

```

AGCGTTTATG GCCGCGTTAA GTCTGAGTGC CGCTTGAGT TGTGAATGA AGTGAACTTC   60
ATTTGTCAGC GTTCGGTTC ATG AAC TGG AAT GTA AGA GGC ACC AGA GGA TTC   112
                Met Asn Trp Asn Val Arg Gly Thr Arg Gly Phe
                -20                      -15

CTG CTC TGT CCC CTG GTT TGC GGC TTG CGA CGT TGG ACA TCC CCG GAT   160
Leu Leu Cys Pro Leu Val Cys Gly Leu Arg Arg Trp Thr Ser Pro Asp
-10                      -5                      1                      5

TGT TGT TTA ATA GAG AAA ACT CAC CGC GGG   190
Cys Cys Leu Ile Glu Lys Thr His Arg Gly
                10                      15

```

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 49..105
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.4
seq RGLLLGLAVAAAA/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

```

AAGATAGAGG CGGCAACCTC GGAAGTGGCG ACGGGTGGGC CTATATAG ATG TTG AGG      57
                                     Met Leu Arg

TGC GGA GGC CGT GGG CTT TTG TTG GGC CTG GCT GTA GCC GCA GCA GCG      105
Cys Gly Gly Arg Gly Leu Leu Leu Gly Leu Ala Val Ala Ala Ala Ala
-15                      -10                      -5

GTA AGG
Val Arg
1

```

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 95..136
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq ILLMIVFSIFLL/CN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

```

ACCCAGAGGC AGAAAGTAAT ATTGCTTACT ATGAGTCTAT ATATCCTGGG GAATTTAAGA      60

TGCCAAAGCA GCTCATTAC ATACAGCGTA AGTA ATG ATT CTC TTA ATG ATT GTA      115
                                     Met Ile Leu Leu Met Ile Val
                                     -10

TTT TCT ATA TTT CTC TTA TTA TGT AAC TTG ACA GAT TTT TAT CTC TTC      163
Phe Ser Ile Phe Leu Leu Leu Cys Asn Leu Thr Asp Phe Tyr Leu Phe
-5                      1                      5

AGG AGC GAT GGG
Arg Ser Asp Gly
10

```

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 149..190
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq SLLFIFRSILISC/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

```
ACAATTGTGTT TTATAAGCCT ATATTAATTG GGTTTTGACT GAATTAATTA TATAACCATT    60
TATCTCAAAA TGAAATGTTT CATAAAATTT ATTTAAWAGT ATATACTGYA TAAGTGTTAA    120
ATTATGAAAT TTAGTGGTCT TATAGAGA ATG TCT TTA TTG TTT ATT TTT AGG        172
                               Met Ser Leu Leu Phe Ile Phe Arg
                               -10

TCA ATT TTG ATC TCC TGC TTT TCA GGA GAC TTT TTT TTT TTT                214
Ser Ile Leu Ile Ser Cys Phe Ser Gly Asp Phe Phe Phe Phe
-5                               1                               5
```

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 27..77
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq SKVLIQLSQAFWA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

```

ACCTGGTATG AATTACAAAA CTGTAA ATG CCT TTG ATT AGT AAA GTT TTG ATA      53
                               Met Pro Leu Ile Ser Lys Val Leu Ile
                               -15                               -10

CAG CTA AGC CAA GCA TTT TGG GCC TCA CCT GAG GGT AGG AAC AGT TCT      101
Gln Leu Ser Gln Ala Phe Trp Ala Ser Pro Glu Gly Arg Asn Ser Ser
      -5                               1                               5

GGG AGT AAG AGG AAG CAG TTG GTA GCT GCA GTG GAG ATG CGA TAC TGT      149
Gly Ser Lys Arg Lys Gln Leu Val Ala Ala Val Glu Met Arg Tyr Cys
      10                               15                               20

AAA AGG CAG CAG GGG                                                    164
Lys Arg Gln Gln Gly
      25

```

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 142..228
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq VLLGSTAMATSLT/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

```

AAGTTGTAAT CCCACTAAGA ACCGCCAGGG CGAGACGAAA GCGACATCGC TTCCATCTTT      60

ACGACCAAGA ATCGCCTTCA GCCCTGTCTG GTGCATCCTT GGCAGAAAGT GAGGAGGRAA      120

ACACCCCCAT TGTTCTTTGG C ATG GAC ACA AGT TCA GTG GGA GGA TTA GAA      171
                               Met Asp Thr Ser Ser Val Gly Gly Leu Glu
                               -25                               -20

TTG ACT GAT CAG ACT CCT GTT TTA TTA GGG AGT ACG GCC ATG GCA ACT      219
Leu Thr Asp Gln Thr Pro Val Leu Leu Gly Ser Thr Ala Met Ala Thr
      -15                               -10                               -5

AGT CTC ACG AAT GTA GGA AAC TCA TTT AGT GGT CCA GCT AAT CCT TTA      267
Ser Leu Thr Asn Val Gly Asn Ser Phe Ser Gly Pro Ala Asn Pro Leu
      1                               5                               10

GTG TCT AGA TCT AAT AAG TTT CAG AAC TCG TCA GTG GAA GAT GAT GAT      315

```

Val	Ser	Arg	Ser	Asn	Lys	Phe	Gln	Asn	Ser	Ser	Val	Glu	Asp	Asp	Asp	
15						20					25					
GAT	GTT	GTT	TTT	ATC	GAA	CCT	GTA	CAA	CCT	CCC	CCA	CCT	TCT	GTA	CCA	363
Asp	Val	Val	Phe	Ile	Glu	Pro	Val	Gln	Pro	Pro	Pro	Pro	Ser	Val	Pro	
30					35				40						45	
GTG	GTA	GCT	GAT	CAA	AGA	ACC	ATA	ACA	TTT	ACA	TCA	TCA	AAA	AAT	GRA	411
Val	Val	Ala	Asp	Gln	Arg	Thr	Ile	Thr	Phe	Thr	Ser	Ser	Lys	Asn	Xaa	
				50				55						60		
GAA	CTA	CAA	GGA	AAT	GAT	TCC	AAA	ATT	ACT	CCT	TCC	TCA	AAA	GAG	TTG	459
Glu	Leu	Gln	Gly	Asn	Asp	Ser	Lys	Ile	Thr	Pro	Ser	Ser	Lys	Glu	Leu	
			65					70						75		
GCA	TCT															465
Ala	Ser															

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 92..184
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq ILLLTHVPPWILE/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

ACACACGTCC	CGCMGTGGAT	ACTGGAGAAT	CCTTGCCACA	CACGTCCTGC	CGTGGACACT	50
GGAGAATCCT	TCTCGCCACA	CACTTCCCAC	C ATG GAC ACT	GGA GAA TCC TTC	112	
			Met Asp Thr Gly Glu Ser Phe			
			-30	-25		
TCG CCA CAC ACG TCC TGC CGT GGA CAC TGG AGA ATC CTT CTA CTC ACA	160					
Ser Pro His Thr Ser Cys Arg Gly His Trp Arg Ile Leu Leu Leu Thr						
-20 -15 -10						
CAC GTC CCA CCG TGG ATA CTG GAG AAT CCT TCT TGC CAC ACA CGT CCC	208					
His Val Pro Pro Trp Ile Leu Glu Asn Pro Ser Cys His Thr Arg Pro						
-5 1 5						
GCC GTG GAC ACT GGA GAA TCC TTC TCG CCA CAA CGG	244					
Ala Val Asp Thr Gly Glu Ser Phe Ser Pro Gln Arg						
10 15 20						

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 154..246
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq LVLLSVLKEPVSR/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

```

ATAGGACTGC TACAAAAACC CCATGTTTAC GAATTGCCA GTGATATTGC CCCCTTCCTG   60
TGTCATCCCA ATTTATGGAT ACGTTATGGT GCCGTGGGAT TTATCACAGT GGTAGCTCGT  120
CAAATAAGTA CAGCTGATGT CTACTGTAAA CTG ATG CCT TAT CTT GAC CCA TAT   174
                               Met Pro Tyr Leu Asp Pro Tyr
                               -30          -25

ATT ACC CAA CCA ATA ATA CAG ATT GAA AGA AAA CTT GTT CTG CTC AGT   222
Ile Thr Gln Pro Ile Ile Gln Ile Glu Arg Lys Leu Val Leu Leu Ser
                               -20          -15          -10

GTT TTA AAG GAA CCA GTA AGT CGT TCT ATA TTT GAT TAT GCT TTG AGG   270
Val Leu Lys Glu Pro Val Ser Arg Ser Ile Phe Asp Tyr Ala Leu Arg
                               -5              1              5

TCT AAA GAT ATT ACT AGC TTG TTC AGA CAT CTT CAC ATG CGT CAG AAG   318
Ser Lys Asp Ile Thr Ser Leu Phe Arg His Leu His Met Arg Gln Lys
          10              15              20

AAA CGA AAT GGT TCT CTT CCC GAC TGC CCT CCG CCA GAG GAT CCT GCC   366
Lys Arg Asn Gly Ser Leu Pro Asp Cys Pro Pro Pro Glu Asp Pro Ala
          25              30              35              40

ATA GCA CAG CTT CTG AAG AAG TTG CTC TCA CAG GGA ATG ACA GAG GAA   414
Ile Ala Gln Leu Leu Lys Lys Leu Leu Ser Gln Gly Met Thr Glu Glu
          45              50              55

GAG GAA GAC AAA CTT CTG GCA CTG AAA GAC TTC ATG ATG               453
Glu Glu Asp Lys Leu Leu Ala Leu Lys Asp Phe Met Met
          60              65

```

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 181..267
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq VLLGSTAMATSLT/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

```

ARRAAAGCCG GGACTGGACC GAGCGGAGTK KTGCGTGTCC CCGAAGGGGG GTKGGCCGGG   60
GGAGGKGAGG TTCGTTCCGC GGAKCCGCAG YCAGAASCGK GRACCAAGAA TCGCCTTCAG   120
CCCTGTCTKG TGCATCCTTG GCAGAAAGTG RKGAKGAAAA CACCCCATT GTTCTTTGGC   180
ATG GAC ACA AGT TCA GTG GGA GGA TTA GAA TTG ACT GAT CAG ACT CCT   228
Met Asp Thr Ser Ser Val Gly Gly Leu Glu Leu Thr Asp Gln Thr Pro
      -25                -20                -15

GTT TTA TTA GGG AGT ACG GCC ATG GCA ACT AGT CTC ACG AAT GTA GGA   276
Val Leu Leu Gly Ser Thr Ala Met Ala Thr Ser Leu Thr Asn Val Gly
      -10                -5                1

AAC TCA TTT AGT GGT CCA GCT AAT CCT TTA GTG TCT   312
Asn Ser Phe Ser Gly Pro Ala Asn Pro Leu Val Ser
      5                10                15

```

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 33..116
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq FGLLDFVQCCDS/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

```

ATTTTTATG ACATCTAWTT ATATTGAGTT GC ATG CAT GTT TTG TTC AAC ATA      53
                               Met His Val Leu Phe Asn Ile
                               -25

GTC ACA ACA AAT WRR RAT AAC CAT TTT GGG TTG TTA GAT TTT GTT GTG      101
Val Thr Thr Asn Xaa Xaa Asn His Phe Gly Leu Leu Asp Phe Val Val
-20                      -15                      -10

CAG TGT TGT GAT TCA TTA AGA AAC CAT ARG WGG TCA TTT CAG TCA TCT      149
Gln Cys Cys Asp Ser Leu Arg Asn His Xaa Xaa Ser Phe Gln Ser Ser
-5                      1                      5                      10

TAC TTG AGG CTA AAT CAT TCA TGR CAT ACA TGT                          182
Tyr Leu Arg Leu Asn His Ser Xaa His Thr Cys
15                      20

```

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 150..215
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq TAYWLSFMSWAQS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

```

ATGTATACTG AGGTTCAAGGA ACTGCTGGAG AGATGACTGG GCACCAAGAG GATGACAGTG      60

ACTCAGCTGG CATCCCTTAG CTGGTTCATG GCAGAGCTGA GTGGCCACTC CTGTCTCTGA      120

CCCCAGCTTC AGTGCTCTTT ATCTCCTCC ATG CCT CCT CAG TCG TGC TGC TCT      173
Met Pro Pro Gln Ser Cys Cys Ser
-20                      -15

```

```

AAG ACT GCT TAC TGG CTT TCC TTC ATG TCC TGG GCA CAG AGC AGT TCT      221
Lys Thr Ala Tyr Trp Leu Ser Phe Met Ser Trp Ala Gln Ser Ser Ser
      -10              -5              1

TTT GGT AGC AGA HTT GAG TCC ACT TCC CCC TGC ACA GAT CAC TGC TCA      269
Phe Gly Ser Arg Xaa Glu Ser Thr Ser Pro Cys Thr Asp His Cys Ser
      5              10              15

GGA CCC AGA GAG GAG CAG CTC TGC TCC AGC AGG GTT TTC CAT TGC ATC      317
Gly Pro Arg Glu Glu Gln Leu Cys Ser Ser Arg Val Phe His Cys Ile
      20              25              30

ACA CAC CCA AAC GGT AGG ATC CAC CGG TGG      347
Thr His Pro Asn Gly Arg Ile His Arg Trp
      35              40

```

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 53..94
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq: SCVFFHFLQGGLG/FG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

```

AACTTTCITC AAGGCGGTTT GGGATTTGGC TCCGCTGGCC GCTGTGCTGG TG ATG TCC      58
                                         Met Ser

TGT GTT TTC TTT CAC TTT CTT CAA GGC GGT TTG GGA TTT GGC TCC GCT      106
Cys Val Phe Phe His Phe Leu Gln Gly Gly Leu Gly Phe Gly Ser Ala
      -10              -5              1

GGC CGC TGT GCT GGT GAC AGG      127
Gly Arg Cys Ala Gly Asp Arg
      5              10

```

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 156..215
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq LILLPIWINMAQI/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

```
AAACTCGAAC TTGGTCGGGG CGCGGATCCC GAGAGGGAAA GTCATAACAA CCGCACGAGE    60
GAGITCGACT GGCGAACTGG AAGGCCACGC CTCCTCCCGC CTGCCCCCTC AGCCCTGTGG    120
CTGGGGGCAG AGCTCAGACT GTCTTCTGAA GATTG ATG TCT ATT TCC TTG AGC      173
                               Met Ser Ile Ser Leu Ser
                               -20                               -15

TCT TTA ATT TTG TTG CCA ATT TGG ATA AAC ATG GCA CAA ATC CAG CAG      221
Ser Leu Ile Leu Leu Pro Ile Trp Ile Asn Met Ala Gln Ile Gln Gln
          -10                      -5                      1

GGA GGT CCA GAT GAA AAA GAA AAG ACT ACC GCA CTG AAA GAT TTA TTA      269
Gly Gly Pro Asp Glu Lys Glu Lys Thr Thr Ala Leu Lys Asp Leu Leu
          5                      10                      15

TCT AGG ATA GAT TTG GAT GAA CTA ATG AAA AAA GAT GAA CCG CCA GGG      317
Ser Arg Ile Asp Leu Asp Glu Leu Met Lys Lys Asp Glu Pro Pro Gly
        20                      25                      30
```

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 50..151
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq SFCNAVVLSPVFQ/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

```

AAGTTATACA GAAGACTTGT AGGAAGGATG GACAAACGTT CTTAAGCCC ATG ACG GCC    58
                                   Met Thr Ala

CTT AAC CTG GTC GCT CCC TTT TCT GAT GGA GAC TCA GGC AGC GTC TCT    106
Leu Asn Leu Val Ala Pro Phe Ser Asp Gly Asp Ser Gly Ser Val Ser
-30                      -25                      -20

CTA GCT TCT TTC TGC AAT GCT GTA GTA CTC TCT CCA GTA TTT CAG GAG    154
Leu Ala Ser Phe Cys Asn Ala Val Val Leu Ser Pro Val Phe Gln Glu
-15                      -10                      -5                      1

GAG GAG CAT TTG CTA TTT CAA AAA CGA AAA ACA AAA ACC TGG CCA CCC    202
Glu Glu His Leu Leu Phe Gln Lys Arg Lys Thr Lys Thr Trp Pro Pro
                    5                      10                      15

AGG
Arg
205

```

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 154..204
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq PVQVLGLLATCQH/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

```

AATATGTAAC CAAAAATAAA GTGTTTCAAT AGTTTATTCC TCTTTCATAT AATGGTCTAG    60

AGAGAGTGTC ATTGGGGCAA AGGGCAAAGA TACAGAGGAT CTGTTTCCCT TCTATCTTGT    120

TTTTCTGTAA TCACCTAGAG CAGTGCTACT CAA ATG TGG TCC AGA CCA GTG CAG    174
                                   Met Trp Ser Arg Pro Val Gln
                                   -15

GTC TTG GGA CTT CTT GCC ACT TGT CAG CAT GCT CCC TCT CCC TCC TTT    222
Val Leu Gly Leu Leu Ala Thr Cys Gln His Ala Pro Ser Pro Ser Phe
-10                      -5                      1                      5

AAA GGT GAG ACA TGT ACA GAA ATT GAG AGT GTT TAT CTG GCC CCC ATG    270

```

```
(A) NAME/KEY: sig_peptide
(B) LOCATION: 271..345
```

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.2
 seq VLLFFCCSPLYSP/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

```

ATGTAATGGA AGCAATCATT TTGAAAAGAG TTAAAGTTTT TTGGTAAGTC AAATAAGGAT   60
CAATGCTGCT GAAAGCTGGG ACAACACACG GGCCCTGACC AAATTGGGGT TTCTTTGTCT   120
ACCTCATACC TTCCAAATCA AAAAATAATT TCCCTAGTAT TTTAATTACT CCCCCAAATC   180
AGGAATAACT TCCTCACTGT GCTGATTTTG GTTCTTTTAA AATAAGGTGG TAATTTGAAG   240
GTAATAGTTA AACCAGTCAT AGATTATTCT ATG CCA TTC TTT TCA AAT CAG CCC   294
                               Met Pro Phe Phe Ser Asn Gln Pro
                               -25                               -20

ACT CAG GTG TCA GTC CTA CTT TTC TTT TGT TGT AGT CCT CTT TAT TCT   342
Thr Gln Val Ser Val Leu Leu Phe Phe Cys Cys Ser Pro Leu Tyr Ser
      -15                               -10                               -5

CCT TTG TTT CTG CTC CAV CTC ATC CCC CAC CAG   375
Pro Leu Phe Leu Leu Xaa Leu Ile Pro His Gln
      1                               5                               10
  
```

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 32..163
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.1
 seq IAVGLTCQHVSHA/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

```

GCTGCGGCCC GGCCCGGCGG GTAAATAACA G ATG CGG GTG AAA GAT CCA ACT   52
                               Met Arg Val Lys Asp Pro Thr
                               -40

AAA GCT TTA CCT GAG AAA GCC AAA AGA AGT AAA AGG CCT ACT GTA CCT   100
Lys Ala Leu Pro Glu Lys Ala Lys Arg Ser Lys Arg Pro Thr Val Pro
      -35                               -30                               -25
  
```

CAT GAT GAA GAC TCT TCA GAT GAT ATT GCT GTA GGT TTA ACT TGC CAA	148
His Asp Glu Asp Ser Ser Asp Asp Ile Ala Val Gly Leu Thr Cys Gln	
-20 -15 -10	
CAT GTA AGT CAT GCT ATC AGC GTG AAT CAT GTA AAG AGA GCA ATA GCT	196
His Val Ser His Ala Ile Ser Val Asn His Val Lys Arg Ala Ile Ala	
-5 1 5 10	
GAG AAT CTG TGG TCA GTT TGC TCA GAA TGT TTA AAA GAA AGA AGA TTC	244
Glu Asn Leu Trp Ser Val Cys Ser Glu Cys Leu Lys Glu Arg Arg Phe	
15 20 25	
TAT GAT GGG CAG CTA GTA CTT ACT TCT GAT ATT TGG TTG TGC CTC AAG	292
Tyr Asp Gly Gln Leu Val Leu Thr Ser Asp Ile Trp Leu Cys Leu Lys	
30 35 40	
TGT GGC TTC CAG GGA TGT GGT AAA AAC TCA GAA AGC CAA CAT TCA TTG	340
Cys Gly Phe Gln Gly Cys Gly Lys Asn Ser Glu Ser Gln His Ser Leu	
45 50 55	
AAG CAC TTT AAG AGT TCC AGA ACA GAG CCC CTC AGG	376
Lys His Phe Lys Ser Ser Arg Thr Glu Pro Leu Arg	
60 65 70	

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 9..140
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq GTYLTSSSPLCQL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

ACTTTAAT ATG GTG TCC TTG GGT TAT TAT TTA ATA TTT GTC CTA TAT CTT	50
Met Val Ser Leu Gly Tyr Tyr Leu Ile Phe Val Leu Tyr Leu	
-40 -35	
TGG CTT TGT TTC ATG CAA ATT AGT GAA GAG AAG TTA ATA GAG GAA CAC	98
Trp Leu Cys Phe Met Gln Ile Ser Glu Glu Lys Leu Ile Glu Glu His	
-30 -25 -20 -15	
ACA GGT ACA TAT TTA ACC TCC AGT TCA CCC CTC TGC CAG CTC CAG CCC	146
Thr Gly Thr Tyr Leu Thr Ser Ser Ser Pro Leu Cys Gln Leu Gln Pro	

-10

-5

1

CCA GGG
Pro Gly

152

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 128..232
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq VLCCLLIATPTFF/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

```

ATATTATTAA ACITTTTATT TTGAGGTTAG TGTGGATTGA AATACTTTC CAACAATTAA      60
CACAAAGGTC CCCTGTGTCC TTTACCCAGT TTCCACAAT GGTAACATCT TACAAAACCTG    120
GAGTACA ATG TCA CTC ACA TCC AGG RTA MYA ATW ATG GWT ACA ATC AAG      169
      Met Ser Leu Thr Ser Arg Xaa Xaa Ile Met Xaa Thr Ile Lys
      -35                -30                -25

ATA CAG AAT AIT TCT ATT ACA AAG GTC TTG TGT TGC CTT CTT ATA GCA      217
Ile Gln Asn Ile Ser Ile Thr Lys Val Leu Cys Cys Leu Leu Ile Ala
      -20                -15                -10

ACA CCT ACT TTC TTC CTA CTC CTT CCC TCA TCC ATT CCA CGG              259
Thr Pro Thr Phe Phe Leu Leu Leu Pro Ser Ser Ile Pro Arg
      -5                1                5

```

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 137..190
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.1
 seq AGVVSTSVAAAVA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

```

AAGCGCAACC GGAAGTAGCC TTCTGGGGGC CGGCTTCCTT TATCTCTGGC GGCCTTGTA 60
TCGTCTCCGA GACTCCCCAC CCCTCCTTCC CTCTTGACCC CCTAGGTTTG ATTGCCCTTT 120
CCCCGAAACA ACTATC ATG ARC GCC GAG GCT GCC GGT GTT GTC TCC ACC TCG 172
          Met Xaa Ala Glu Ala Ala Gly Val Val Ser Thr Ser
                    -15                      -10

GTG GCC GCG GCI GTT GCT GCT GTC GCT GCT CCT GCT GGG GCC GGG      217
Val Ala Ala Ala Val Ala Ala Val Ala Ala Pro Ala Gly Ala Gly
      -5              1              5

```

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 101..145
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4
 seq IMSSCLALTYTNS/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

```

ITGGTATCTG GAGIGTTGTA GTGTGTTTGT ATTGCTTAT AAATAAGTAT TATAGATAAA 60
GATAAACTTC ATAAAGAGTG GATATTTTGG GGAAATTTTC ATG TGG ATA ATG TCA 115
          Met Trp Ile Met Ser
                    -15

TCC TGT CTG GCA TTG ACA TAC ACA AAT TCA ATC TCA CAT AGT CTT TGC 163
Ser Cys Leu Ala Leu Thr Tyr Thr Asn Ser Ile Ser His Ser Leu Cys
-10              -5              1              5

```

CTT GAG AGA GCG TAC AGT CTA TTC AAA GIT GAC
 Leu Glu Arg Ala Tyr Ser Leu Phe Lys Val Asp
 10 15

196

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 65..124
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq SNALVLVTRGSSS/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

ACAGTGTGGC TCGGTTGAAT AGGAGAGCTT TAACTGCATT CTCTTGAGAG AATGCAGTBG 60
 AAGA ATG CCA AGA GGA GTG TAC AAT TCA AAT GCG TTA GTG CTT GTA ACA 109
 Met Pro Arg Gly Val Tyr Asn Ser Asn Ala Leu Val Leu Val Thr
 -20 -15 -10
 CGT GGT TCC AGT TCT CTC CCT CTT GGC TTG TAT GGT ATA AAT TGT GTA 157
 Arg Gly Ser Ser Ser Leu Pro Leu Gly Leu Tyr Gly Ile Asn Cys Val
 -5 1 5 10
 CAG GTA ATT AAG TTA TTT TAT AGA GGC CAT CTC CAC TGG GAA ACT TTG 205
 Gln Val Ile Lys Leu Phe Tyr Arg Gly His Leu His Trp Glu Thr Leu
 15 20 25
 CTG CCA TCG 214
 Leu Pro Ser
 30

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 210..341
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq FLLPCVHPFSVIA/VY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

```

AATTTATGAT AGGAAATGAT TGATCAAGTG TCACACAGCT GATTATCAGG TCTCAGTCTA    60
ATATTTATTC CTTATTGGTC TCTGCTTAAC TTCAAGTAGG TTATAGATTC CTTAATGGAC    120
TGATAGITTA TGTCTTATAG CTTTACCTTT CAGGCGCTTA GTTTCATATT GGGAACATGA    180
CAAGTGAATA ATAAATACAT GATAGCTCT ATG ATT GAA CCC TGT GAG AAA ATG      233
                               Met Ile Glu Pro Cys Glu Lys Met
                               -40
AAG CAT TAT GAT ATG AAT TGG TTT CTG TGT ATG TAT GAG TGT TTT TTT      281
Lys His Tyr Asp Met Asn Trp Phe Leu Cys Met Tyr Glu Cys Phe Phe
-35                      -30                      -25
TTY CAT CTT TTG GAA ACA GAA TTT CTG CTC CCC TGT GTA CAC CCT TTC      329
Phe His Leu Leu Glu Thr Glu Phe Leu Leu Pro Cys Val His Pro Phe
-20                      -15                      -10                      -5
TCT GTA ATT GCA GTG TAT GTT TTT                                      353
Ser Val Ile Ala Val Tyr Val Phe
1

```

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 134..298
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq AALCGISLSQXFP/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

```

AGCCTCCGCC TTTGCCTTCG CAGCCGCCTC CAGGGCAATT TGCATATTTC TCCAAAGAAC    60
CATCCAGAAC CTGAGCAGCC TGTCTTCAGA CAGAGATAGG CCCACGGCTG TTTCTTGAAA    120
TCTGGCGCTG GGA ATG GCC ATG TGG AAC AGG CCA TGC CAG ARG CTG CCT    169
      Met Ala Met Trp Asn Arg Pro Cys Gln Xaa Leu Pro
      -55                      -50                      -45
CAG CAG CCT CTG GTA GCT GAG CCC ACT GCA GAG GGG GAG CCA CAC CTG    217
Gln Gln Pro Leu Val Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu
      -40                      -35                      -30
CCC ACG GGC CGG GAG CTG ACT GAG GCC AAC CGC TTC GCC TAT GCT GCC    265
Pro Thr Gly Arg Glu Leu Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala
      -25                      -20                      -15
CTC TGT GGC ATC TCC CTG TCC CAG TCA TTT CCT GAA CCG GGG    307
Leu Cys Gly Ile Ser Leu Ser Gln Xaa Phe Pro Glu Pro Gly
      -10                      -5                      1

```

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 130..180
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq CLLVSYAVDSAAG/RF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

```

ATTGTCAAAA AGACATCAAA CTCAACTTCT GGGAAGACAG ATTTTAAATA CACATACTTG    60
GCTAATACTC ACAAACATAT CTAAAGTTTT GGCAAAATTA TGAGGGTGAT GGGTKGGTAC    120
TACCTGGC ATG GAG CAG GTG TGT CTT TTG GTT TCT TAT GCA GTT GAC TCT    171
      Met Glu Gln Val Cys Leu Leu Val Ser Tyr Ala Val Asp Ser
      -15                      -10                      -5
GCT GCA GGG AGA TTC GGG    189
Ala Ala Gly Arg Phe Gly
      1

```

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 20..103
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq ATLRCWASTPVSG/RL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

```

ACAAAGAGGC AGCTCCGGA ATG AGA AAG ATA AGC CAC TGC CTC CAC TGC TGG      52
      Met Arg Lys Ile Ser His Cys Leu His Cys Trp
                        -25                      -20

CCC GAG TCG GGG GCA ACA TTG AGG TGC TGG GCT TCA ACA CCC GTC AGC      100
Pro Glu Ser Gly Ala Thr Leu Arg Cys Trp Ala Ser Thr Pro Val Ser
      -15                      -10                      -5

SGA AGG CTT TCC TCA ATG GCT GTK RWG SSG CKG GGG GAA AKG CCA CCA      148
Gly Arg Leu Ser Ser Met Ala Val Xaa Xaa Xaa Gly Glu Xaa Pro Pro
      1                      5                      10                      15

CAG GAT GCC TTC ACC ACA CAG TGG CTG GTG CGG GAC CTG AGG GGC AAG      196
Gln Asp Ala Phe Thr Thr Gln Trp Leu Val Arg Asp Leu Arg Gly Lys
                        20                      25                      30

ACT GAG AAG GAG TTT AAG GCC TAT GTG TCT TTG TTC ATG CGC CAT CTG      244
Thr Glu Lys Glu Phe Lys Ala Tyr Val Ser Leu Phe Met Arg His Leu
                        35                      40                      45

TGT GAG CCT GGG GCA GAC GGC TCT GAA ACC TTT GCC GAT GGG GTC CCT      292
Cys Glu Pro Gly Ala Asp Gly Ser Glu Thr Phe Ala Asp Gly Val Pro
                        50                      55                      60

CGG GAG GGA CTG AGT CGC CAG CAG GTG TTG ACC CGC ATT GGA GTC ATG      340
Arg Glu Gly Leu Ser Arg Gln Gln Val Leu Thr Arg Ile Gly Val Met
      65                      70                      75

TCT CTC GTC AAA AAG AAG GGG CAG      364
Ser Leu Val Lys Lys Lys Gly Gln
      80                      85

```

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 172..237
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq LLHPCGSITLTSS/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

```

AAAATTTTTT TAGCCTCTAA CATGAAAGGG TCTCTTCATT GTTCTCATTT GTCTTACCCG    60
CCATCCAGTG TTAAGCAGTA TGTTAAAGAG CTTCTTCTTT ACAACTTTTC CCCTCACATT    120
ATTTTYCTAC ATGCAGCAAC TTCTTTAACC AAGTTGTTTG ATTAGGAGTA A ATG TGC    177
                                     Met Cys
ATA AAC GAT CAT ATT ATT AAG CTT CTG CAC CCA TGT GGC AGC ATC ACT    225
Ile Asn Asp His Ile Ile Lys Leu Leu His Pro Cys Gly Ser Ile Thr
-20              -15              -10              -5
TTA ACT TCT TCC TCA ACC ACA CGG                                249
Leu Thr Ser Ser Ser Thr Thr Arg
      1

```

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 135..185
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4
seq VALQCGLTIPALX/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

```

AGAAGGGGTG TCAAACCTCCA ATGGAAAAGG TTTAGGAAAA GACCTTTTAC AAATCCAAAG   60
ATGTTTCACA GTGGGCGAGG CTGGTGTGGC GACAGTAGTG GCCCACATGG CTGGGTGGG   120
AGCCAGCTCT GCCC ATG AGG TGC CGT GTG GCT TTG CAG TGT GGC CTC ACA   170
          Met Arg Cys Arg Val Ala Leu Gln Cys Gly Leu Thr
          -15                               -10

ATC CCA GCT TTG TNT CTT CCC CAG GGA GAT GAG GCT GGT GAT GCT CAA   218
Ile Pro Ala Leu Xaa Leu Pro Gln Gly Asp Glu Ala Gly Asp Ala Gln
-5              1              5              10

GAT CTC AGA GGC CCT GCC CAG GCT GAG TAT CTG TAT ATA ATA TCC CCC   266
Asp Leu Arg Gly Pro Ala Gln Ala Glu Tyr Leu Tyr Ile Ile Ser Pro
          15              20              25

TCG                               269
Ser

```

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 83..366
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq LTS AFLWLPR LHI/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

```

ATATRACTCA GTTTTCTGTT GTCTTTAGCT ACTGATGCAA ATGIGAAGAA TGAAAGTCTT   60
TCATCTGTGC AGCAGCTTGG CATTAAA ATG ACT GTC AGG TAT GGC AAA TTC CTC   114
          Met Thr Val Arg Tyr Gly Lys Phe Leu
          -90                               -85

AGT CTC TTA AAA GAT GGT GCA GAA AAT GAT CTT ACC TGG GTT TTA AAG   162
Ser Leu Leu Lys Asp Gly Ala Glu Asn Asp Leu Thr Trp Val Leu Lys
          -80              -75              -70

```

CAT TGT GAG AGA TTC CTG AAA CAG CAG CAA ACT TCC ATA AAA TCT TCT	210
His Cys Glu Arg Phe Leu Lys Gln Gln Gln Thr Ser Ile Lys Ser Ser	
-65 -60 -55	
CTT CTC TGC CTG CAA GGG AAT TAT GCT GGC CAT GAC TGG TTT GTA TCT	258
Leu Leu Cys Leu Gln Gly Asn Tyr Ala Gly His Asp Trp Phe Val Ser	
-50 -45 -40	
TCT CTG TTC ATG ATA ATG TTG GGA GAC AAA GAA AAA ACA TTC CAA TTT	306
Ser Leu Phe Met Ile Met Leu Gly Asp Lys Glu Lys Thr Phe Gln Phe	
-35 -30 -25	
CTT CAT CAA TTC TCC AGG CTT CTG ACT TCT GCT TTT CTT TGG TTG CCA	354
Leu His Gln Phe Ser Arg Leu Leu Thr Ser Ala Phe Leu Trp Leu Pro	
-20 -15 -10 -5	
AGG CTA CAT ATT TCT GTA AGA CTT CAA TCT GTT TTT AAA GGA GGG TTT	402
Arg Leu His Ile Ser Val Arg Leu Gln Ser Val Phe Lys Gly Gly Phe	
1 5 10	
GAM ATT TTA AGA ACA TTA TAC TTA CAT TCA MCG GGA CGG	441
Xaa Ile Leu Arg Thr Leu Tyr Leu His Ser Xaa Gly Arg	
15 20 25	

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 160..219
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq FFWVVLFSAGCKV/IT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

AACAGAGCCA CAGAATGCTG AGCAGTCAAC AGCATTTCTT GTTCCAAGAT CACCCTTCTG	60
AGTACCTCTC TGGCTGCCAA ATTGCCAGG. CCTTCACAGT TTGATTCCAT TTCTCAGCTC	120
CAAGCATTAG GTAAACCCAC CAAGCAATCC TAGCCTGTG ATG GCG TTT GAC GTC	174
Met Ala Phe Asp Val	
-20	
AGC TGC TTC TTT TGG GTG GTG CTG TTT TCT GCC GGC TGT AAA GTC ATC	222

Ser Cys Phe Phe Trp Val Val Leu Phe Ser Ala Gly Cys Lys Val Ile
 -15 -10 -5 1

ACC TCC TGG GAT CAG ATG TGC ATT GAG AAA GAA GCC ACA 261
 Thr Ser Trp Asp Gln Met Cys Ile Glu Lys Glu Ala Thr
 5 10

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 167..232
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq HLSSTTSPPWTHA/AI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

AAAAACGCCT TGAGGATAAG GAAGGAGAAT CAGCAAGTCC CGAGTTCCTA CGGTGTGTCA 60
 GCATCGTGCT CCCACTCCCG GGAGAGAGGC ATTATCTTCA GTTTACAAAA GGGGAAAACA 120
 GGTCTGGGGT TTCCAGAGTC CGCGGTTTTC CTAAGAAGCC GCAGTG ATG TTG ACG 175
 Met Leu Thr
 -20
 CGG CTG GTC CTC AGT GCA CAC CTG AGT AGC ACG ACC TCT CCG CCC TGG 223
 Arg Leu Val Leu Ser Ala His Leu Ser Ser Thr Thr Ser Pro Pro Trp
 -15 -10 -5
 ACG CAC GCT GCC ATC AGC TGG GAG CTG GAC AAC GTG CTG ATG CCT AGT 271
 Thr His Ala Ala Ile Ser Trp Glu Leu Asp Asn Val Leu Met Pro Ser
 1 5 10
 CCC AGA ATC TGG CCC CTG 289
 Pro Arg Ile Trp Pro Leu
 15

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 326..445
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq CVNLLLGFEPVIS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

```

ATAAACTTA GGGGAAGAT TTGCCTCTCA CTTTTTTTCT TGGAAATGT GGGCAGCAAT   60
TTTAAAGAGA ACATGAAAAT GGAGTAGGTT GAAACCAACA TTCAGAACTT CCTTTCATGG  120
ATTGAACTT AAAGCTGAGG GAGGKTTTRA GGGTGGARKT RAGGAAGGGC TAGAAGATAG  180
CAAATTTTCA AGTCATATCA GAGAATATGA ACTGTCAGTG TTTCCAATGT TTCTCTTGGC  240
TCTGCACAGC ACTTCCAAGC CCTTTTGCTC ACTGTTTTCG TTCTGCCACA CCTAGGAGAA  300
GATTCAGAGC TTGCTGAGGC AAAAC ATG CGA TAT TTC CAA GGG CCT TCC CCC   352
                Met Arg Tyr Phe Gln Gly Pro Ser Pro
                -40                      -35

TAT TCT GAA ATA GAA ATT GAG CTT TGT GAT CAT GTG TAT TCA TTC CAA   400
Tyr Ser Glu Ile Glu Ile Glu Leu Cys Asp His Val Tyr Ser Phe Gln
   -30                      -25                      -20

GGT CTA TGT GTT AAC CTT TTG CTA GGA TTT GAA CCT GTT ATT AGT AGG   448
Gly Leu Cys Val Asn Leu Leu Leu Gly Phe Glu Pro Val Ile Ser Arg
   -15                      -10                      -5                      1

AGC CGR MGC AGT TCA CTT GCT GTT GAG TCT   478
Ser Arg Asa Ser Ser Leu Ala Val Glu Ser
      5                      10

```

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 48..170
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq LASLECYVPSTNQ/WQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

```

ACTGCAGATA CGATCCCCGC TTCAACACCT GGATACACCT GGCCAGS ATG AAN HAG      56
                                     Met Xaa Xaa
                                     -40

AAG CGC ACG CAC TKV VNS STG AGC GTG TTC AAC GGG CTC GTG TAC GCC      104
Lys Arg Thr His Xaa Xaa Xaa Ser Val Phe Asn Gly Leu Val Tyr Ala
-35                               -30                               -25

GCG GGC GGC CGC AAC GCA GAA GGA AGC CTG GCC TCG CTG GAG TGC TAC      152
Ala Gly Gly Arg Asn Ala Glu Gly Ser Leu Ala Ser Leu Glu Cys Tyr
-20                               -15                               -10

GTG CCC TCC ACC AAT CAG TGG CAG CCG AAG HHN SCC CTG GAG GTG GCG      200
Val Pro Ser Thr Asn Gln Trp Gln Pro Lys Xaa Xaa Leu Glu Val Ala
-5                               1                               5                               10

CGC TGC TGC CAC GCT AGC GCG GTC GCC GAC GGC CGC GTG CTG GTG ACC      248
Arg Cys Cys His Ala Ser Ala Val Ala Asp Gly Arg Val Leu Val Thr
15                               20                               25

GGA GGC TTG
Gly Gly Leu
257

```

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 249..362
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq LLFFHLLLNDFFT/FY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

```

ACATCCAGCT CTGGTAGTTT AGGCTCAATC TTACGGTGTA ATTATACAGA ATAATTAGAG   60
GCAGCTGTAT CCTTGTTTCT GATTTTAAAA TCTGRATGTT TCTYCAATC TTTGTGTACT  120
TCCCTTCAT TTGGTACATA TAGAAGTCTT CTTATGTGTT ATTAAAGTCT TCTAAGATAG  180
TATTCTGGTC ATTGGAGACA CCAAAAATCT ATGGGCACAG TCCTGTTCTT GTTTCTTTTG  240
CCAATAGA ATG TTC CTT AAG GTT CAG TCA CAG TCC TTT TAC DTC CCT TAC   290
      Met Phe Leu Lys Val Gln Ser Gln Ser Phe Tyr Xaa Pro Tyr
            -35                -30                -25

AGA GAT TGT TTA AAT TTC CAC AAA AGC ACG TAT TTA CTC TTC TTT CAC   338
Arg Asp Cys Leu Asn Phe His Lys Ser Thr Tyr Leu Leu Phe Phe His
            -20                -15                -10

TTG TTA CTA AAT GAC TTC TTC ACA TTT TAC NTT GCT AAA               377
Leu Leu Leu Asn Asp Phe Phe Thr Phe Tyr Xaa Ala Lys
            -5                1                5

```

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 119..199
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq WIIIIYTFQCNS/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

```

CAGAATGTTT TTTGCTGCCT CGCTTACATG GCAAAACTCA CAAACCACCT ATACAATCCA   60
AAAGAGGGGA AACAGTCAT CTCATATTAA TTATGGTCCA TTTCBATGAT AGGATATT   118
ATG CAA CCA TTA AAA ATC ATA TTT TAT CTG AGT GTT AGT ATA TGG ATT   166
Met Gln Pro Leu Lys Ile Ile Phe Tyr Leu Ser Val Ser Ile Trp Ile
      -25                -20                -15

ATT TTA ATT ATT TAT ACT TTT CAG TGT AAT TCT TCT CTG AGC ATA CTA   214
Ile Leu Ile Ile Tyr Thr Phe Gln Cys Asn Ser Ser Leu Ser Ile Leu
      -10                -5                1                5

CTT TTT GAG TTA               226
Leu Leu Glu Leu

```

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 10..66
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq RVAACATAAAPLQA/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

```

AAGTGATGG ATG ATG AGA ACG ACA GCG AGA GTC GCT GCG TGT ACT GCT GCA   51
Met Met Arg Thr Thr Ala Arg Val Ala Ala Cys Thr Ala Ala
               -15               -10

GCC CCA TTG CAA GCC CAC GGT GCA GRC ATT CAG CAG GRT CCA GAC AGS   99
Ala Pro Leu Gln Ala His Gly Ala Xaa Ile Gln Gln Xaa Pro Asp Xaa
-5               1               5               10

CTC TGS TCT RGA AGG CTC AGC AGA GRR GGR CTT TCT GCA GGG CGR CTG   147
Leu Xaa Ser Xaa Arg Leu Ser Arg Xaa Gly Leu Ser Ala Gly Arg Leu
               15               20               25

CAC CAR AGC GAA ACA GAA GCT GAA CTG GAR GCC CCG GGT CGC GCG   192
His Gln Ser Glu Thr Glu Ala Glu Leu Glu Ala Pro Gly Arg Ala
               30               35               40

```

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: 140..241
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.8
 seq RWASSCLHPSARS/SN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

```

AASCCCAASG TGCTGCCGTT GCCCGTACAA CTCGGACTTG CTGTTGCTCG AGCCGCGTCT   60
GCACGGGTCT CGGACCGAGC GGAGTCCMAG CCTCGGTCCC GGAGCCCACC TTCGCCTCGC   120
CCTTGCCCAG CCTGCGGTG ATG GAG GCG GCC ACC ACA CTG CAC CCA GGC CCG   172
               Met Glu Ala Ala Thr Thr Leu His Pro Gly Pro
                   -30                               -25

CGC CCG GCG CTG CCC CTC GGG GCC CGG GCC CGC TGG GCG AGT TCC TGC   220
Arg Pro Ala Leu Pro Leu Gly Ala Arg Ala Arg Trp Ala Ser Ser Cys
                   -20                               -15                               -10

CTC CAC CCG AGT GCC CGG TCT TCG AAC CCA GCT GGG AAG AGT TCG CGG   268
Leu His Pro Ser Ala Arg Ser Ser Asn Pro Ala Gly Lys Ser Ser Arg
                   -5                               1                               5

ACC CCT   274
Thr Pro
10

```

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 92..178
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.8
 seq LCPVIFFPSNCWK/EY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

```

AAGGAAGGAC ATTTTTTTTT TCTTGACTA ACTAGGCTGG ATTYCCAAA TTGTTTGAGT   60
GGCCCGCTGCC CCTCTTAATG CTTCTGTAAG A ATG CAA GGT GTC AGG GGA CCT   112
               Met Gln Gly Val Arg Gly Pro
                   -25

GTG TCC TTT TCC TGG AGC ACA ACC ATG TTG TGT CCT GTT ATA TTC TTT   160

```

Val Ser Phe Ser Trp Ser Thr Thr Met Leu Cys Pro Val Ile Phe Phe
 -20 -15 -10

CCA TCC AAC TGT TGG AAA GAA TAT AAC AGG ACA CAG 196
 Pro Ser Asn Cys Trp Lys Glu Tyr Asn Arg Thr Gln
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 177..230
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq FXLLFXFXFFRQ/XG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

ACAAGTCTGT CCTCCCTAGG CTGGCAGCTC TGTCAGCACC CAGGTTGTTA GAATAGTTGT 60
 TAAAACAGGT CATTCTGTTG CCAAGTAATT ACGGGGCCTT GSACTCAGTA ACCTTCCCCA 120
 CGAAGCAGGC CGTAGTGTGC TTAGTGCTCT CCCTGSCCTT TCCATCCCCT ACTTTG ATG 179
 Met
 TKG GRR TTT TCT TTC YTT TTA CTT TTC YTT TAW TTT CYT TTT TTC CGC 227
 Xaa Xaa Phe Ser Phe Xaa Leu Leu Phe Xaa Xaa Phe Xaa Phe Phe Arg
 -15 -10 -5
 CAG KCT GGG 236
 Gln Xaa Gly
 1

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 359..427
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.8
 seq SVRLLEFRFSVIMA/SE
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

```
ACACTGTGAA ATGCAATTGT GCCTTGAATA AGAAGGTACC TAGAAGCCAA ATTAAAGTAA   60
TAATGACTTC TTATTGGCTT TGATTTTTCa TTGCAGTATA TGGGAATTGT ACAGCAGGAA  120
ATGCTTATCA TTAATTTCTG ATGTTTTTTA AAGCACAACG CGAAACATTT CGATCATACA  180
TACATAGCAG TAGAGATCTG TGCCCTTCAG GTACATTGWA TCTGACCATC AGTTTATATA  240
TGTCATTGAA TTTTAAGAAT ACTCATGTTA ATAATAGTCA TCTATCCTTG CATTTTGAAA  300
CTGTTCTAAT CTTAGTGAAC TTGAATTGGA TTTCTGGGTA AAAGAATGTG TTTCTTTT   358
ATG TTG CTT CTG TCC GAA GCC TTG TCA GAA TCT GTC AGA CTC TTG TTT   406
Met Leu Leu Leu Ser Glu Ala Leu Ser Glu Ser Val Arg Leu Leu Phe
      -20                      -15                      -10

AGG TTT AGT GTG ATC ATG GCG TCA GAG AAG CAA AGC TTT CAA ATA       451
Arg Phe Ser Val Ile Met Ala Ser Glu Lys Gln Ser Phe Gln Ile
      -5                      1                      5
```

(2) INFORMATION FOR SEQ ID NO: 193:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 319..369
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.8
 seq SLPCTTAFPLLSS/KV
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:


```

ATTCTTCTCT GGTTACCTCT ATCTACCCCC GAGTCAACAA GCCCTGCCTG ATTACGCAGC   60
AGCAGTTTCTT CCTGGAGAGT ATATGCCCTT CCCTACCAGA GTGGCTGTGC TCTGTGGACC  120
AACGGCATT TT GTGCCGTGGC TGGTGTTC ACCATTCCAG TGGGTGGCT GCAGAGTTAT  180
CCTTTGTGGG TGGGAGAGAG CACCAGGCCT CAGGAATCTC CCTGCTGGTC CCAGCCTCCA  240
TCTCCTCTC CCCAACCTG AACCTCTCCC GCAACCTGCA CCTCCCCGA GAAGCCAGCC  300
ACAGAGGCAG AGAGCATC ATG GCT CTT ATC AGC CTG CCA TGC ACG ACA GCT   351
                Met Ala Leu Ile Ser Leu Pro Cys Thr Thr Ala
                -15                               -10

TTC CCT TTA CTG TCC AGC AAG GTT TCC CAG CTT CTC TTG CCC CTC AGC   399
Phe Pro Leu Leu Ser Ser Lys Val Ser Gln Leu Leu Leu Pro Leu Ser
   -5                1                5                10

```

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 83..193
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq RVVALPLVRATCT/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

```

AGTGGAGAGT CGAGCCTGGG GTCGGCGGAG ACWGCTGGTG TCTGAAGCCG CTCGCGCCCA   60
GGGTGACCCT GTTTCAGCA CG ATG TCT GAA GAA GAG GCG GCT CAG ATC CCC   112
                Met Ser Glu Glu Glu Ala Ala Gln Ile Pro
                -35                               -30

AGA TCC AGT GTG TGG GAG CAG GAC CAG CAG AAC GTG GTG CAG CGT GTG   160
Arg Ser Ser Val Trp Glu Gln Asp Gln Gln Asn Val Val Gln Arg Val
   -25                -20                -15

GTG GCT CTG CCC CTG GTC AGG GCC ACG TGC ACC GCG GTC TGC GAT GTT   208
Val Ala Leu Pro Leu Val Arg Ala Thr Cys Thr Ala Val Cys Asp Val
   -10                -5                1                5

TAC AGT GCA GCC AAG GAC AGG CAC CCG CTG CTG GGC TCC GCC TGG   253
Tyr Ser Ala Ala Lys Asp Arg His Pro Leu Leu Gly Ser Ala Trp

```

10

15

20

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 8..223
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq LAELTVDPQGALA/IR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

```

AAAAAAG ATG GCG GCG GCG GCG GCA GCT GGT GCG GCC TCC GGG CTG CCG      49
      Met Ala Ala Ala Ala Ala Ala Gly Ala Ala Ser Gly Leu Pro
                -70                      -65                      -60

GGT CCA GTG GCA CAA GGA TTA AAG GAA GCG TTA GTG GAT ACG CTC ACC      97
Gly Pro Val Ala Gln Gly Leu Lys Glu Ala Leu Val Asp Thr Leu Thr
                -55                      -50                      -45

GGG ATC CTA TCC CCA GTA CAG GAG GTG CGG GCG GCT GCT GAA GAA CAG     145
Gly Ile Leu Ser Pro Val Gln Glu Val Arg Ala Ala Ala Glu Glu Gln
                -40                      -35                      -30

ATT AAG GTG CTG GAG GTG ACG GAG GAA TTT GGT GTT CAC TTG GCA GAA     193
Ile Lys Val Leu Glu Val Thr Glu Glu Phe Gly Val His Leu Ala Glu
                -25                      -20                      -15

CTG ACT GTA GAT CCC CAG GGG GCA CTG GCA ATC CGT CAG CTG GCA TCA     241
Leu Thr Val Asp Pro Gln Gly Ala Leu Ala Ile Arg Gln Leu Ala Ser
-10                      -5                      1                      5

GTC ATC TTG AAA CAA TAT GTG GAG ACT CAC TGG TGT GCC CAA TCA GAG     289
Val Ile Leu Lys Gln Tyr Val Glu Thr His Trp Cys Ala Gln Ser Glu
                10                      15                      20

AAA TTT AGG                                                                298
Lys Phe Arg
                25

```

(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 114..464
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq XXXYLNFCPVCYC/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

```

GIGAATTTCG CAGCGGGAGC GCGCTCGCGG WCCGCGCGTT CTCGCTTTC CCGGCTCCGT   60
CGCTGACGCG TCGTAGASTT GGSVWGCGGG AAGGCAACGG CAGCGGGATC GGG ATG   116
                                     Met
AAC AGC GGC GGC GGC TTC GGT TTG GGC TTA GGC TTC GGC CTC ACC CCC   164
Asn Ser Gly Gly Gly Phe Gly Leu Gly Leu Gly Phe Gly Leu Thr Pro
-115                               -110                               -105
ACG TCG GTG ATT CAG GTG ACG AAT CTG TCG TCG GCG GTG ACC AGC GAG   212
Thr Ser Val Ile Gln Val Thr Asn Leu Ser Ser Ala Val Thr Ser Glu
-100                               -95                               -90                               -85
CAG ATG CGG ACG CTT TTT TCC TTC CTA GGA GAA ATC GAG GAG CTG CGG   260
Gln Met Arg Thr Leu Phe Ser Phe Leu Gly Glu Ile Glu Glu Leu Arg
-80                               -75                               -70
CTC TAC CCC CCG GAC AAC GCA CCT CTT GCT TTT TCC TCB DRA GTA TGT   308
Leu Tyr Pro Pro Asp Asn Ala Pro Leu Ala Phe Ser Ser Xaa Val Cys
-65                               -60                               -55
TAT GTT AAG TTT CGT GAT CCA TCA AGT GTT GGA GTG GCC CAG CAT CTA   356
Tyr Val Lys Phe Arg Asp Pro Ser Ser Val Gly Val Ala Gln His Leu
-50                               -45                               -40
ACT AAC ACG GTT TTT ATT GAC AGA GST CTG RAT AGT TGT TCC TTG TGC   404
Thr Asn Thr Val Phe Ile Asp Arg Xaa Leu Xaa Ser Cys Ser Leu Cys
-35                               -30                               -25
AGA AGG TTG GTA TCT CGC TTT KTT TGN HBT TAT TTG AAT TTC TGT CCT   452
Arg Arg Leu Val Ser Arg Phe Xaa Xaa Xaa Tyr Leu Asn Phe Cys Pro
-20                               -15                               -10                               -5
GTC TGT TAT TGC TTT AGC TTT CCT AGA GAT TGG CAA GTA GAC AGT ACT   500
Val Cys Tyr Cys Phe Ser Phe Pro Arg Asp Trp Gln Val Asp Ser Thr
1                               5                               10
CTC   503

```

Leu

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 47..85
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq MIEMLIFLDCVLS/SK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

```

ATTAACAAAG AGCAAGTTTA ACCTGAGTGG TCAACTTTTG CAGCAG ATG ATT GAR      55
                                   Met Ile Glu

ATG CTA ATA TTT CTA GAC TGT GTC CTG TCT TCC AAA GAT ACA ATA ACC      103
Met Leu Ile Phe Leu Asp Cys Val Leu Ser Ser Lys Asp Thr Ile Thr
-10                               -5                               1                               5

ATG TTT GTG AAG TTC ATA CCT ATT TTT CCT TTT CCT TTG CAG TTT TAT      151
Met Phe Val Lys Phe Ile Pro Ile Phe Pro Phe Pro Leu Gln Phe Tyr
                               10                               15                               20

TTG CCC TCT TTC CTT CTT TTG GAG                                      175
Leu Pro Ser Phe Leu Leu Leu Glu
                               25                               30

```

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 49..285
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq VIGSLLVLTMLTC/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

```

ACATCACAAA AATTAGGTGA CCATGGTTAT GATAATTCTT TGCCTAGT ATG CAT CCA    57
                                   Met His Pro

TTT CTA GCT GCC CAC GGA CCT GCA TTT CAC AAA GGC TAC AAG CAT AGC    105
Phe Leu Ala Ala His Gly Pro Ala Phe His Lys Gly Tyr Lys His Ser
-75                               -70                               -65

ACA ATT AAC ATT GTG GAT ATT TAT CCA ATG ATG TGC CAC ATC CTG GGA    153
Thr Ile Asn Ile Val Asp Ile Tyr Pro Met Met Cys His Ile Leu Gly
-60                               -55                               -50                               -45

TTA AAA CCA CAT CCC AAT AAT GGG ACC TTT GGT CAT ACT AAG TGC TTG    201
Leu Lys Pro His Pro Asn Asn Gly Thr Phe Gly His Thr Lys Cys Leu
                               -40                               -35                               -30

TTA GTT GAC CAG TGG TGC ATT AAT CTC CCA GAA GCC ATC GCG ATT GTT    249
Leu Val Asp Gln Trp Cys Ile Asn Leu Pro Glu Ala Ile Ala Ile Val
                               -25                               -20                               -15

ATC GGT TCA CTC TTG GTG TTA ACC ATG CTA ACA TGC CGC CGG            291
Ile Gly Ser Leu Leu Val Leu Thr Met Leu Thr Cys Arg Arg
                               -10                               -5                               1
  
```

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 33..74
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq IWPMASVATLWS/FT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

```

ATCTTAGTGT GACACATGAA CCCCTCCCT TC ATG ATC TGG CCT ATG TCT GCC    53
                                   Met Ile Trp Pro Met Ser Ala
                                   -10
  
```

TCT GTA GCT ACT CTC TGG TCC TTT ACC TCT TAC ATA AGC TAC CCA AGC 101
 Ser Val Ala Thr Leu Trp Ser Phe Thr Ser Tyr Ile Ser Tyr Pro Ser
 -5 1 5

AGG TTT TAC TAT GAT GCT TGG 122
 Arg Phe Tyr Tyr Asp Ala Trp
 10 15

(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 12..104
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq LFIYLVFVECLLC/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

AAGGGTAATG G ATG GGA ATT GAT ATT TTC TAT CCT TCA CAC ATC CCA GAC 50
 Met Gly Ile Asp Ile Phe Tyr Pro Ser His Ile Pro Asp
 -30 -25 -20

TTT CAT CCT ATT CAT TTA TTC ATT TAT CTA GTG TTT GTA GAG TGC CTT 98
 Phe His Pro Ile His Leu Phe Ile Tyr Leu Val Phe Val Glu Cys Leu
 -15 -10 -5

CTG TGT ACC AGG AAC TGR GAW AGK TTG TCC KGA TTC AAC TGT GAT AAC 146
 Leu Cys Thr Arg Asn Xaa Xaa Xaa Leu Ser Xaa Phe Asn Cys Asp Asn
 1 5 10

GCT CAA ATA ATC TTC ACA ACA GGC TCA TCC TCT AGT GGA GGA AAT AAA 194
 Ala Gln Ile Ile Phe Thr Thr Gly Ser Ser Ser Ser Gly Gly Asn Lys
 15 20 25 30

CCA TTT AAA AGT AGT TTA TGT ACA GTA CAT AGA GGC CAA GAA AGG GAA 242
 Pro Phe Lys Ser Ser Leu Cys Thr Val His Arg Gly Gln Glu Arg Glu
 35 40 45

AGA ATA GAG TGC CAA GGG AAT GGG 266
 Arg Ile Glu Cys Gln Gly Asn Gly
 50

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 24..284
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq LILQASLKGELEA/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

```

AAATAGCTGA TTATGAACGT TTG ATG AAA GAA CTA AAT CAA AAG TTA ACT AAT    53
      Met Lys Glu Leu Asn Gln Lys Leu Thr Asn
      -85                                -80

AAA AAC AAC AAG ATA GAA GAT TTG GAG CAA GAA ATA AAA ATT CAA AAA    101
Lys Asn Asn Lys Ile Glu Asp Leu Glu Gln Glu Ile Lys Ile Gln Lys
      -75                                -70                                -65

CAG AAA CAA GAA ACC CTA CAA GAA GAA ATA ACT TCA TTA CAG TCT TCA    149
Gln Lys Gln Glu Thr Leu Gln Glu Glu Ile Thr Ser Leu Gln Ser Ser
      -60                                -55                                -50

GTA CAA GAA TAT GAA GAA AAA AAC WCC AAA ATC AAG CAA TTG CTT GTG    197
Val Gln Glu Tyr Glu Glu Lys Asn Xaa Lys Ile Lys Gln Leu Leu Val
      -45                                -40                                -35                                -30

AAA ACC AAA AAG GAA CTG GCA GAT TCA AAG CAA GCA GAA ACT GAT CAC    245
Lys Thr Lys Lys Glu Leu Ala Asp Ser Lys Gln Ala Glu Thr Asp His
      -25                                -20                                -15

TTA ATA CTT CAA GCA TCT TTA AAA GGT GAG CTG GAG GCA AGC CAG CAG    293
Leu Ile Leu Gln Ala Ser Leu Lys Gly Glu Leu Glu Ala Ser Gln Gln
      -10                                -5                                1

CAA GTA GAA GTC TAT AAA GTA AGG GTT TTA CTT TTT AAG ATT AAA AAA    341
Gln Val Glu Val Tyr Lys Val Arg Val Leu Leu Phe Lys Ile Lys Lys
      5                                10                                15

ATG TTT TTT CAT GTA GAA GTG AGG AAC GGC                                371
Met Phe Phe His Val Glu Val Arg Asn Gly
      20                                25

```

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 33..371
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq RLLLCILIIVCYI/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

```

ACAGTCCTAC CTTTGCTGAT GCCTACTCTA AT ATG GGA AAC ACT CTA AAG GAG      53
                               Met Gly Asn Thr Leu Lys Glu
                               -110

ATG CAG GAT GTT CAG GGA GCC TTG CAG TGT TAT ACG CGT GCC ATC CAA      101
Met Gln Asp Val Gln Gly Ala Leu Gln Cys Tyr Thr Arg Ala Ile Gln
-105                      -100                      -95

ATT AAT CCT GCA TTT GCA GAT GCA CAT AGC AAT CTG GCT TCC ATT CAT      149
Ile Asn Pro Ala Phe Ala Asp Ala His Ser Asn Leu Ala Ser Ile His
-90                      -85                      -80                      -75

AAG GAT TCA GGG AAT ATT CCA GAA GCC ATA GCT TCT TAC CGC ACG GCT      197
Lys Asp Ser Gly Asn Ile Pro Glu Ala Ile Ala Ser Tyr Arg Thr Ala
                      -70                      -65                      -60

CTG AAA CTT AAG CCT GAT TTT CCT GAT GCT TAT TGT AAC TTG GCT CAT      245
Leu Lys Leu Lys Pro Asp Phe Pro Asp Ala Tyr Cys Asn Leu Ala His
                      -55                      -50                      -45

TGC CTG CAG ATT GTC TGT GAT TGG ACA GAC TAT GAT GAG CGA ATG AAG      293
Cys Leu Gln Ile Val Cys Asp Trp Thr Asp Tyr Asp Glu Arg Met Lys
                      -40                      -35                      -30

AAG TTG GTC AGT ATT GTG GCT GAC CAG TTA GAG AAG AAT AGG TTG CTT      341
Lys Leu Val Ser Ile Val Ala Asp Gln Leu Glu Lys Asn Arg Leu Leu
                      -25                      -20                      -15

CTG TGC ATC CTC ATC ATA GTA TGC TAT ATC CTC TTT CTC ATG      383
Leu Cys Ile Leu Ile Ile Val Cys Tyr Ile Leu Phe Leu Met
-10                      -5                      1

```

(2) INFORMATION FOR SEQ ID NO: 203:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 92..208
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq VAYAIPSIPSLFC/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

```
ACATGTTGAG TACTTTTTC TCACCTGTTT TTCCATTCCT GTTAGCCGGA GCAAAGGGC   60
CTCCAACCTCC TCTTTTAGAG AGAAATGACT A ATG CTC ATA CTA GCA GAT ACC   112
                               Met Leu Ile Leu Ala Asp Thr
                               -35
AGA CGT GTC CAA GGA GGT ACC TTG GGC TTA ATT CCA GCA GTT CTC AAC   160
Arg Arg Val Gln Gly Gly Thr Leu Gly Leu Ile Pro Ala Val Leu Asn
   -30               -25               -20
AGA GTC CAC GTG GCA TAT GCT ATA CCC AGC ATA CCT AGC CTC TTC TGC   208
Arg Val His Val Ala Tyr Ala Ile Pro Ser Ile Pro Ser Leu Phe Cys
   -15               -10               -5
CAG CGC TGG                               217
Gln Arg Trp
1
```

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 343..402
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6

seq CVFLFPLISNTSS/YK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

```

CACACAATTA ATATTAATGG ATAATAATT GGAGTAATGA TTATTAGCTA CTGAATGCTG   60
ATAATAGAAG TCATATTTAA ATGCTTACTT AGTTACTTAA GTTAGTCAAG GACTCTGAAA  120
AAAATAAGGT TTAAAGTTAA CAGTGTATC AGTCATTCCC AGTTATCTTC TTATTTAAGA  180
ACAAGATGGT AATGCAGTTG CCTTTGTTA TTAAATAGA AAAAATTAAA TCAGGATAAA  240
ATGACCCAAC TACAGTGATG TATTTGGACA CACTACTTCT TATCTTTCAA TATAGACTTT  300
TATTTCTGGA TTACCATAGA TGGAAATAGT ATTACTGGAC AT ATG TTG GTA GGT   354
                               Met Leu Val Gly
                               -20

AIT TAC TTC TGT GTT TTT CTT TTT CCC TTA ATT TCG AAT ACT TCT AGC   402
Ile Tyr Phe Cys Val Phe Leu Phe Pro Leu Ile Ser Asn Thr Ser Ser
  -15                -10                -5

TAC AAA AAT TGT CAT AAA ACT TTG CAA CAC ACT ATA CCT CCC CAC GGG   450
Tyr Lys Asn Cys His Lys Thr Leu Gln His Thr Ile Pro Pro His Gly
   1                5                10                15

```

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..126
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LLLQGACPLIFL/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

```

ATG TTT CTC GCT CCC TCT CTG CTG ATC ACA AAG CTG CTG ACC GGG TCA   43
Met Phe Leu Ala Pro Ser Leu Leu Ile Thr Lys Leu Leu Thr Gly Ser
  -40                -35                -30

GAA AGT CCT GAT GGA AAT CCA CCA GCG CTG GGC AGG CCC CTC CTC CTC   96
Glu Ser Pro Asp Gly Asn Pro Pro Ala Leu Gly Arg Pro Leu Leu Leu
  -25                -20                -15

```

```

CAG GGA GCT TGT CCT TGC CTA ATT TTT CTT CGT CCT GAT GAG AAC AAA   144
Gln Gly Ala Cys Pro Cys Leu Ile Phe Leu Arg Pro Asp Glu Asn Lys
-10                      -5                      1                      5

AAA GAG GGG GRG GAG GAA AAG AAA AAC CAC AAA CTT CCT TTG AAA ACC   192
Lys Glu Gly Xaa Glu Glu Lys Lys Asn His Lys Leu Pro Leu Lys Thr
                      10                      15                      20

AGC TTA GGG   201
Ser Leu Gly
                      25

```

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 235..288
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq SKSCLFYQLQKVSQ/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

```

AAAGGTGGCT TCAGGACCAC CTCCTGAGAG CTTGCTTGTA TTTCATGTAT ATTTCCCCAA   60
ATATATCAGC ATCTGACCCT TGGCTTCTGG GAGAAAGACA GAGGCGGAAC CCTGGCCGCC   120
CCAGAGAGAG GCAGCTGTGG GGGCAGAGAT GTAACAACCC TTTGAACCTT GACCTTGGAC   180
GCCAGGCTGT CCGGGAGCTT CTCCACAAT GGCTGTTTTG GGGATGTGAC CTGG ATG   237
                                         Met
GAC CCA TCT GCT AGC AAA TCC TGT CTG TTT TAC CTC CAA AAA GTA TCT   285
Asp Pro Ser Ala Ser Lys Ser Cys Leu Phe Tyr Leu Gln Lys Val Ser
-15                      -10                      -5

GGA ATT CCA GGG CTT CTC ACC   306
Gly Ile Pro Gly Leu Leu Thr
1                      5

```

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 54..191
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq RWLCLQAYLASFS/LE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

```

ACGIGTCCTC AGGATTTTCC TCTTGGGCTG GACAGTTTGC TCCCCTGGAG GGT ATG      56
                                     Met

AGC CTG ACT GCT AGT GGG CCA AGA GCT GCC TGG GAG GAA AGG GTG GGG      104
Ser Leu Thr Ala Ser Gly Pro Arg Ala Ala Trp Glu Glu Arg Val Gly
-45                -40                -35                -30

GGT CTC CAC ACT TGG GGT GCC AAC ATT CCT ACC GCC CCT GAT TCC CAG      152
Gly Leu His Thr Trp Gly Ala Asn Ile Pro Thr Ala Pro Asp Ser Gln
                -25                -20                -15

CGG TGG CTC TGT CTT CAG GCG TAC CTG GCA TCC TTC AGT CTT GAG AGC      200
Arg Trp Leu Cys Leu Gln Ala Tyr Leu Ala Ser Phe Ser Leu Glu Ser
                -10                -5                1

CCC CAC AGA ATC TAC CTK GAA TCT CCT CCC ACG CTC CTT TTC CCC CCG      248
Pro His Arg Ile Tyr Leu Glu Ser Pro Pro Thr Leu Leu Phe Pro Pro
      5                10                15

CCG
Pro
20
251

```

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 117..182
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq AQLASPLLPGATP/VA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

```

ACCGCAGAAA ATGCTAGGTG CAAAGTTTGT CGAAAGAAAG GTGAGGATGA CAAATTGATC    60
TTGTGTGATG AGTGTAATAA AGCCTTYCCA CCTGTTTTGT CTGAGGCCCG CCCTCT ATG    119
                                     Met
AAG TAC CAG ATG GTG AGT GGC AGT GCC CAG CTT GCC AGC CCG CTA CTG    167
Lys Tyr Gln Met Val Ser Gly Ser Ala Gln Leu Ala Ser Pro Leu Leu
  -20                      -15                      -10
CCA GGC GCA ACT CCC GTG GCA GGA ACT ATA CTG AAG AGT CTG CTT CTG    215
Pro Gly Ala Thr Pro Val Ala Gly Thr Ile Leu Lys Ser Leu Leu Leu
  -5                      1                      5                      10
AGG ACA GTG AAG ATG ATG AGA GTG ATG    242
Arg Thr Val Lys Met Met Arg Val Met
      15                      20

```

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 229..333
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq CFWGLMYXWLLLG/SX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

```

ACATCTGATC GATAATTATG TCACCTGTAC CTGTCGCCAG CTTGICITGT TATGACGTTA    60
GTTTACTGCT TAGAATATC TAGTAGATGG CTGGAAATCT GCAGGCAAG TGCAGAGGGA    120
GTGAGCCTGC GAGGAGAGGG SCTGGGCAAA GTGAMBGCCC TGGGCCGCAG AGTTCTTATC    180

```

```

TAAAAAATGG.GAACAGTAGT GTCTTCCTAA AGGCACCATG GACTTAAA ATG AAT GGC   237
                                     Met Asn Gly
                                     -35

ACG TTT CCT GGG ACT TAT GTA TAT TTG GTT GCT TAT GGG GAC TTA CGT   285
Thr Phe Pro Gly Thr Tyr Val Tyr Leu Val Ala Tyr Gly Asp Leu Arg
-30                               -25                               -20

ATA TTT GGT TGC TTT TGG GGA CTT ATG TAT ATK TGG TTG CTT TTG GGG   333
Ile Phe Gly Cys Phe Trp Gly Leu Met Tyr Xaa Trp Leu Leu Leu Gly
-15                               -10                               -5

TCT NAA GGG
Ser Xaa Gly
1

```

342

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 66..157
id AA134726
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 216..282
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 152..218
id AA134726
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..342
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 220..279
id AA134726
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 64..103
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..40
 id AA134726
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 98..130
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 34..66
 id AA134726
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 81..285
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..205
 id R17226
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 50..112
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 12.7
 seq ILFLLSWSGPLQG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

```

GAGGCTGACT GTACGTCCT TCTACTCTGG CACCACTCTC CAGGCTGCC ATG GGG CCC   58
                                     Met Gly Pro
                                     -20

AGC ACC CCT CTC CTC ATC TTG TTC CTT TTG TCA TGG TCG GGA CCC CTC   106
Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser Gly Pro Leu
      -15                      -10                      -5

CAA GGA CAG CAG CAC CAC CTT GTG GAG TAC ATG GAA CGC CGA CTA GCT   154
Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg Arg Leu Ala
      1                      5                      10

GCT TTA GAG GAA CGG CTG GCC CAG TGC CAG GAC CAG AGT AGT CGG CAT   202
Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser Ser Arg His
      15                      20                      25                      30

GCT GCT GAG CTG CGG AAC TTC AAG AAC AAG ATG CTG CCA CTG CTG GAG   250
Ala Ala Glu Leu Arg Asn Phe Lys Asn Lys Met Leu Pro Leu Leu Glu
      35                      40                      45

GTG GCA GAG AAG GAG CGG GAG GCA CTC AGA ACT GAG GCC GRC ACC ATC   298
Val Ala Glu Lys Glu Arg Glu Ala Leu Arg Thr Glu Ala Xaa Thr Ile
      50                      55                      60

TCN NVN GGA GTG GAT CGT CTG GAG CGG GAG GTA GAC TAT CTG   340
Ser Xaa Gly Val Asp Arg Leu Glu Arg Glu Val Asp Tyr Leu

```

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- [illegible]

(ix) FEATURE:

- [illegible]

(ix). FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 76..141
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.5
seq LMLLVSSLSFVCG/VL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

AAAATAGGAG	TCTCTGGTAC	TGCAAACCCA	CAGCCTGGAC	TCAGAGCTCA	AGTCTGAAC	60										
CTACCTCCAG	ACAGA	ATG	AAG	TTC	ATC	TCG	ACA	TCT	CTG	CTT	CTC	ATG	CTG	111		
		Met	Lys	Phe	Ile	Ser	Thr	Ser	Leu	Leu	Leu	Met	Leu			
				-20					-15							
CTG	GTC	AGC	AGC	CTC	TCT	CCA	GTC	CAA	GGT	GTT	CTG	GAG	GTC	TAT	TAC	159
Leu	Val	Ser	Ser	Leu	Ser	Pro	Val	Gln	Gly	Val	Leu	Glu	Val	Tyr	Tyr	
-10				-5					1					5		
ACA	AGC	TTG	AGG	TGT	AGA	TGT	GTC	CAA	GAG	AGC	TCA	GTC	TTT	ATC	CCT	207
Thr	Ser	Leu	Arg	Cys	Arg	Cys	Val	Gln	Glu	Ser	Ser	Val	Phe	Ile	Pro	
			10					15					20			


```

AGA CGC TTC ATT GAT CGA ATT CAA ATC TTG CCC CGT GGG AAT GGT TGT    255
Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn Gly Cys
      25              30              35

CCA AGA AAA GAA ATC ATA GTC TGG AAG AAG AAC AAG TCA ATT GTG TGT    303
Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile Val Cys
      40              45              50

GTG GAC CTC AAG CAT AGG                                321
Val Asp Leu Lys His Arg
      55              60

```

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..186
id T07474
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 16..156
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8
seq VLELLAAVCLVRG/GH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

```

AGTTTACGTG CCATC ATG AAT TAT CAG TAT GGT TTC AAC ATG GTC ATG TCT    51
      Met Asn Tyr Gln Tyr Gly Phe Asn Met Val Met Ser
            -45              -40

CAT CCA CAC GCT GTC AAT GAG ATT GCA CTA AGC CTG AAC AAC AAG AAT    99
His Pro His Ala Val Asn Glu Ile Ala Leu Ser Leu Asn Asn Lys Asn
-35      -30              -25              -20

CCC AGA ACA AAA GCC CTT GTC TTA GAA CTG TTG GCA GCC GTT TGT CTT    147
Pro Arg Thr Lys Ala Leu Val Leu Glu Leu Leu Ala Ala Val Cys Leu
      -15              -10              -5

GTC AGA GGC GGG CAT GAA ATC ATT TTA TCA GCA TTT GAT AAC TTT AAA    195

```

Val	Arg	Gly	Gly	His	Glu	Ile	Ile	Leu	Ser	Ala	Phe	Asp	Asn	Phe	Lys	
			1				5					10				
GAG	GTT	TGT	GGA	GAA	AAA	CAG	CGC	TTT	GAG	AAG	TTG	ATG	GAA	CAT	TTC	243
Glu	Val	Cys	Gly	Glu	Lys	Gln	Arg	Phe	Glu	Lys	Leu	Met	Glu	His	Phe	
	15					20					25					
AGG	AAT	GAA	GAC	AAT	AAC	ATA	GAT	TTT	ATG	GTG	GCT	TCT	ATG	CAG	TTT	291
Arg	Asn	Glu	Asp	Asn	Asn	Ile	Asp	Phe	Met	Val	Ala	Ser	Met	Gln	Phe	
30					35					40					45	
ATT	AAT	ATT	GTA	GTC	CAT	TCA	GTA	GAA	GAT	ATG	AAT	TTC	AGA	GTT	CAC	339
Ile	Asn	Ile	Val	Val	His	Ser	Val	Glu	Asp	Met	Asn	Phe	Arg	Val	His	
				50					55					60		
CTG	CAG	TAT	GAA	TTT	ACC	AAA	TTA	GGC	CTG	GMC	GAA	TAC	TTG	GRC	AAG	387
Leu	Gln	Tyr	Glu	Phe	Thr	Lys	Leu	Gly	Leu	Xaa	Glu	Tyr	Leu	Xaa	Lys	
			65					70					75			
CTG	AAA	CAC	ACT	GAG	AGT	GAC	AAG	CTT	CAA	GTC	CAG	ATC				426
Leu	Lys	His	Thr	Glu	Ser	Asp	Lys	Leu	Gln	Val	Gln	Ile				
	80						85					90				

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi). ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 246..387
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..142
id HUM75821
est

(ix) FEATURE:

- ```
(A) NAME/KEY: other
(B) LOCATION: 246..387
(C) IDENTIFICATION METHOD: blastn
(D). OTHER INFORMATION: identity 100
 . region 1..142
 . id T08488
 : est
```

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 261..387

(C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 1..127  
                           id R54273  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 205..288  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.7  
                           seq LVMCFLSYFGTFA/VE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

```

ATTGGTAATT TTCAGCTCAC AAATGATGAA GAAATCCATA ACGTCGGAAC TTCCTTGACC 60
TTTGGATTG GCACATTGAC CTGCTGGATC CAGGCTGCGC TGACACTCAA GGTCAACATC 120
AASAATGAAG GACGGAGAGT TGAATTCCA CGGGTTATTC TGTCGGCATC TATCACTCTC 180
TGTGTGGTCC TCTACTTCAT CCTC ATG GCC CAA AGC ATC CAC ATG TAT GCA 231
 Met Ala Gln Ser Ile His Met Tyr Ala
 -25 -20

GCC AGG GTC CAG TGG GGC CTG GTC ATG TGC TTC CTG TCT TAT TTT GGC 279
Ala Arg Val Gln Trp Gly Leu Val Met Cys Phe Leu Ser Tyr Phe Gly
 -15 -10 -5

ACC TTT GCC GTG GAG TTC CGG CAT TAC CGC TAT GAG ATT GTT TGC TCT 327
Thr Phe Ala Val Glu Phe Arg His Tyr Arg Tyr Glu Ile Val Cys Ser
 1 5 10

GAG TAC CAG GAG AAT TTC CTA AGC TTC TCA GAA AGC CTG TCA GAA GCT 375
Glu Tyr Gln Glu Asn Phe Leu Ser Phe Ser Glu Ser Leu Ser Glu Ala
 15 20 25

TCT GAA TAT CAG 387
Ser Glu Tyr Gln
 30

```

## (2) INFORMATION FOR SEQ ID NO: 214:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 124..335  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 1..212  
                           id AA081335  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 212..309  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 1..98  
                           id H88204  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 296..335  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 82..121  
                           id H88204  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 284..335  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 1..52  
                           id W31695  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 75..138  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.1  
                           seq LHLFHLIRPXQG/WX

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

```

ACTCTCTGCT GAACTCCCAA AGGGAGTGTG IGTATTTCCT CCCGTTCTTN ATCAGAGCCC 60
CCAAAATAAG TAGGA ATG GGC AGT GGC TAT TCA CAT TCA CTA CAC CTT TTC 111
 Met Gly Ser Gly Tyr Ser His Ser Leu His Leu Phe
 -20 -15 -10

CAT TTG CTA ATA AGG CCC TGS CAA GGT TGG RAG GRA ATT GTC CCT GCC 159
His Leu Leu Ile Arg Pro Xaa Gln Gly Trp Xaa Xaa Ile Val Pro Ala
 -5 1 5

TGC TTC TGG AGA AAG AAG ATA TTG ACA CCA TCT ACG GGC ACC ATG GAA 207
Cys Phe Trp Arg Lys Lys Ile Leu Thr Pro Ser Thr Gly Thr Met Glu
 10 15 20

CTG CTT CAA GTG ACC ATT CTT TTT CTT CTG CCC AGT ATT TGC AGC AGT 255
Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys Ser Ser
 25 30 35

```

AAC AGC ACA GGT GTT TTA GAG GCA GCT AAT AAT TCA CTT GTT GTT ACT 303  
 Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val Val Thr  
 40 45 50 55

ACA ACA AAA CCA TCT ATA ACA ACA CCA AAC ACG TGG 339  
 Thr Thr Lys Pro Ser Ile Thr Thr Pro Asn Thr Trp  
 60 65

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 209..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..116  
id AA081350  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 277..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 3..50  
id AA046671  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 157..204
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq CFSLVLLLSIWT/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

AGGGAAATCC GGATGTCTCG GTTATGAAGT GGAGCAGTGA GTGTGAGCCT CAACATAGTT 60  
 CCAGAACTCT CCATCCGGAC TAGTTATTGA GCATCTGCCT CTCATATCAC CAGTGGCCAT 120  
 CTGAGGTGTT TCCCTGGCTC TGAAGGGGTA GGCACG ATG GCC AGG TGC TTC AGC 174  
 Met Ala Arg Cys Phe Ser  
 -15

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CTG | GTG | TTG | CTT | CTC | ACT | TCC | ATC | TGG | ACC | ACG | AGG | CTC | CTG | GTC | CAA | 222 |
| Leu | Val | Leu | Leu | Leu | Thr | Ser | Ile | Trp | Thr | Thr | Arg | Leu | Leu | Val | Gln |     |
| -10 |     |     |     |     | -5  |     |     | .   |     | 1   |     |     |     | 5   |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GGC | TCT | TTG | CGT | GCA | GAA | GAG | CTT | TCC | ATC | CAG | GTG | TCA | TGC | AGA | ATT | 270 |
| Gly | Ser | Leu | Arg | Ala | Glu | Glu | Leu | Ser | Ile | Gln | Val | Ser | Cys | Arg | Ile |     |
|     |     |     | 10  |     |     |     |     | 15  |     |     |     |     | 20  |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| ATG | GNN | RTC | ACC | CTT | GTG | AGC | AAA | AAG | GCG | AAC | CAG | CAG | CTG | AAT | TTC | 318 |
| Met | Xaa | Xaa | Thr | Leu | Val | Ser | Lys | Lys | Ala | Asn | Gln | Gln | Leu | Asn | Phe |     |
|     |     | 25  |     |     |     |     | 30  |     |     |     |     | 35  |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| ACA | GAA | NNV | NAA | GGA | GGC | CWW | WAR | GCT | GCT | GGG | ACT | AAG | TTT | GGC |     | 363 |
| Thr | Glu | Xaa | Xaa | Gly | Gly | Xaa | Xaa | Ala | Ala | Gly | Thr | Lys | Phe | Gly |     |     |
|     | 40  |     |     |     |     | 45  |     |     |     |     | 50  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 20..194  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 144..318  
id AA045920  
est

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 194..257  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 319..382  
id AA045920  
est

(ix) FEATURE:

- (A) NAME/KEY: other  
(B) LOCATION: 20..226  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 153..359  
id N25870  
est

(12) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 220..262  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 355..397  
id N25870  
est

(ix) FEATURE:

[illegible]

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 212..267  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 335..390  
id H99323  
est

(ix) FEATURE:

[illegible]

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 171..269  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.7  
seq MTCLSVLFQYATS/HP

(xi) SEQUENCE DESCRIPTION: SEO ID NO: 216:

|                                                                    |         |
|--------------------------------------------------------------------|---------|
| AATCTTGTGCA GAAGTCGTCG AAAATATTTA CACCAGCAGC TCCAGTTCAT ACCAATAAAG | 60      |
| AAGATCCTGC TACCCAAACT AATTTGGGRW TTATCCAWGC ATTTGKCGCT GCCATATCAG  | 120     |
| TTATTAWTGK ATCYGAATTG GGTGATAAGA CATTTTTTAT AGCAGCCATC ATG GCA     | 176     |
|                                                                    | Met Ala |
| ATG CGC TAT AAC CGC CTG ACC GTG CTG GCT GGT GCA ATG CTT GCC TTG    | 224     |
| Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala Met Leu Ala Leu    |         |
| -30 -25 -20                                                        |         |
| GGA CTA ATG ACA TGC TTG TCA GTT TTG TTT GGC TAT GCC ACC AGT CAT    | 272     |
| Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly Tyr Ala Thr Ser His    |         |
| -15 -10 -5 1                                                       |         |
| CCC CAG GGC CTA TAC ATA                                            | 290     |
| Pro Gln Gly Leu Tyr Ile                                            |         |

## (2) INFORMATION FOR SEQ ID NO: 217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 319..370
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 31..82  
id R51759  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 288..318
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..31  
id R51759  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 211..288
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq RQLLLPLPPFSFP/AP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

AGTCAATTCT AGGAGCCATC AAGCATGAAA GTGGTTCTGT CTCCTGAGCG CAASCTCGCC 60

GGACCCCTGG GCGAAGGCCT GGA CTTCAG ATGTGTGTTT CCTGTGCGGG TGGACAGAGG 120

GGGCCCTTAT GACCCACATT GCAGCCCCAT TCCACCACCC CTCCTCCCC AGAGCAGTCT 180

CTGCCGAGGG ACAGCACCTG TGTCCCTTCG ATG CCA CAA CAG CCA GTT GAA CAG 234  
Met Pro Gln Gln Pro Val Glu Gln  
-25 -20

GGG AGC CCT TTG CTC AGG CAG CTT CTC CTG CCT CTC CCT CCT TTC TCC 282  
Gly Ser Pro Leu Leu Arg Gln Leu Leu Pro Leu Pro Phe Ser  
-15 -10 -5



|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TTC CCT GCC CCA TCC CCG TGC CCT TCT TGG CCT GTG GCG CTG GGG AGC | 330 |
| Phe Pro Ala Pro Ser Pro Cys Pro Ser Trp Pro Val Ala Leu Gly Ser |     |
| 1 5 10                                                          |     |
| CAT GGT GTG GCA TAC TGG GGC TCC TGC TCC TTG GGS CAC             | 369 |
| His Gly Val Ala Tyr Trp Gly Ser Cys Ser Leu Gly His             |     |
| 15 20 25                                                        |     |

## (2) INFORMATION FOR SEQ ID NO: 218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 117..390
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..274  
id C16636  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 121..360
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2  
seq RASLLPMLLGSWA/FL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AAAAAAGAGC TGGTTCCTG GCAGGCTGGA GGGCAGGAGC TGGGGCCACC CTGGTCTGGG  | 60  |
| ATAGTTGGGC AGGGAGGCTG TCTACCTGGT CTTCCAGAAT GGACGGCCCT GTGGCAGAGC | 120 |
| ATG CCA AGC AGG AGC CCT TTC ACG TGG TCA CAC CTC TGT TGG AGA GCT   | 168 |
| Met Pro Ser Arg Ser Pro Phe Thr Trp Ser His Leu Cys Trp Arg Ala   |     |
| -80 -75 -70 -65                                                   |     |
| GGG CGC TGT CCC AGG TGG CGG GCA TGC CTG TCT TCC TCA AGT GTG AGA   | 216 |
| Gly Arg Cys Pro Arg Trp Arg Ala Cys Leu Ser Ser Ser Ser Val Arg   |     |
| -60 -55 -50                                                       |     |
| ATG TGC AGC CCA GCG GCT CCT TCA AGA TTC GGG GCA TTG GGC ATN TCT   | 264 |
| Met Cys Ser Pro Ala Ala Pro Ser Arg Phe Gly Ala Leu Gly Xaa Ser   |     |
| -45 -40 -35                                                       |     |
| GCC AGG AGA TGG CCA AGA AGG GAT GCA GAC ACC TGG TGT GCT CCT CAG   | 312 |

Ala Arg Arg Trp Pro Arg Arg Asp Ala Asp Thr Trp Cys Ala Pro Gln  
-30 -25 -20  
GGG GTA ATG CGG GCA TCG CTG CTG CCT ATG CTG CTA GGA AGC TGG GCA 360  
Gly Val Met Arg Ala Ser Leu Leu Pro Met Leu Leu Gly Ser Trp Ala  
-15 -10 -5  
TTC CTG CCA CCA TCG TGC TCC CCG AGA GCA 390  
Phe Leu Pro Pro Ser Cys Ser Pro Arg Ala  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 219:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..409
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 50..373  
id AA147010  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..450
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 156..474  
id AA142584  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 222..450
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..229  
id AA043641  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..304
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 72..275  
id T18932

est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 132..243  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
 region 146..257  
 id AA123074  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 165..284  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6  
 seq LTYGIILTHGASG/DM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

```

AACGCTGTGG CGGGGCAGGC GAGGCGGTCTG CTTGAGCGC GCTAGTCAGC TCCCTGAAGG 60
GAGTGACGGC GGTGGGTGC CCGCGGCCAC TTTGCTTC CCGGGGAGAT GTCCTTTGCT 120
TCTCAGATGT AAKGCACTT TAAGTTTGW ATTCAACAGT GAAA ATG AGT CAT ACA 176
 Met Ser His Thr
 -40

GAG GTT AAA TTA AAA ATA CCT TTT GGA AAT AAA TTA CTA GAT GCT GTT 224
Glu Val Lys Leu Lys Ile Pro Phe Gly Asn Lys Leu Leu Asp Ala Val
-35 -30 -25

TGT TTG GTA CCT AAC AAG AGC TTA ACA TAT GGA ATA ATT CTT ACA CAT 272
Cys Leu Val Pro Asn Lys Ser Leu Thr Tyr Gly Ile Ile Leu Thr His
-20 -15 -10 -5

GGA GCA TCA GGA GAT ATG AAT CTT CCT CAT TTG ATG TCA CTG GCA TCC 320
Gly Ala Ser Gly Asp Met Asn Leu Pro His Leu Met Ser Leu Ala Ser
 1 5 10

CAT CTT GCA TCT CAT GGG TTT TTC TGC CTG AGA TTT ACC TGT AAA GGC 368
His Leu Ala Ser His Gly Phe Phe Cys Leu Arg Phe Thr Cys Lys Gly
 15 20 25

CTT AAT ATT GTA CAT AGA ATT AAG GCG TAT AAA TCA GTT TTG AAT TAC 416
Leu Asn Ile Val His Arg Ile Lys Ala Tyr Lys Ser Val Leu Asn Tyr
 30 35 40

CTG AAG ACA TCA GGM RAA TAC AAA CTT GCA GGT 449
Leu Lys Thr Ser Gly Xaa Tyr Lys Leu Ala Gly
45 50 55

```

## (2) INFORMATION FOR SEQ ID NO: 220:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 75..254  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..180  
id T31666  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 73..126  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 88..141  
id R58665  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 23..77  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 39..93  
id R58665  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 157..231  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 63..137  
id R14990  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 95..144  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..50  
id R14990  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 135..254  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..120  
id T26956

est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 31..150
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq LCXEFXSVASCDA/AV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

```

AAAAAGGGGC GGTGCAGAGG CGGCAGGAAG ATG GAG TTG GGG AGT TGC CTG GAG 54
 Met Glu Leu Gly Ser Cys Leu Glu
 -40 -35

GGC GGG AGG GAG GCG GCG GAG GAA GAG GGC GAG CCT GAG GTG AAA AAG 102
Gly Gly Arg Glu Ala Ala Glu Glu Glu Gly Glu Pro Glu Val Lys Lys
 -30 -25 -20

CGG CGA CTT CTG TGT STR GAG TTT RCC TCG GTC GCA AGC TGC GAT GCC 150
Arg Arg Leu Leu Cys Xaa Glu Phe Xaa Ser Val Ala Ser Cys Asp Ala
 -15 -10 -5

GCA GTG GCT CAG TGC TTC CTG GCC GAK AAC GAC TGG GAG ATG GAA AGG 198
Ala Val Ala Gln Cys Phe Leu Ala Xaa Asn Asp Trp Glu Met Glu Arg
 1 5 10 15

GCT CTG AAC TCC TAC TTC GAG CCT CCG GTG GAG GAG AGC GCC TTG GAA 246
Ala Leu Asn Ser Tyr Phe Glu Pro Pro Val Glu Glu Ser Ala Leu Glu
 20 25 30

CGC CGA CCA DGG
Arg Arg Pro Xaa
 35

```

## (2) INFORMATION FOR SEQ ID NO: 221:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 52..231  
id AA099777  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 85..135  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 1..51  
                           id AA099777  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 138..222  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 83..167  
                           id HSB16C031  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 80..135  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 27..82  
                           id HSB16C031  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 145..314  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 91  
                           region 43..212  
                           id AA068028  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 148..255  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.8  
                           seq AFVSGLLIGQCSS/QK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

```

AGGCAGTGAA TTGAGACCGG AGGGAATCTG GCCCCTAGAG GCTGGTACTT GGGCCCGAAA 60
CCCCCATCTC CGGCGGAGAG ACCGTCCGAG GTAATTGTCT GCCACGAGTG CACATTCTGA 120
AAACAGGRGR WTTTAAGKTT CCTAAAA ATG GGA AGA ACC TAC ATT GTA GAA GAG 174
 Met Gly Arg Thr Tyr Ile Val Glu Glu
 -35 -30

ACT GTT GGC CAG TAT CTT TCA AAC ATA AAT CTC CAA GGA AAG GCT TTT 222
Thr Val Gly Gln Tyr Leu Ser Asn Ile Asn Leu Gln Gly Lys Ala Phe
 -25 -20 -15

GTC TCT GGC CTT TTA ATA GGA CAG TGT TCG TCA CAA AAG GAT TAT GTG 270
Val Ser Gly Leu Leu Ile Gly Gln Cys Ser Ser Gln Lys Asp Tyr Val

```

|                                                                 |    |    |    |     |
|-----------------------------------------------------------------|----|----|----|-----|
| -10                                                             | -5 | 1  | 5  |     |
| ATT CTT GCC ACT AGA ACG CCA CCC AAA GAG GAG CAA AGT GAG AAC TTG |    |    |    | 318 |
| Ile Leu Ala Thr Arg Thr Pro Pro Lys Glu Glu Gln Ser Glu Asn Leu |    |    |    |     |
|                                                                 | 10 | 15 | 20 |     |

## (2) INFORMATION FOR SEQ ID NO: 222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 227..433
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..207  
id R16604  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 432..474
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 207..249  
id R16604  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 227..440
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..214  
id N99558  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 109..171
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq CLSCLLIPLALWS/II

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

AGTATTTTCAC ACTGAGATTG TCGGCTGCGG GTATATTCCA ATTCCCCGTC TCCTCATGAA 60

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| TATGAAGTGA AGGGCTCTGA CCCTGGAAGT GGTCTAAGC AGGGCAAA ATG GGG TCT | 117 |
| Met Gly Ser                                                     |     |
| -20                                                             |     |
| CGG AAG TGT GGA GGC TGC CTA AGT TGT TTG CTG ATT CCG CTT GCA CTT | 165 |
| Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu Leu Ile Pro Leu Ala Leu |     |
| -15 -10 -5                                                      |     |
| TGG AGT ATA ATC GTG AAC ATA TTA TTG TAT TTC CCG AAT GGG CAA ACT | 213 |
| Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr Phe Pro Asn Gly Gln Thr |     |
| 1 5 10                                                          |     |
| TCC TAT GCA TCC AGC AAT AAA CTC ACC AAC TAC GTG TGG TAT TTT GAA | 261 |
| Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn Tyr Val Trp Tyr Phe Glu |     |
| 15 20 25 30                                                     |     |
| GGA ATC TGT TTC TCA GGC ATC ATG ATG CTT ATA GTA ACA ACA GTT CTT | 309 |
| Gly Ile Cys Phe Ser Gly Ile Met Met Leu Ile Val Thr Thr Val Leu |     |
| 35 40 45                                                        |     |
| CTG GTA CTG GAG AAT AAT AAC AAC TAT AAA TGT TGC CAG AGT GAA AAC | 357 |
| Leu Val Leu Glu Asn Asn Asn Asn Tyr Lys Cys Cys Gln Ser Glu Asn |     |
| 50 55 60                                                        |     |
| TGC AGC AAA AAA TAT GTG ACA CTG CTG TCA ATT ATC TTT TCT TCC CTC | 405 |
| Cys Ser Lys Lys Tyr Val Thr Leu Leu Ser Ile Ile Phe Ser Ser Leu |     |
| 65 70 75                                                        |     |
| GGA ATT GCT TTT TCT GGA TAC TGC CTG GTC ATC TCT GCC TTG GGT CTT | 453 |
| Gly Ile Ala Phe Ser Gly Tyr Cys Leu Val Ile Ser Ala Leu Gly Leu |     |
| 80 85 90                                                        |     |
| GTC CAA GGG CCA TAT TGC CGC                                     | 474 |
| Val Gln Gly Pro Tyr Cys Arg                                     |     |
| 95 100                                                          |     |

## (2) INFORMATION FOR SEQ ID NO: 223:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..341
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..214  
id N99558



est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 399..459  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
 region 278..338  
 id N99558  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 359..407  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
 region 237..285  
 id N99558  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 128..334  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 1..207  
 id R16604  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 333..386  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 207..260  
 id R16604  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 10..72  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.6  
 seq CLSCLLIPLALWS/II

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

```

AAGGGCAAA ATG GGG TCT CGG AAG TGT GGA GGC TGC CTA AGT TGT TTG CTG 51
 Met Gly Ser Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu Leu
 -20 -15 -10

ATT CCG CTT GCA CTT TGG AGT ATA ATC GTG AAC ATA ITA TTG TAT TTC 99
 Ile Pro Leu Ala Leu Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr Phe
 -5 1 5

CCG AAT GGG CAA ACT TCC TAT GCA TCC AGC AAT AAA CTC ACC AAC TAC 147
 Pro Asn Gly Gln Thr Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn Tyr
 10 15 20 25

GTG TGG TAT TTT GAA GGA ATC TGT TTC TCA GGC ATC ATG ATG CTT ATA 195

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Trp | Tyr | Phe | Glu | Gly | Ile | Cys | Phe | Ser | Gly | Ile | Met | Met | Leu | Ile |     |  |
|     |     |     |     | 30  |     |     |     |     | 35  |     |     |     |     | 40  |     |     |  |
| GTA | ACA | ACA | GTT | CTT | CTG | GTA | CTG | GAG | AAT | AAT | AAC | AAC | TAT | AAA | TGT | 243 |  |
| Val | Thr | Thr | Val | Leu | Leu | Val | Leu | Glu | Asn | Asn | Asn | Asn | Tyr | Lys | Cys |     |  |
|     |     |     | 45  |     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |  |
| TGC | CAG | AGT | GAA | AAC | TGC | AGC | AAA | AAA | TAT | GTG | ACA | CTG | CTG | TCA | ATT | 291 |  |
| Cys | Gln | Ser | Glu | Asn | Cys | Ser | Lys | Lys | Tyr | Val | Thr | Leu | Leu | Ser | Ile |     |  |
|     |     |     | 60  |     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |  |
| ATC | TTT | TCT | TCC | CTC | GGA | ATT | GCT | TTT | TCT | GGA | TAC | TGC | CTG | GTC | ATC | 339 |  |
| Ile | Phe | Ser | Ser | Leu | Gly | Ile | Ala | Phe | Ser | Gly | Tyr | Cys | Leu | Val | Ile |     |  |
|     |     |     | 75  |     |     | 80  |     |     |     |     | 85  |     |     |     |     |     |  |
| TCT | GCC | TTG | GGT | CTT | GTC | CAA | GGG | CCA | TAT | TGC | CGC | ACC | CTT | GAT | GGC | 387 |  |
| Ser | Ala | Leu | Gly | Leu | Val | Gln | Gly | Pro | Tyr | Cys | Arg | Thr | Leu | Asp | Gly |     |  |
|     |     |     | 90  |     |     | 95  |     |     |     | 100 |     |     |     |     | 105 |     |  |
| TGG | GAG | TAT | GCT | TTT | GAA | GGC | ACT | RCT | GGA | CGT | TTC | CTT | ACA | GAT | TCT | 435 |  |
| Trp | Glu | Tyr | Ala | Phe | Glu | Gly | Thr | Xaa | Gly | Arg | Phe | Leu | Thr | Asp | Ser |     |  |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |     |     |  |
| AGC | ATA | TGG | ATT | CAG | TGC | CTG | GAA |     |     |     |     |     |     |     |     | 459 |  |
| Ser | Ile | Trp | Ile | Gln | Cys | Leu | Glu |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     | 125 |     |     |     |     |     |     |     |     |     |     |     |     |  |

## (2) INFORMATION FOR SEQ ID NO: 224:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 6..344  
id H09880  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 403..454
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 355..401  
id H09880  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 60..399  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 56..395  
id H29351  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 393..432  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 391..430  
id H29351  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 65..369  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 41..345  
id H94779  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 118..455  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..338  
id N27248  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 122..399  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..278  
id T74091  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 393..434  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 273..314  
id T74091  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 346..403  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.5  
seq SFLPSALVIWTS/AF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

```

ACTCCTTTTA GCATAGGGGC TTCGGCGCCA GCGGCCAGCG CTAGTCGGTC TGGTAAGTGC 60
CTGATGCCGA GTTCCGTCTC TCGCGTCTTT TCCTGGTCCC AGGCAAAGCG GASGNAGATC 120
CTCAAACGGC CTAGTGCTTC GCGCTTCCGG AGAAAATCAG CGGTCTAATT AATTCCTCTG 180
GTTTGTGTA GAGTTACCA AGAATCTTCA ACCCTTTCCC ACAAAGCTA ATTGAGTACA 240
CGTTCCTGTT GAGTACACGT TCCTGTTGAT TTACAAAAGG TGCAGGTATG AGCAGGTCTG 300
AAGACTAACA TTTTGTGAAG TTGTAAACA GAAACCTGT TAGAA ATG TGG TGG TTT 357
 Met Trp Trp Phe
 -20

CAG CAA GGC CTC AGT TTC CTT CCT TCA GCC CTT GTA ATT TGG ACA TCT 405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
 -15 -10 -5

GCT GCT TTC ATA TTT TCA TAC ATT ACT GCA GTA ACA CTC CAC CAT ATA 453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
 1 5 10 15

```

## (2) INFORMATION FOR SEQ ID NO: 225:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..277
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 29..295  
id AA041777  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 56..277
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..222  
id HSC1QB111  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 135..281  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 56..202  
 id H10738  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 81..133  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 1..53  
 id H10738  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 75..277  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 6..208  
 id HSC2KE111  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 89..263  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
 region 2..176  
 id W24981  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 106..228  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.4  
 seq PLIFSLWCSGVLL/HI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

```

AAGAGTGCGC GGRSATTGGG GCTTTCAGC TCTCACAGAA CCTTCAGCAT CCCAGCTGC 60
CGGTCTTGGC ATCTTCGAAG TAAGGAGAGT TTTAGATGCT TCTGG ATG TTC AAT GCT 117
 Met Phe Asn Ala
 -40

AGC ACC TTT ACA GAC TGG AGC AGC TCG ATT TTC TTC GTA TTT ACT TTC 165
Ser Thr Phe Thr Asp Trp Ser Ser Ser Ile Phe Phe Val Phe Thr Phe
-35 -30 -25

AAG AGC AAG AAA AGT GCT GGG CTC CCA CTT ATT TTC TCC CTG TGG TGT 213
Lys Ser Lys Lys Ser Ala Gly Leu Pro Leu Ile Phe Ser Leu Trp Cys
-20 -15 -10

TCC GGA GTT CTG CTC CAT ATC CAC CAG AAA GCT GGC GGC CCA CGG CTT 261

```

Ser Gly Val Leu Leu His Ile His Gln Lys Ala Gly Gly Pro Arg Leu  
-5 1 5 10  
TGG CGC ATC CAT GGC GAG CAG  
Trp Arg Ile His Gly Glu Gln  
15

282

## (2) INFORMATION FOR SEQ ID NO: 226:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 155..334
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 98.3  
region 1..181  
id HSU90144  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 218..323
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 90..200  
id T70246  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..216
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..89  
id T70246  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 170..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 50..208  
id T70127  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 219..328  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 62..171  
                           id AA114263  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 159..218  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 1..60  
                           id AA114263  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 222..308  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 13.4  
                           seq SLLLVQLLTPTCSA/QF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

```

GACTCTTACT GTTTCATG GTGAGAAGAC AATATTGCT TTCTCTTTT CCTTCTTCC 60
GGATGAGAGG NTAAGCCATA ATAGAAAGAA TGGAGAATTA TTGATTGACC GTCCTTATTC 120
TGTGGGCTCT GATTCTCCAA TGGGAATACC AAGGGATGGT TTTCCATACT GGAACCCWWA 180
GGTAAAGACA CTCAAGGACA GACATTTTGG GCAGAGCATA G ATG AAA ATG GCA AGT 236
 Met Lys Met Ala Ser
 -25

TCC CTG GCT TTC CTT CTG CTC AAC TTT CAT GTC TCC CTC CTC TTG GTC : 284
Ser Leu Ala Phe Leu Leu Leu Asn Phe His Val Ser Leu Leu Leu Val
 -20 -15 -10

CAG CTG CTC ACT CCT TGC TCA GCT CAG TTT TCT GTG CTT GGA CCT CTG 332
Gln Leu Leu Thr Pro Cys Ser Ala Gln Phe Ser Val Leu Gly Pro Leu
 -5 1 5

```

## (2) INFORMATION FOR SEQ ID NO: 227:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 414 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 182..411  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
 region 1..230  
 id C15003  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 182..411  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
 region 1..230  
 id HUM407E11B  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 182..369  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 1..188  
 id C15677  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 212..369  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
 region 26..183  
 id HUM169E08B  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 274..399  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.2  
 seq LLFDLVCFEFCQS/DD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

```

ACCAGGAACA TCCAGCTATT TATGATAGCA TTTGCTTCAT TATGTCAAGT TCAACAAATG 60
TTGACTTGCT GGTGAAGGTG GGGGAGGTTG TGGACAGCT CTTTGATTG GATGAGAAAC 120
TAATGTTAAG AATGGGTCAG AAATGGGGCT GCTCAGCCTC TGGACCAACC CCAGGAAGAG 180
TCTGAAGAGC AGCCAGTGTT TCGGCTTGTT CCCTGTATAC TTGAAGCTGC CAAACAAGTA 240
CGTTCTGAAA ATCCAGAATG GCTTGATGTT TAC ATG CAC ATT TTA CAA CTG CTT 294
 Met His Ile Leu Gln Leu Leu
 -40
ACT ACA GTG GAT GAT GGA ATT CAA GCA ATT GTA CAT TGT CCT GAC ACT 342
Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His Cys Pro Asp Thr

```



|                                                                 |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|
| -35                                                             | -30 | -25 | -20 |     |
| GGA AAA GAC ATT TGG AAT TTA CTT TTT GAC CTG GTC TGC CAT GAA TTC |     |     |     | 390 |
| Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp Leu Val Cys His Glu Phe |     |     |     |     |
|                                                                 | -15 | -10 | -5  |     |
| TGC CAG TCT GAT GAT CCA GCC CGG                                 |     |     |     | 414 |
| Cys Gln Ser Asp Asp Pro Ala Arg                                 |     |     |     |     |
|                                                                 | 1   | 5   |     |     |

## (2) INFORMATION FOR SEQ ID NO: 228:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..96
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..31  
id AA017364  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 114..242
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq PMQLLQVLSDVLA/EI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AAACCGTTGC CAAGGAGCTC GACTCTGGGA GCGGTCTAGA GCCCGGGCGC CTCCTGGGGG | 60  |
| GTGGGGAAAC GGTTCGTGA GGAGAATTG AGTTAAATTA ATAAGACCTA ATT ATG      | 116 |
|                                                                   | Met |
| AGT GAT CAA ATT AAA TTC ATT ATG GAC AGT CTC AAT AAG GAG CCC TTT   | 164 |
| Ser Asp Gln Ile Lys Phe Ile Met Asp Ser Leu Asn Lys Glu Pro Phe   |     |
| -40 -35 -30                                                       |     |
| AGG AAG AAC TAT AAT TTA ATC ACG TTT GWT TCC TTG GAG CCA ATG CAA   | 212 |
| Arg Lys Asn Tyr Asn Leu Ile Thr Phe Xaa Ser Leu Glu Pro Met Gln   |     |
| -25 -20 -15                                                       |     |
| CTA TTA CAA GTT CTC AGT GAT GTT CTG GCT GAG ATT GAC CCA AAG CAA   | 260 |
| Leu Leu Gln Val Leu Ser Asp Val Leu Ala Glu Ile Asp Pro Lys Gln   |     |

|                                                                 |     |   |   |  |
|-----------------------------------------------------------------|-----|---|---|--|
| -10                                                             | -5  | 1 | 5 |  |
| CTT GTG GAT ATC AGA GAG GAG ATG CCA GAG CAG ACA GCC AAA CGA ATG | 308 |   |   |  |
| Leu Val Asp Ile Arg Glu Glu Met Pro Glu Gln Thr Ala Lys Arg Met |     |   |   |  |
| 10 15 20                                                        |     |   |   |  |
| TTG AGC CTT CTT GGT ATT CTT AAG TAC AAA CCT TCA GGA AAT GCC ACA | 356 |   |   |  |
| Leu Ser Leu Leu Gly Ile Leu Lys Tyr Lys Pro Ser Gly Asn Ala Thr |     |   |   |  |
| 25 30 35                                                        |     |   |   |  |
| GAT ATG AGT ACT TTT CGT CAG GGT TTG GTG ATT GGA AGT AAA CCT GTA | 404 |   |   |  |
| Asp Met Ser Thr Phe Arg Gln Gly Leu Val Ile Gly Ser Lys Pro Val |     |   |   |  |
| 40 45 50                                                        |     |   |   |  |
| ATT TAC CCA GTG CTC                                             | 419 |   |   |  |
| Ile Tyr Pro Val Leu                                             |     |   |   |  |
| 55                                                              |     |   |   |  |

## (2) INFORMATION FOR SEQ ID NO: 229:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..203
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..151  
id T34361  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 205..358
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 152..305  
id T34361  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 205..342
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 131..263  
id HSC16A051  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 74..203
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 1..130  
id HSC16A051  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 340..373
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 267..300  
id HSC16A051  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 41..236  
id T35252  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 255..302
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 236..283  
id T35252  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..146
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 57..143  
id H92421  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 205..278
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 200..273  
id H92421  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..203
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 85..227

id T19059  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 205..270  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 228..293  
id T19059  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 93..329  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.6  
seq IIHAXGLVRECLA/XT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

```

AAGACCTGGG CGTCTGGAAT GATCTACGTG CTAAATACA CCACTCGCCA CCATTTTCTC 60
CAGCTGGGAG TGTCCACTCG CCTTCCACCA GC ATG GCA ACG TCK TCA CAG KAC 113
 Met Ala Thr Ser Ser Gln Xaa
 -75

CGC CAG CTG CTC AGT GAC TAC GGG CCA CCG TCC CTA GGC TAC ACC CAG 161
Arg Gln Leu Leu Ser Asp Tyr Gly Pro Pro Ser Leu Gly Tyr Thr Gln
 -70 -65 -60

GGA ACT GGG AAC AGC CAR RTG CCC CAA AGC AAA TAC GCG GAG CTG CTG 209
Gly Thr Gly Asn Ser Gln Xaa Pro Gln Ser Lys Tyr Ala Glu Leu Leu
 -55 -50 -45

GCC ATC ATT GRA GAG CTG GGG AAG GAG ATC AGA CCC ATG TAC GCA GGG 257
Ala Ile Ile Xaa Glu Leu Gly Lys Glu Ile Arg Pro Met Tyr Ala Gly
 -40 -35 -30 -25

AGC AAG AGT GCC ATG GAG AGG CTG AAG CGC GGC ATC ATT CAC GCT MSA 305
Ser Lys Ser Ala Met Glu Arg Leu Lys Arg Gly Ile Ile His Ala Xaa
 -20 -15 -10

GGM CTR GTT CGG GAG TGC TTG GCA GAM ACG GAA CGA ATG CCA GAT CCT 353
Gly Leu Val Arg Glu Cys Leu Ala Xaa Thr Glu Arg Met Pro Asp Pro
 -5 1 5

AGC TGC CTT GTT GGT TTT 371
Ser Cys Leu Val Gly Phe
 10

```

## (2) INFORMATION FOR SEQ ID NO: 230:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 107..234  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..128  
id N88564  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 59..103  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.5  
seq LLGAAVAALGRG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

```

AACCGGCAGC TGAACCCACC CGGCGCCACG GGACTTTGAC GCGTGCTCTG CGCTTGCC 58
ATG AGA CTC CTG GGA GCT GCA GCC GTC GCG GCT CTG GGG CGC GGA AGG 106
Met Arg Leu Leu Gly Ala Ala Ala Val Ala Ala Leu Gly Arg Gly Arg
-15 -10 -5 1
GCC CCC GCC TCC CTA GGC TGG CAG AGG AAG CAG GTT AAT TGG AAG GCC 154
Ala Pro Ala Ser Leu Gly Trp Gln Arg Lys Gln Val Asn Trp Lys Ala
 5 10 15
TGC CGA TGG TCT TCA TCA GGG GTG ATT CCT AAT GAA AAA ATA CGA AAT 202
Cys Arg Trp Ser Ser Ser Gly Val Ile Pro Asn Glu Lys Ile Arg Asn
 20 25 30
ATT GGA ATC TCA GCT CAC ATT GAT TCT GGG AAG 235
Ile Gly Ile Ser Ala His Ile Asp Ser Gly Lys
 35 40

```

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 13..162  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 20..169  
                           id N41898  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 26..162  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 38..174  
                           id H69272  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 45..162  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 1..118  
                           id N20619  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 13..60  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.5  
                           seq RLLRRFLASVIS/RK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

```

AATTGCAGGG AG ATG GCT CAG CGA CTT CTT CTG AGG AGG TTC CTG GCC TCT 51
 Met Ala Gln Arg Leu Leu Arg Arg Phe Leu Ala Ser
 -15 -10 -5

GTC ATC TCC AGG AAG CCC TCT CAG GGT CAG TGG CCA CCC CTC ACT TCC 99
Val Ile Ser Arg Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser
 1 5 10

AGA GCC CTG CAG ACC CCA CAA TGC AGT CCT GGT GGC CTG ACT GTA ACA 147
Arg Ala Leu Gln Thr Pro Gln Cys Ser Pro Gly Gly Leu Thr Val Thr
 15 20 25

CCC AAC CCA GCG CCG GGG 165
Pro Asn Pro Ala Pro Gly
 30 35

```

## (2) INFORMATION FOR SEQ ID NO: 232:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs  
 (B) TYPE: NUCLEIC ACID.

(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 59..214  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..156  
id AA069390  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 122..169  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.4  
seq LNSLSALAE LAVG/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

```
AAGGAGAGTC ACGTGAGAGT GGGCGGAGGG GGTGGAGGTT TGTCTCCGCT GTTTCATCTC 60
TATGGCTGTC AGAGGTGGGC GGCTTTGACC GAGAGGCTGC TGGAGCTCGT GTTGGACGC 120
G ATG TTT CGT CTG AAC TCA CTT TCT GCT TTG GCA GAA CTG GCT GTG GGT 169
Met Phe Arg Leu Asn Ser Leu Ser Ala Leu Ala Glu Leu Ala Val Gly
 -15 -10 -5

TCT CGA TGG TAC CAT GGA GGA TCA CAG CCC ATC CAG ATC CGG CTA GCG 217
Ser Arg Trp Tyr His Gly Gly Ser Gln Pro Ile Gln Ile Arg Leu Ala
 1 5 10 15
```

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 358 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 44..169  
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 1..126  
id AA094226  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 170..231  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 126..187  
id AA094226  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 230..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 185..216  
id AA094226  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 44..195  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 129..280  
id R13710  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 193..254  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 279..340  
id R13710  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 44..282  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 172..410  
id R54574  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 44..184  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 159..299  
id T78111  
est

(ix) FEATURE:

(A) NAME/KEY: other



(B) LOCATION: 182..222  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 298..338  
                           id T78111  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 220..254  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 337..371  
                           id T78111  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 89..271  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
                           seq YTAHSVLAGPRWA/DP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GCGGCGCGGC CGTAAAGCGC CATTACGCAG AGAGAAAGTT ACGAGAAACT CGTTTTCATC | 60  |
| TTCTTGTTT CATCTTAATA CCAACGTC ATG TCT GGT TCT AAT GGT TCC AAA     | 112 |
| Met Ser Gly Ser Asn Gly Ser Lys                                   |     |
| -60 -55                                                           |     |
| GAA AAT TCT CAC AAT AAG GCT CGG ACG TCT CCT TAC CCA GGT TCA AAA   | 160 |
| Glu Asn Ser His Asn Lys Ala Arg Thr Ser Pro Tyr Pro Gly Ser Lys   |     |
| -50 -45 -40                                                       |     |
| GTT GAA CGA AGC CAG GTT CCT AAT GAG AAA GTG GGC TGG CTT GTT GAG   | 208 |
| Val Glu Arg Ser Gln Val Pro Asn Glu Lys Val Gly Trp Leu Val Glu   |     |
| -35 -30 -25                                                       |     |
| TGG CAA GAC TAT AAG CCT GTG GAA TAC ACT GCA GTC TCT GTC TTG GCT   | 256 |
| Trp Gln Asp Tyr Lys Pro Val Glu Tyr Thr Ala Val Ser Val Leu Ala   |     |
| -20 -15 -10                                                       |     |
| GGA CCC AGG TGG GCA GAT CCT CAG ATC AGT GAA AGT AAT TTT TCT CCC   | 304 |
| Gly Pro Arg Trp Ala Asp Pro Gln Ile Ser Glu Ser Asn Phe Ser Pro   |     |
| -5 1 5 10                                                         |     |
| AAG TTT AAC GAA AAG GAT GGG CAT GTT GAG AGA AAG AGC AAG AAT GGC   | 352 |
| Lys Phe Asn Glu Lys Asp Gly His Val Glu Arg Lys Ser Lys Asn Gly   |     |
| 15 20 25                                                          |     |
| CTG TAT                                                           | 358 |
| Leu Tyr                                                           |     |

## (2) INFORMATION FOR SEQ ID NO: 234:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 base pairs

(B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 294..347  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                                   region 297..350  
                                   id AA038489  
                                   est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 134..347  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                                   region 1..214  
                                   id AA111922  
                                   est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 284..331  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.5  
                                   seq TLMFSLTAQWXTS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

```

AAAAAAAGC TGCTGGACCC CAGGGAGAGC TGACCACTGC CCGAGCAGCC GGCTGAATCC 60
ACCTCCACAA TGCSGCTCTC AGGAACCCCG GYCCCTAATA AGAAGAGGAA ATCCAGCAAG 120
CTGATCATGG AACICACTGG AGGTGGACAG GAGAGCTCAG GCTTGAACCT GGGCAAAAAG 180
ATCAGTGTCC CAAGGSATGT GATGTTGGAG GAACTGTCCG TGCTTACCAA CCGGGGCTCC 240
AAGATGTTCA AACTGSGGCA GATGAGGGTG GAGAAGTTTA TTT ATG AGA ACC ACC 295
 Met Arg Thr Thr
 -15

CTG ATG TTT TCT CTG ACA GCT CAA TGG WTC ACT TCC AGA AST TCC TTC 343
Leu Met Phe Ser Leu Thr Ala Gln Trp Xaa Thr Ser Arg Ser Ser Phe
 -10 -5 1

CAA 346
Gln
5

```

(2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 384 base pairs
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: DOUBLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo Sapiens
  - (D) DEVELOPMENTAL STAGE: Fetal
  - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
  - (A) NAME/KEY: other
  - (B) LOCATION: 35..384
  - (C) IDENTIFICATION METHOD: blastn
  - (D) OTHER INFORMATION: identity 98  
region 8..357  
id H11129  
est
- (ix) FEATURE:
  - (A) NAME/KEY: other
  - (B) LOCATION: 43..346
  - (C) IDENTIFICATION METHOD: blastn
  - (D) OTHER INFORMATION: identity 99  
region 16..319  
id R11829  
est
- (ix) FEATURE:
  - (A) NAME/KEY: other
  - (B) LOCATION: 50..302
  - (C) IDENTIFICATION METHOD: blastn
  - (D) OTHER INFORMATION: identity 99  
region 1..253  
id R18811  
est
- (ix) FEATURE:
  - (A) NAME/KEY: other
  - (B) LOCATION: 302..366
  - (C) IDENTIFICATION METHOD: blastn
  - (D) OTHER INFORMATION: identity 96  
region 254..318  
id R18811  
est
- (ix) FEATURE:
  - (A) NAME/KEY: other
  - (B) LOCATION: 183..371
  - (C) IDENTIFICATION METHOD: blastn
  - (D) OTHER INFORMATION: identity 96  
region 6..194  
id R10511  
est
- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide

(B) LOCATION: 73..147  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 14.1  
 seq LLLLLLLTLLAFA/GY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

```

ACTGCGCGGA TCGGCGTCCG CAGCGGGCGG CTGCTGAGCT GCCTIGAGGT GCAGTGTGG 60
GGATCCAGAG CC ATG TCG GAC CTG CTA CTA CTG GGC CTG ATT GGG GGC CTG 111
 Met Ser Asp Leu Leu Leu Leu Gly Leu Ile Gly Gly Leu
 -25 -20 -15

ACT CTC TTA CTG CTG CTG ACG CTG CTG GCC TTT GCC GGG TAC TCA GGG 159
Thr Leu Leu Leu Leu Leu Thr Leu Leu Ala Phe Ala Gly Tyr Ser Gly
 -10 -5 1

CTA CTG GCT GGG GTG GAA GTG AGT GCT GGG TCA CCC CCC ATC CGC AAC 207
Leu Leu Ala Gly Val Glu Val Ser Ala Gly Ser Pro Pro Ile Arg Asn
 5 10 15 20

GTC ACT GTG GCC TAC AAG TTC CAC ATG GGG CTC TAT GGT GAG ACT GGG 255
Val Thr Val Ala Tyr Lys Phe His Met Gly Leu Tyr Gly Glu Thr Gly
 25 30 35

CGG CTT TTC ACT GAG AGC TGC AGC ATC TCT CCC AAG CTC CGC TCC ATC 303
Arg Leu Phe Thr Glu Ser Cys Ser Ile Ser Pro Lys Leu Arg Ser Ile
 40 45 50

GCT GTC TAC TAT GAC AAC CCC CAC ATG GTG CCC CCT GAT AAG TGC CGA 351
Ala Val Tyr Tyr Asp Asn Pro His Met Val Pro Pro Asp Lys Cys Arg
 55 60 65

TGT GCC GTG GGC AGC ATC CTG AGT GAA GGT GAG 384
Cys Ala Val Gly Ser Ile Leu Ser Glu Gly Glu
 70 75

```

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 269 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 75..213  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 29..172  
 id T64530

est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 36..131
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.4  
seq LWSLALWLPLALS/VS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

```

AATCCGGACT GATAACCAGC CGGCCAGACT GAGGG ATG GAA GGC ACT GAG ATG 53
 Met Glu Gly Thr Glu Met
 -30

GGG GCC CGT CCA GGC GGA CAC CCG CRG AAA TGG AGC TTT CTG TGG TCT 101
Gly Ala Arg Pro Gly Gly His Pro Xaa Lys Trp Ser Phe Leu Trp Ser
-25 -20 -15

CTT GCA CTC TGG CTG CCT CTT GCC CTC TCT GTG TCT CTC TTT CTT GGT 149
Leu Ala Leu Trp Leu Pro Leu Ala Leu Ser Val Ser Leu Phe Leu Gly
-10 -5 1 5

CTC TCC CTC TCT CCT CCT CAG CCT GGT CTT TCT CTT TGG TGC ACA CTT 197
Leu Ser Leu Ser Pro Pro Gln Pro Gly Leu Ser Leu Trp Cys Thr Leu
10 15 20

AGT TAT TGT TGT GAG CAA TGG AAG TTC AAA GGA ACT CCC TCT CCA GCT 245
Ser Tyr Cys Cys Glu Gln Trp Lys Phe Lys Gly Thr Pro Ser Pro Ala
25 30 35

CTT CTG AAT CTK GGG ACA CGC GGG 269
Leu Leu Asn Leu Gly Thr Arg Gly
40 45

```

## (2) INFORMATION FOR SEQ ID NO: 237:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 220..396
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 207..383  
id N26787  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 108..207  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 95..194  
id N28787  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 220..316  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 209..305  
id AA019783  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 108..207  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 97..196  
id AA019783  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 307..392  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 297..382  
id AA019783  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 108..207  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 99..198  
id H86396  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 307..374  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 300..367  
id H86396  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 255..313  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 247..305

id H86396  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 220..336  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 210..326  
id H86516  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 108..207  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 98..197  
id H86516  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 327..368  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 318..359  
id H86516  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 108..207  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 111..210  
id AA059290  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 272..354  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 285..367  
id AA059290  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 220..286  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 223..289  
id AA059290  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 139..302  
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.2  
seq LLFALGSLGLIFA/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

```

ARCGGTTAGT GGACCGGGAC CGGTAVGGGT GCTGTWGCCA TCATGGCTGA CCCCMMCCC 60
CGGBACMCTC GCTCCTCGAT CGAGGACGAC TTCANMTMNG GCAGGCAAGC GTGGCCTCCG 120
CCACCGTGYM BNTCCGA ATG VCC TTT CTG AGA AAA GTC TMN AGC ATT CTT 170
 Met Xaa Phe Leu Arg Lys Val Xaa Ser Ile Leu
 -55 -50 -45

TCT CTG CAG GTT CTC TTA ACT ACA GTG ACT TCA ACA GTT TTT TTA TAC 218
Ser Leu Gln Val Leu Leu Thr Thr Val Thr Ser Thr Val Phe Leu Tyr
 -40 -35 -30

TTT GAG TCT GTA CGG ACA TTT GTA CMT GAG AGT CCT GCC TTA ATT TTG 266
Phe Glu Ser Val Arg Thr Phe Val Xaa Glu Ser Pro Ala Leu Ile Leu
 -25 -20 -15

CTG TTT GCC CTC GGA TCT CTG GGT TTG ATT TTT GCG TTG ATT TTA AAC 314
Leu Phe Ala Leu Gly Ser Leu Gly Leu Ile Phe Ala Leu Ile Leu Asn
 -10 -5 1

AGV CAT AAG TAT CCC CTT AAC CTG TAC CTA CTT TTT GGA TTT ACG CTG 362
Xaa His Lys Tyr Pro Leu Asn Leu Tyr Leu Leu Phe Gly Phe Thr Leu
 5 10 15 20

TTG GMA GCT CTG ACT GTG GCA GTT GTT GTT ACT 395
Leu Xaa Ala Leu Thr Val Ala Val Val Val Thr
 25 30

```

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..155
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 24..126  
id AA075942  
est

(ix) FEATURE:

- (A) NAME/KEY: other



(B) LOCATION: 66..136  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 37..107  
                           id AA262924  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 22..135  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 10.8  
                           seq MLLLLLLLGSGQG/PQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AAAGGGTCGT TGGTGGGAAA G ATG GCG GCG ACT CTG GGA CCC CTT GGG TCG | 51  |
| Met Ala Ala Thr Leu Gly Pro Leu Gly Ser                         |     |
| -35 -30                                                         |     |
| TGG CAG CAG TGG CGG CGA TGT TTG TCG GCT CGG GAT GGG TCC AGG ATG | 99  |
| Trp Gln Gln Trp Arg Arg Cys Leu Ser Ala Arg Asp Gly Ser Arg Met |     |
| -25 -20 -15                                                     |     |
| TTA CTC CTT CTT CTT TTG TTG GGG TCT GGG CAG GGG CCA CAG CAA GTC | 147 |
| Leu Leu Leu Leu Leu Leu Gly Ser Gly Gln Gly Pro Gln Gln Val     |     |
| -10 -5 1                                                        |     |
| GGG GCG GGG                                                     | 156 |
| Gly Ala Gly                                                     |     |
| 5                                                               |     |

## (2) INFORMATION FOR SEQ ID NO: 239:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(64..95)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
                           region 79..110  
                           id N98118  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 195..317  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 9.9  
 seq ILPFLLPFPVNA/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

```

ATAGTGATCC TTTTCCTTCT CCCACTCCGT AAGTTTCTAT CCTTGGCCTC CTATTCTTTT 60
TACTACATAT ATACTTTATA TATACATATA TACTTGGAAC AGGCTTAATG AGTTCCAAGG 120
TTTCAAGTAT AATAGAAGGA TAGTTTCCCT AATATTTCTT CAAAACAGAT TTCTCTTCTG 180
AAATCCAGAG TCAT ATG TCC AGT TGG ATG TAT CTT GGA TAC CCC ATT GTC 230
 Met Ser Ser Trp Met Tyr Leu Gly Tyr Pro Ile Val
 -40 -35 -30

ACC TCA AAC ACT ACT TGT CTA AAA CTG ATC TCA TCA TCT TTT CCC CAA 278
Thr Ser Asn Thr Thr Cys Leu Lys Leu Ile Ser Ser Ser Phe Pro Gln
 -25 -20 -15

ATC CTT CCT TTT CTT CTA TTT CCC TTC CCA GTG AAT GCC AGA TCT CAC 326
Ile Leu Pro Phe Leu Leu Phe Pro Phe Pro Val Asn Ala Arg Ser His
 -10 -5 1

TYA GTT GCT CAA ACT AAA AGC CCG AGG 353
Xaa Val Ala Gln Thr Lys Ser Pro Arg
 5 10

```

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 88..132  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 352..396  
 id AA021024  
 est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 46..108  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 9.7  
 seq QLCLLLLPSCSLS/VS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

```

ACCTCTTGGG GCCTACTTTG GGATGAAGTR GCCTCCCTCA GCAGC ATG GCC CCT GGG 57
 Met Ala Pro Gly
 -20

GTC ATC ATC ATC CAG CTC TGC CTC TTG CTC CTG CCT TCC TGC TCC CTT 105
Val Ile Ile Ile Gln Leu Cys Leu Leu Leu Leu Pro Ser Cys Ser Leu
 -15 -10 -5

TCT GTT TCC GGA TGT TCC TGC CCT AGT GCC TGC TTC AGC ACC ACC AGC 153
Ser Val Ser Ser Gly Cys Ser Cys Pro Ser Ala Cys Phe Ser Thr Thr Ser
 1 5 10 15

CGC GAG 159
Arg Glu

```

## (2) INFORMATION FOR SEQ ID NO: 241:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 179..213  
id N78639  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 193..232  
id AA150442  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 99..377
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.6  
seq LSLSLGASAPVQC/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

```

ACATGCTCAG GGTCAGGTTT CAGCCCCAGC TGAGGGCTGA GGGGAGTGGG TGGACATGGG 60
GCAGGGAGCT GGAAGAACAC TCGAGAGACA GCAGGTAG ATG AGA CAT GGC TTT ATT 116
 Met Arg His Gly Phe Ile
 -90

CAG CAG CAG TTT TCA TTA ACA GCT TTC TCA MAC STT WRG SCW ATC TTC 164
Gln Gln Gln Phe Ser Leu Thr Ala Phe Ser Xaa Xaa Xaa Xaa Ile Phe
 -85 -80 -75

ACA CTG KST GSC CTG TCT CAG TTG CTT AGT TCA GCA GCT CCC AAA CAC 212
Thr Leu Xaa Xaa Leu Ser Gln Leu Leu Ser Ser Ala Ala Pro Lys His
 -70 -65 -60

ACA GCT GCA CCG ACG GCC CTC CCT TGC CTT CAG GGT CAG CAG CTT AAC 260
Thr Ala Ala Pro Thr Ala Leu Pro Cys Leu Gln Gly Gln Gln Leu Asn
 -55 -50 -45 -40

TCT CTC TCT CTG GGC ACA AGT GAG CTG AGC TGT GTC CTG GCT TCC TCC 308
Ser Leu Ser Leu Gly Thr Ser Glu Leu Ser Cys Val Leu Ala Ser Ser
 -35 -30 -25

TGT CTA TCT ACA AAG ACA GAC CCC TCT GGT CTC TCT CTC TCT TTG GGT 356
Cys Leu Ser Thr Lys Thr Asp Pro Ser Gly Leu Ser Leu Ser Leu Gly
 -20 -15 -10

GCC AGC GCA CCT GTA CAG TGT CAG CAG GAC AAT TAT ACC TTT TGC KNN 404
Ala Ser Ala Pro Val Gln Cys Gln Gln Asp Asn Tyr Thr Phe Cys Xaa
 -5 1 5

CAA TAC TGG CTT AGA GCA AGG CAT 428
Gln Tyr Trp Leu Arg Ala Arg His
10 15

```

(2) INFORMATION FOR SEQ ID NO: 242:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 325..371
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 277..323  
id: AA015589

est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 325..371  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
 region 277..323  
 id AA019963  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 140..262  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 9.5  
 seq LIIFLSFLPFINS/SF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

```

ACAAGTGGGA TAGGTCTGT GACAGAATTG TGTGATACAG GTCAAACAGG AGTTGGGTTA 60
TGGGGAAAT GCCAGTTGAA ATATGTTTG ATCTTTGGAG AAACCTATTT TTTCATTTAA 120
CCTGTTCTTT AAATCCAGT ATG TTC CAG AAC ATA CAA AAA TGT TTA AAT GTT 172
 Met Phe Gln Asn Ile Gln Lys Cys Leu Asn Val
 -40 -35

CCA TTT GTA AGA GGA TAT CAT GTA TTT TAT ATC AAT TTA AAT GCA GTT 220
Pro Phe Val Arg Gly Tyr His Val Phe Tyr Ile Asn Leu Asn Ala Val
-30 -25 -20 -15

ATC CTA ATC ATT TTT CTT TCA TTT TTA CCC TTT ATT AAC TCT TCA TTT 268
Ile Leu Ile Ile Phe Leu Ser Phe Leu Pro Phe Ile Asn Ser Ser Phe
 -10 -5 1

GTT TAC AAA ACA AAT CCA CTC TAT GAC GCA ATC TCT AAT TAT GTG TTT 316
Val Tyr Lys Thr Asn Pro Leu Tyr Asp Ala Ile Ser Asn Tyr Val Phe
 5 10 15

TCT TTC AGG TAT CCA AAC CTT GRA ASC TTT GCT CTA GAT GTC AGG CTT 364
Ser Phe Arg Tyr Pro Asn Leu Xaa Xaa Phe Ala Leu Asp Val Arg Leu
 20 25 30

GTT TTT
Val Phe
 35

```

## (2) INFORMATION FOR SEQ ID NO: 243:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (D) DEVELOPMENTAL STAGE: Fetal  
    (F) TISSUE TYPE: kidney
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: complement(215..358)  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 97  
                            region 165..308  
                            id R98055  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 185..289  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 97  
                            region 252..356  
                            id W23510  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 136..186  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 98  
                            region 202..252  
                            id W23510  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 73..109  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 97  
                            region 139..175  
                            id W23510  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 315..352  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 92  
                            region 385..422  
                            id W23510  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: complement(215..358)  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 97  
                            region 144..287  
                            id T46976  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other

(B) LOCATION: complement(227..358)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 167..298  
                           id AA084768  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(248..358)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 169..279  
                           id R50108  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(215..250)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 278..313  
                           id R50108  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 281..340  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 9.2  
                           seq FPVLALFLSGSLA/LF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

```

AGAGTGAGAC GGGCAGATGG AGGAGGGGATI GTAATGGCGG YAGCGGCAGC TCCCSTGCTC 60
TGACCCACGG CAGGCATACA GCATCCGATT TAATCTGGAT CCATTCCGGC GCCTTCCTCT 120
CCCAGTCACC CAGAGGGCCC CAACCCCGGC GGCCTTTTCT TCCTCAAATG TCCTCGGCTC 180
TATACCGTGC CTGGGTCTTT TCTCTTTCTC TCIGCCTGGA AGATTCTTTC TTCCCTCTTT 240
TGTCTTGCCC ACTCCTGTTT ACCCTTCAAG TTCAAGTTC ATG TCA CTG TCT CAG 295
 Met Ser Leu Ser Gln
 -20

AGA GGT TTT CCT GTG CTC GCC CTG TTT CTC TCA GGA AGC CTT GCT CTT 343
Arg Gly Phe Pro Val Leu Ala Leu Phe Leu Ser Gly Ser Leu Ala Leu
-15 -10 -5 1

TTC CAT CAT ACC TCT GGG 361
Phe His His Thr Ser Gly
 5

```

## (2) INFORMATION FOR SEQ ID NO: 244:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..132
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..114  
id N87112  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 194..267
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 174..247  
id N87112  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..195
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 111..176  
id N87112  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 68..267
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..200  
id T68050  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..209
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 1..147  
id AA157180  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..195
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98



region 1..130  
id AA094982  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 190..264  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 5..79  
id W00395  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 59..145  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.9  
seq ALLIVCDVPSASA/QR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

```

ACCCACCCTC AGACCTAGCC GGAGCAAAGT TTCACTTATA GAAGGGAGAG AAGCGAAC 58

ATG GCA GCG CGT TGG CGG TTT TGG TGT GTC TCT GTG ACC ATG GTG GTG 106
Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val
 -25 -20 -15

GCG CTG CTC ATC GTT TGC GAC GTT CCC TCA GCC TCT GCC CAA AGA AAG 154
Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln Arg Lys
 -10 -5 1

AAG GAG ATG GTG TTA TCT GAA AAG GTT AGT CAG CTG ATG GAA TGG ACT 202
Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met Glu Trp Thr
 5 10 15

AAC AAA AGA CCT GTA ATA AGA ATG AAT GGA GAC AAG TTC CGT CGC CTT 250
Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys Phe Arg Arg Leu
 20 25 30 35

GTG AAA GGN CCA CCG AGG 268
Val Lys Xaa Pro Pro Arg
 40

```

## (2) INFORMATION FOR SEQ ID NO: 245:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 45..241  
id H81225  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..123
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..38  
id H81225  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 2..208  
id W01412  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 129..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..199  
id AA044118  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 13..209  
id W42797  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 209..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 95..213  
id R39635  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..209
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 15..94

id R39635  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 191..286
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8  
seq VPMLLLIVGGSFG/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

```

AACAAAGTATG TTACGATGGC TCGATTGCTT TTGCCTAGCG GAAACCATTC ACTAAGGACC 60
GAGCACCAAA TAACCAAGGA AAAGGAAGTG AGTTAAGGAC GTACTCGTCT TGGTGAGAGC 120
GTGAGCTGCT GAGATTTGGG AGTCTGCGCT AGGCCCGCTT GGAGTTCTGA GCCGATGGAA 180
GASTTCACTC ATG TTT GCA CCC GCG GTG ATG CGT GCT TTT CGC AAG AAC 229
 Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn
 -30 -25 -20

AAG ACT CTC GGC TAT GGA GTC CCC ATG TTG TTG CTG ATT GTT GGA GGT 277
Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly
 -15 -10 -5

TCT TTT GGT CTT CGT GAG TTT TCT CNA ATC CGA TAT GAT GCT GTG AAG 325
Ser Phe Gly Leu Arg Glu Phe Ser Xaa Ile Arg Tyr Asp Ala Val Lys
 1 5 10

GGG 328
Gly

```

## (2) INFORMATION FOR SEQ ID NO: 246:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 106..210
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 104..203  
id AA131932  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 298..342  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 293..337  
id AA131932  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 86..291  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 67..272  
id AA001989  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 29..102  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 11..84  
id AA001989  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 102..331  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 76..305  
id W32996  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 55..96  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 31..72  
id W32996  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 236..377  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 165..306  
id AA121218  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 106..235  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 34..163  
id AA121218  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 70..180
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5  
seq LLVLLLYAPVGFC/LL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

```

AAGAGCSSCT GCGGCCGGGC GCGAAAATGG CGGCGCGGCG GACGGCCNGG CGCTCCTGAA 60
GCAGCAGTT ATG GAG CTT CCC TCA GGG CCG GGG CCG GAG CGG CTC TTT GAC 111
 Met Glu Leu Pro Ser Gly Pro Gly Pro Glu Arg Leu Phe Asp
 -35 -30 -25

TCG CAC CGG CTT CCG GGT GAC TGC TTC CTA CTG CTC GTG CTG CTG CTC 159
Ser His Arg Leu Pro Gly Asp Cys Phe Leu Leu Leu Val Leu Leu Leu
 -20 -15 -10

TAC GCG CCA GTC GGG TTC TGC CTC CTC GTC CTG SGC CTC TTT CTC GGG 207
Tyr Ala Pro Val Gly Phe Cys Leu Leu Val Leu Xaa Leu Phe Leu Gly
 -5 1 5

ATC CAC GTC TTC CTG GTC AGC TGC GCG CTG CCA GAC AGC GTC CTT CGC 255
Ile His Val Phe Leu Val Ser Cys Ala Leu Pro Asp Ser Val Leu Arg
 10 15 20 25

AGA TTC GTA GTG CGG ACC ATG TGT GCG GTG CTA GGG CTC GTG GCC CGG 303
Arg Phe Val Val Arg Thr Met Cys Ala Val Leu Gly Leu Val Ala Arg
 30 35 40

CAG GAG GAC TCC GGA CTC CGG GAT CAC AGT GTC AGG GTC CTC ATT TCC 351
Gln Glu Asp Ser Gly Leu Arg Asp His Ser Val Arg Val Leu Ile Ser
 45 50 55

AAC CAT GTG ACA CCT TTC GAC CAC CAG 378
Asn His Val Thr Pro Phe Asp His Gln
 60 65

```

## (2) INFORMATION FOR SEQ ID NO: 247:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 38..181
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 1..144  
id W60505  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 186..312  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 150..276  
id W60505  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 305..346  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 270..311  
id W60505  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 38..312  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..275  
id W60589  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 305..346  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 269..310  
id W60589  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 32..175  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..144  
id R33763  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 176..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 144..229  
id R33763  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 268..312  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 238..282  
id R33763  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 305..337  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 276..308  
id R33763  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 33..176  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 3..146  
id AA123856  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 181..346  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 88..253  
id HSB31E112  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 93..181  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..89  
id HSB31E112  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 106..375  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.4  
seq SLVLLTVTPSXRR/QE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

AGGACTTCCC CCGGGCTGAG CTGCGCASGG GGTTTTGGCC AAATTGGGCG AGGGCACAAA 60

ATAACCACTT ACCCCTTCTC ACCGAGGAAG AGCGGGAGAA AGGGT ATG GCA CAG TCA 117  
Met Ala Gln Ser  
-90

CAG GGG TGG GTG RAA AGR TAC KTC AAG GCC TTT TGT AAA GGC TTC TTT 165  
Gln Gly Trp Val Xaa Arg Tyr Xaa Lys Ala Phe Cys Lys Gly Phe Phe

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| -85                                                             | -80 | -75 |     |
| GTG GCG GTG CCT GTG GCA GTG ACT TTC TTG GAT CGG GTC GCC TGT GTG | 213 |     |     |
| Val Ala Val Pro Val Ala Val Thr Phe Leu Asp Arg Val Ala Cys Val |     |     |     |
| -70                                                             | -65 | -60 | -55 |
| GCA AGA GTA GAA GGA GCA TCG ATG CAG CCT TCT TTG AAT CCT GGG GGG | 261 |     |     |
| Ala Arg Val Glu Gly Ala Ser Met Gln Pro Ser Leu Asn Pro Gly Gly |     |     |     |
| -50                                                             | -45 | -40 |     |
| AGC NAG TCA TCT GAT GTG GTG SDD DTG AAC CAC TGG AAA GTG AGG AAT | 309 |     |     |
| Ser Xaa Ser Ser Asp Val Val Xaa Xaa Asn His Trp Lys Val Arg Asn |     |     |     |
| -35                                                             | -30 | -25 |     |
| TTT GAA GTA CAC CGT GGT GAC ATT GTA TCA TTG GTG TTG CTC ACT GTG | 357 |     |     |
| Phe Glu Val His Arg Gly Asp Ile Val Ser Leu Val Leu Leu Thr Val |     |     |     |
| -20                                                             | -15 | -10 |     |
| ACG CCC TCC ASC CGA CAA CAG GAG                                 | 381 |     |     |
| Thr Pro Ser Xaa Arg Gln Gln Glu                                 |     |     |     |
| -5                                                              | 1   |     |     |

## (2) INFORMATION FOR SEQ ID NO: 248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..158
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 11..158  
id H56585  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 201..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 201..322  
id H56585  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 151..322
- (C) IDENTIFICATION METHOD: blastn



(D) OTHER INFORMATION: identity 93  
region 119..290  
id AAL47898  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 39..159  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 8..128  
id AAL47898  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 201..322  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 83..204  
id R52248  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 170..202  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 51..83  
id R52248  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 177..264  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 87..174  
id H54950  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 284..315  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 192..223  
id H54950  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(199..320)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 40..161  
id W22146  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 67..135  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 8.1  
 seq WLLVLSFVFGCNV/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

```

AGCCGCTGTT GTTGTGGTCC CCATGGAGCT GCCGTAGCGG ACCCAGCACA GCCAGGAGCG 60
TCCGGG ATG AGC TCA GCC GCG GCC GAC CAC TGG GCG TGG TTG CTG GTG 108
 Met Ser Ser Ala Ala Ala Asp His Trp Ala Trp Leu Leu Val
 -20 -15 -10
CTC AGC TTC GTG TTT GGA TGC AAT GTT CTT AGG ATC CTC CKC CCG GBC 156
Leu Ser Phe Val Phe Gly Cys Asn Val Leu Arg Ile Leu Xaa Pro Xaa
 -5 1 5
YTC STM ATC STG CAK GTC CAG GGT GCT GCA GAA GGA CGC GGA SAG GAG 204
Xaa Xaa Ile Xaa Xaa Val Gln Gly Ala Ala Glu Gly Arg Gly Xaa Glu
 10 15 20
TCA CAG ATG AGA GCG GAG ATC CAG GAC ATG AAG CAG GAG CTC TCC ACA 252
Ser Gln Met Arg Ala Glu Ile Gln Asp Met Lys Gln Glu Leu Ser Thr
 25 30 35
GTC ARC ATG ATG GAC GAG TTT GCC AGA TAT GCC AGG CTG GAN AGA AAG 300
Val Asn Met Met Asp Glu Phe Ala Arg Tyr Ala Arg Leu Xaa Arg Lys
 40 45 50 55
ATC AAC AAG ATG ACG GAT AAG 321
Ile Asn Lys Met Thr Asp Lys
 60

```

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 196..382  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
                           region 10..196  
                           id HSC2EA121  
                           est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 121..205  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 134..218  
                           id AA095017  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 197..252  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 209..264  
                           id AA095017  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 281..340  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 8  
                           seq HVFFLLLLAHIIA/LE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

```

GTTTTGTTT GTGTGTGCGT GTTGTGGCC TCCATCCCCA CTCCCAGAC TCCACTTCTC 60
CAGGCCTCTC TCCCGCCTTT TCATCCCGCA TCCGCAGGAC ACCCAATCAC CGGGGCAACA 120
GGATGCCTTC CGCGCCTTCC ACCCTGACCT GGAATTCGTG GGCAAGTTCT TGAAACCCCT 180
GCTGATTGGT GAACTGGCCC CGGAGGAGCC CAGCCAGGAC CACGGCAAGA ACTCAAAGAT 240
CACTGAGGAC TTCGGGGCCC TGAGGAAGAC GGCTGAGGAC ATG AAC CTG TTC AAG 295
 Met Asn Leu Phe Lys
 -20

ACC AAC CAC GTG TTC TTC CTC CTC CTC CTG GCC CAC ATC ATC GCC CTG 343
Thr Asn His Val Phe Phe Leu Leu Leu Leu Ala His Ile Ile Ala Leu
-15 -10 -5 1

GAG AGC ATT GCA TGG TTC ACT GTC TTT TAC TTT GGC AAT 382
Glu Ser Ile Ala Trp Phe Thr Val Phe Tyr Phe Gly Asn
 5 10

```

## (2) INFORMATION FOR SEQ ID NO: 250:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 80..300  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 101..321  
id H21228  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 60..300  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 117..357  
id R72127  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..59  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 77..117  
id R72127  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 60..204  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 63..207  
id H18908  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 195..269  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 199..273  
id H18908  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..59  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 23..63  
id H18908  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 65..203  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95

region 144..282  
id W93461  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..59  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 98..138  
id W93461  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 252..288  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 333..369  
id W93461  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 228..259  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 308..339  
id W93461  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 136..300  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 93..257  
id HUM085F04B  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 170..241  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

|             |             |             |             |             |             |     |
|-------------|-------------|-------------|-------------|-------------|-------------|-----|
| AATCACGTGG  | CTGCCACCCA  | GGGGCATTCT  | TCGGGGGTGC  | ATCAGAGGGA  | GGGCAGAGCC  | 60  |
| TCAGGATCTA  | AGCGAAGGCT  | TCCCCGGGTG  | TAATTCCTG   | GGCTGTTTGT  | GAGGAGAGAT  | 120 |
| CGAATTCGCC  | TCCTGCTCTC  | AGGCCTCTCT  | GCTCCTGTCT  | TTGTTTGG    | ATG CCG GCG | 178 |
|             |             |             |             |             | Met Pro Ala |     |
| CTG CTG CCT | GTG GCC TCC | CGC CTT TTG | TTG CTA CCC | CGA GTC TTG | CTG         | 226 |
| Leu Leu Pro | Val Ala Ser | Arg Leu Leu | Leu Leu Pro | Arg Val Leu | Leu         |     |
| -20         |             | -15         |             | -10         |             |     |

ACC ATG GCC TCT GGA AGC CCT CCG ACC CAG CCC TCG CCG GCC TCG GAT 274  
Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro Ala Ser Asp  
-5 1 5 10  
TCC GGC TCT GGC TAC GTT CCG GGC 298  
Ser Gly Ser Gly Tyr Val Pro Gly  
15

## (2) INFORMATION FOR SEQ ID NO: 251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..286  
id HUM085F04B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 147..245
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 167..265  
id R64509  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 99..161
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 118..180  
id R64509  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 245..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 266..307  
id R64509  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 147..262  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 182..297  
id H85714  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 99..161  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 133..195  
id H85714  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 95..286  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 159..350  
id H21228  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 201..236  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 151..236  
id AA009893  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 148..206  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 97..155  
id AA009893  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 99..160  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 49..110  
id AA009893  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 1..198  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG ATA GGG TCG GGA TTG GCT GGC TCT GGA GGC GCA GGT GGT CCT TCT | 48  |
| Met Ile Gly Ser Gly Leu Ala Gly Ser Gly Gly Ala Gly Gly Pro Ser |     |
| -65 -60 -55                                                     |     |
| TCT ACT GTC ACA TGG TGC GCG CTG TTT TCT AAT CAC GTG GCT GCM ACC | 96  |
| Ser Thr Val Thr Trp Cys Ala Leu Phe Ser Asn His Val Ala Ala Thr |     |
| -50 -45 -40 -35                                                 |     |
| CAG GCC TCT CTG CTC CTG TCT TTT GTT TGG ATG CCG GCG CTG CTG CCT | 144 |
| Gln Ala Ser Leu Leu Leu Ser Phe Val Trp Met Pro Ala Leu Leu Pro |     |
| -30 -25 -20                                                     |     |
| GTG GCC TCC CGC CTT TTG TTG CTA CCC CGA GTC TTG CTG ACC ATG GCC | 192 |
| Val Ala Ser Arg Leu Leu Leu Leu Pro Arg Val Leu Leu Thr Met Ala |     |
| -15 -10 -5                                                      |     |
| TCT GGA AGC CCT CCG ACC CAG CCC TCG CCG GCC TCG GAT TCC GGC TCT | 240 |
| Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro Ala Ser Asp Ser Gly Ser |     |
| 1 5 10                                                          |     |
| GGC TAC GTT CCG GGC TCG GTC TCT GCA GCC TTT GTT ACT TGC CCC AGG | 288 |
| Gly Tyr Val Pro Gly Ser Val Ser Ala Ala Phe Val Thr Cys Pro Arg |     |
| 15 20 25 30                                                     |     |

## (2) INFORMATION FOR SEQ ID NO: 252:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 53..340  
id AA056366  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 80..367  
id R77008  
est



## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 77..268  
id W75983  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 223..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 269..365  
id W75983  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 129..320  
id W39055  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 223..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 321..417  
id W39055  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..236
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 84..288  
id N48534  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 264..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 318..373  
id N48534  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 11..82
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

```

ATTGTTTGG ATG CCG GCG CTG CTG CCT GTG GCC TCC CGC CTT TTG TTG 49
 Met Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu
 -20 -15

CTA CCC CGA GTC TTG CTG ACC ATG GCC TCT GGA AGC CCT CCG ACC CAG 97
Leu Pro Arg Val Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln
-10 -5 1 5

CCC TCG CCG GCC TCG GAT TCC GGC TCT GGC TAC GTT CCG GGC TCG GTC 145
Pro Ser Pro Ala Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly Ser Val
 10 15 20

TCT GCA GCC TTT GTT ACT TGC CCC AAC GAG AAG GTC GCC AAG GAG ATC 193
Ser Ala Ala Phe Val Thr Cys Pro Asn Glu Lys Val Ala Lys Glu Ile
 25 30 35

GCC AGG GCC GTG GTG GAG AAG CGC CTA GCA GCC TGC GTC AAC CTC ATC 241
Ala Arg Ala Val Val Glu Lys Arg Leu Ala Ala Cys Val Asn Leu Ile
 40 45 50

CCT CAG ATT ACA TCC ATC TAT GAG TGG AAA GGG AHG ATC GAG GAA GAC 289
Pro Gln Ile Thr Ser Ile Tyr Glu Trp Lys Gly Xaa Ile Glu Glu Asp
 55 60 65

AGT GAG GTG CTG ATG ATG ATT AAA ACC CAA GCG 322
Ser Glu Val Leu Met Met Ile Lys Thr Gln Ala
70 75 80

```

## (2) INFORMATION FOR SEQ ID NO: 253:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 247..302  
id T80036  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 33..308

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.6

seq FLLLTVALSYS/VH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

```

AAGATGGAAC TGGTAGTCAG CTGGAGAGCA GC ATG GAG GCG TCC TGG GGG AGC 53
 Met Glu Ala Ser Trp Gly Ser
 -90

TTC AAC GCT GAG CGG GGC TGG TAT GTC TCT GTG CAG CAG CCT GAA GAA 101
Phe Asn Ala Glu Arg Gly Trp Tyr Val Ser Val Gln Gln Pro Glu Glu
-85 -80 -75 -70

GCG GAG GCC GAA GAG TTG AGT CCG TTG CTA AGC AAC GAA CTT CAC AGA 149
Ala Glu Ala Glu Glu Leu Ser Pro Leu Leu Ser Asn Glu Leu His Arg
 -65 -60 -55

CAG CGA TCC CCA GGT GTT TCA TTT GGT TTA TCA GTG TTT AAT TTG ATG 197
Gln Arg Ser Pro Gly Val Ser Phe Gly Leu Ser Val Phe Asn Leu Met
 -50 -45 -40

AAT GCC ATC ATG GGA AGT GGC ATC CTT GGC TTA GCT TAT GTT ATG GCT 245
Asn Ala Ile Met Gly Ser Gly Ile Leu Gly Leu Ala Tyr Val Met Ala
 -35 -30 -25

AAT ACC GGT GTC TTT GGA TTT AGC TTC TTG CTG CTG ACA GTT GCT CTC 293
Asn Thr Gly Val Phe Gly Phe Ser Phe Leu Leu Leu Thr Val Ala Leu
 -20 -15 -10

CTG GCT TCT TAC TCA GTC CAT CTT CTG CTT AGT ATG TGT ATT CAG ACA 341
Leu Ala Ser Tyr Ser Val His Leu Leu Leu Ser Met Cys Ile Gln Thr
-5 1 5 10

GCT GTA ACA TCT TAT GAA GAT CTT GGA CTC TTT GCA TTT GGA TTA CCT 389
Ala Val Thr Ser Tyr Glu Asp Leu Gly Leu Phe Ala Phe Gly Leu Pro
 15 20 25

GGA CTG
Gly Leu
395

```

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 13..132

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..115  
id T10447  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 78..128  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.6  
seq FFLLLRFFLRIDG/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

```
ATTTTGAAGA AGTTCTCCTT TTTGAGGATG AACTTCATGA TCATGGAGTT TCAAGCCTGA 60
GTGTGAAGAT TAGAGTA ATG CCT TCT AGC TTT TTC CTG CTG TTG CGG TTT 110
 Met Pro Ser Ser Phe Phe Leu Leu Leu Arg Phe
 -15 -10

TTC TTG AGA ATT GAC GGG GTG CCG 134
Phe Leu Arg Ile Asp Gly Val Pro
-5 1
```

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 44..276  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..233  
id N83601  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 51..276  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 15..240  
id N56180  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 69..216  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 23..170  
id R57553  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 46..75  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..30  
id R57553  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 58..142  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 42..126  
id R57171  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 18..56  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..39  
id R57171  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 142..182  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 97..137  
id N88966  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 49..83  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..35  
id N88966  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 200..256  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.6  
seq FIVGIYFLSSCRA/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

```

AGTCTTTGTC CTGAGCCAC GATTCCAGAG CTGGCTGGAC CCAAGGAGGT GAAGAGTCAC 60
TTTTCAGCCC CAGGAAGGGC AAAGAAGAGA GARAATCAGC CTGTCTGCTC TCTCCTTGGC 120
TCAACAAGGC CTCTAACAGT CTTCTGTCCT CTATTCTGCA CACGGCATAT TTGGGAACGA 180
GAAACAAAAG TTTTCCCAA ATG AAG AGA ACT CAC TTG TTT ATT GTG GGG ATT 232
 Met Lys Arg Thr His Leu Phe Ile Val Gly Ile
 -15 -10

TAT TTT CTG TCC TCT TGC AGG GCA GAA GAG GGG CTT AAT TTC CCC ACA 280
Tyr Phe Leu Ser Ser Cys Arg Ala Glu Gly Leu Asn Phe Pro Thr
 -5 1 5

TAT GAT GGG AAG GAC CGA GTG GTA AGT CTT TCC GAG AAG AAC TTC AAG 328
Tyr Asp Gly Lys Asp Arg Val Val Ser Leu Ser Glu Lys Asn Phe Lys
 10 15 20

CAG GTT TTA 337
Gln Val Leu
 25

```

## (2) INFORMATION FOR SEQ ID NO: 256:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 57..182  
id AA019348  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 215..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 173..287  
id AA019348  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..98

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..56  
id AA019348  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 98..217  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 57..176  
id AA013099  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 211..329  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 171..289  
id AA013099  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 43..98  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..56  
id AA013099  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 215..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 130..234  
id R54717  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 142..223  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 58..139  
id R54717  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 95..149  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 10..64  
id R54717  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 105..173  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..69  
id AAl12675  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 215..267  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 108..160  
id AAl12675  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 296..329  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 185..218  
id AAl12675  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 167..196  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 62..91  
id AAl12675  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 88..223  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 3..138  
id H27167  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 215..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 129..233  
id H27167  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 145..213  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.4  
seq VLLLAALPPVLLP/GA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:



```

AGAGTGTTTCG CCGCCGCCGC GGCCGCCACC TGGAGTTTCT TCAGACTCCA GATTTCCCTG 60
TCAACCACGA GGAGTCCAGA GAGGAAACGC GGAGGAGACA ACAGTACCTG ACGCCTCTTT 120
CAGCCCGGGA TCGCCCCAGC AGGG ATG GGC GAC AAG ATC TGG CTG CCC TTC 171
 Met Gly Asp Lys Ile Trp Leu Pro Phe
 -20 -15

CCC GTG CTC CTT CTG GCC GCT CTG CCT CCG GTG CTG CTG CCT GGG GCG 219
Pro Val Leu Leu Leu Ala Ala Leu Pro Pro Val Leu Leu Pro Gly Ala
 -10 -5 1

GCC GGC TTC ACA CCT TCC CTC GAT AGC GAC TTC ACC TTT ACC CTT CCC 267
Ala Gly Phe Thr Pro Ser Leu Asp Ser Asp Phe Thr Phe Thr Leu Pro
 5 10 15

GCC GGC CAG AAG GAG TGC TTC TAC CAG CCC ATG CCC CTG RAG GCC TCG 315
Ala Gly Gln Lys Glu Cys Phe Tyr Gln Pro Met Pro Leu Xaa Ala Ser
 20 25 30

CTG GAG ATC GAG 327
Leu Glu Ile Glu
35

```

## (2) INFORMATION FOR SEQ ID NO: 257:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 166..415
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..250  
id HSU52870  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 182..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 156..311  
id T35951  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..132
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 7..107  
id T35951  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 109..166  
id T35951  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 182..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 156..302  
id T35949  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..132
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 7..107  
id T35949  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 109..166  
id T35949  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 233..409
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 53..229  
id W17267  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..476
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 220..295  
id W17267

est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 182..399  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 54..271  
 id HSC34G011  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 136..192  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 7..63  
 id HSC34G011  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 306..416  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.3  
 seq LLSACLVTWGLG/EP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

```

AATTCATTTT TCACTCCTCC CTCCTAGGTC ACACTTTTCA GAAAAAGAAT CTGCATCCTG 60
GAAACCAGAA GAAAAATATG AGACGGGGAA TCATCGTGTG ATGTGTGTGC TGCCTTTGGC 120
TKWGTGTGTX GAAGTYCCKG CTCAGGTGTT AGGTACAGTG TGTTTGATCG TGGTGGCTTG 180
AGGGGAACCC GCTGTTTACA GCTGTGACTG CGGCTGCACT CAGAGAAGCT GCCCTTGGCT 240
GCTCGTAGCG CCGGGCCTTC TCTCCTCGTC ATCATCCAGA GCAGCCAGTG TCCGGGAGGC 300
ADVNG ATG CCC CAC TCC AGC CTG CAT CCA TCC ATC CCG TGT CCC AGG GGT 350
Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly
 -35 -30 -25

CAC GGG GCC CAG AAG GCA GCC TTG GIT CTG CTG AGT GCC TGC CTG GTG 398
His Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val
 -20 -15 -10

ACC CTT TGG GGG CTA GGA GAG CCA CCA GAG CAC ACT CTC CGG TAC CTG 446
Thr Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu
 -5 1 5 10

GTG CTC CAM CTA GCC TCC CTG CAG CTG GGA 476
Val Leu Xaa Leu Ala Ser Leu Gln Leu Gly
 15 20

```

## (2) INFORMATION FOR SEQ ID NO: 258:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(28..221)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 32..225  
id AA025879  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..154)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 97..250  
id N33067  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(144..221)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 31..103  
id N33067  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..221)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 31..251  
id AA132495  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..221)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 31..251  
id AA063545  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(23..221)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 47..240  
id N99132  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 59..145
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3  
seq HLLLLLLPAPTLK/GL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

```

ACACTCGGGC CCCACTCAAG GATGTAGGGC CTTTCTGGC CCCTGACCCC TCCCTGGC 58
ATG GGA GCG TGG GGA CGG GGC TGG CCT TGG GAG GAG CGG CAG GGG CAT 106
Met Gly Ala Trp Gly Arg Gly Trp Pro Trp Glu Glu Arg Gln Gly His
 -25 -20 -15
CAC CTC CTT CTG CTG CTT CTC CCT GCT CCT ACC CTC AAG GGC CTG GGG 154
His Leu Leu Leu Leu Leu Pro Ala Pro Thr Leu Lys Gly Leu Gly
 -10 -5 1
GCT GCC CAG CTG CCT CTA TGC CCT TCT GGG GGT CTC AGC CCA CTG CTG 202
Ala Ala Gln Leu Pro Leu Cys Pro Ser Gly Gly Leu Ser Pro Leu Leu
 5 10 15
ACA CTT CTG CAA TCC GGG 220
Thr Leu Leu Gln Ser Gly
 20 25

```

## (2) INFORMATION FOR SEQ ID NO: 259:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 56..429
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 65..438  
id W27019  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(79..429)

(C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 91..441  
                           id W26783  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 284..390  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 343..449  
                           id W85233  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 57..281  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.2  
                           seq LLFIIGLIGCCAT/IR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

```

ACTCTCGGTG AGCGCRSCCC GCTCTCCGGG CCGGGTCTTC GCGGGCCACC GGCGCC ATG 59
 Met
 -75

GGC CAG TGC GGC ATC ACC TCC TCC AAG ACC GTG CTG GTC TTT CTC AAC 107
Gly Gln Cys Gly Ile Thr Ser Ser Lys Thr Val Leu Val Phe Leu Asn
 -70 -65 -60

CTC ATC TTC TGG GGG GCA GCT GGC ATT TTA TGC TAT GTG GGA GCC TAT 155
Leu Ile Phe Trp Gly Ala Ala Gly Ile Leu Cys Tyr Val Gly Ala Tyr
 -55 -50 -45

GTC TTC ATC ACT TAT GAT GAC TAT GAC CAC TTC TTT GAA GAT GTG TAC 203
Val Phe Ile Thr Tyr Asp Asp Tyr Asp His Phe Phe Glu Asp Val Tyr
 -40 -35 -30

ACG CTC ATC CCT GCT GTA GTG ATC ATA GCT GTA AGA GCC CTG CTT TTC 251
Thr Leu Ile Pro Ala Val Val Ile Ile Ala Val Arg Ala Leu Leu Phe
 -25 -20 -15

ATC ATT GGG CTA ATT GGC TGC TGT GCC ACA ATC CGG GAA AGT CGC TGT 299
Ile Ile Gly Leu Ile Gly Cys Cys Ala Thr Ile Arg Glu Ser Arg Cys
-10 -5 1 5

GGA CTT GCC ACG TTT GTC ATC ATC CTG CTC TTG GTT TTT GTC ACA GAA 347
Gly Leu Ala Thr Phe Val Ile Ile Leu Leu Leu Val Phe Val Thr Glu
 10 15 20

GTT GTT GTA GTG GTT TTG GGA TAT GTT TAC AGA GCA AAG GTG GAA AAT 395
Val Val Val Val Val Leu Gly Tyr Val Tyr Arg Ala Lys Val Glu Asn
 25 30 35

GAG GTT GAT CGC AGC ATT CAG AAA GTG TAT AAG 428
Glu Val Asp Arg Ser Ile Gln Lys Val Tyr Lys
 40 45

```

## (2) INFORMATION FOR SEQ ID NO: 260;

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 167..425
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 106..364  
id N39913  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..170
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..108  
id N39913  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..188
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 39..166  
id HUM527C01B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 188..303
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 165..280  
id HUM527C01B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..61
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..38  
id HUM527C01B  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 81..275  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7  
 seq IGHFLCLVILVYC/AE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

```

AAGAGGATTT GGCGCCCTCC TCTGTGGATT CTGGCCAGGC CGGTTTCGGC GGTGCTGTG 60
AGAGCGGGCT TCCCAACACC ATG CCG KCC GCC TTC TCT GTC AGC TCT TTC CCC 113
 Met Pro Xaa Ala Phe Ser Val Ser Ser Phe Pro
 -65 -60 -55

GTC AGC ATC CCA GCC GTG CTC ACG CAG ACG GAC TGG ACT GAG CCC TGG 161
Val Ser Ile Pro Ala Val Leu Thr Gln Thr Asp Trp Thr Glu Pro Trp
 -50 -45 -40

CTC ATG GGG CTG GCC ACC TTC CAC GCG CTC TGC GTG CTC CTC ACC TGC 209
Leu Met Gly Leu Ala Thr Phe His Ala Leu Cys Val Leu Leu Thr Cys
 -35 -30 -25

TTG TCC TCC CGA AGC TAC AGA CTA CAG ATC GGG CAC TTT CTG TGT CTA 257
Leu Ser Ser Arg Ser Tyr Arg Leu Gln Ile Gly His Phe Leu Cys Leu
 -20 -15 -10

GTC ATC TTA GTC TAC TGT GCT GAA TAC ATC AAT GAG GCG GCT GCG ATG 305
Val Ile Leu Val Tyr Cys Ala Glu Tyr Ile Asn Glu Ala Ala Ala Met
 -5 1 5 10

AAC TGG AGA TTA TTT TCG MAA TAC CAG TAT TTC GAC TCC AGG GGG ATG 353
Asn Trp Arg Leu Phe Ser Xaa Tyr Gln Tyr Phe Asp Ser Arg Gly Met
 15 20 25

TTC ATT TCT ATA GTA TTT TCA GCC CCA CTG CTG GTG AAT GCC ATG ATC 401
Phe Ile Ser Ile Val Phe Ser Ala Pro Leu Leu Val Asn Ala Met Ile
 30 35 40

ATT GTG GTT ATG TGG GTA TGG AAG 425
Ile Val Val Met Trp Val Trp Lys
 45 50

```

## (2) INFORMATION FOR SEQ ID NO: 261:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (iii) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney



## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 133..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 11..43  
id HUM153A05B  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 136..177  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.7  
seq LLLSLFFPLRISL/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

```
ATTTTCTCC GGTACAGCCT GGAACGTAG GTCCGCGCC TGTGATAAGT AAGGTTGGAT 60
TTTCTCTTCC CTGAGGTGAA GGATGCCCCG RAGSCCTCGG CAGGACCGCG CGGAACGGG 120
CCTTCTGCCC AAAAG ATG CTG CTT CTC TCC TTA TTC TTT CCC CTC AGA ATC 171
 Met Leu Leu Leu Ser Leu Phe Phe Pro Leu Arg Ile
 -10 -5

TCG CTG TCT CCT TCC AAC CAC CTG TGG TCG SCA TCC TCC GGG 213
Ser Leu Ser Pro Ser Asn His Leu Trp Ser Ala Ser Ser Gly
 1 5 10
```

## (2) INFORMATION FOR SEQ ID NO: 262:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 16..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..304  
id HSC26A021  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 17..174

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..158  
id W07871  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 205..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 192..306  
id W07871  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 174..203  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 159..188  
id W07871  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 169..305  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 144..280  
id T75539  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 64..172  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 41..149  
id T75539  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 175..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 161..305  
id H94774  
est

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 24..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 10..151  
id H94774  
est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 228..319  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 203..294  
                           id W89738  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 43..102  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 91  
                           region 22..81  
                           id W89738  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 82..150  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.6  
                           seq LILVLQLLLRIRR/NR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

```

ACTCGCACCC GGAACAACAA AGCAAGGAAG ACGGAGTCCG AGCCTCGGGG GCTCCTAGCA 60
ACGGGCCCGGG GCGGGAGTTC C ATG GAG ACT GGG GAG CGC GCC CGT CTC ATC 111
 Met Glu Thr Gly Glu Arg Ala Arg Leu Ile
 -20 -15

CTC ATC CTT GTC CTC CAG CTT CTC CTT CGC ATC CGA CGC AAC CSG CAG 159
Leu Ile Leu Val Leu Gln Leu Leu Leu Arg Ile Arg Arg Asn Arg Gln
-10 -5 1

CAG CGC TGC SCC GCG TCC TCA GCC ACC GCT CCC TCT TCC CAC GGA TGT 207
Gln Arg Cys Xaa Ala Ser Ser Ala Thr Ala Pro Ser Ser His Gly Cys
 5 10 15

GAT CTT CGT GGT GGA AAG CTA AAT TTT AAA ACC ACC CCA ATG GAT GCA 255
Asp Leu Arg Gly Gly Lys Leu Asn Phe Lys Thr Thr Pro Met Asp Ala
 20 25 30 35

GAC AGT GAT GTT GCA TTG GAC ATT CTA ATT ACA AAT GTA GTC TGT GTT 303
Asp Ser Asp Val Ala Leu Asp Ile Leu Ile Thr Asn Val Val Cys Val
 40 45 50

TTT AGA ACA AGA TGT CGG 321
Phe Arg Thr Arg Cys Arg
 55

```

## (2) INFORMATION FOR SEQ ID NO: 263:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 2..88  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 18..104  
                           id R56970  
                           est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 128..250  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.4  
                           seq ILGCSSVCQLCTG/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

```

AGGAGTTAAG AAATGTCGTT CTTCAGATTT AAAAAGAAAA CCTTIACTGA ATCAGCTGAG 60
TGTTAATAAT ACGAATTTC TTKTCNTGCC AATKCDRMYC TGRDDCAGRA RATCSNWGAA 120
CAGGGWT ATG TGT GGA TTW YAG TTT TCT CTG CCT TGC CTA CGA CTG TTT 169
 Met Cys Gly Xaa Xaa Phe Ser Leu Pro Cys Leu Arg Leu Phe
 -40 -35 -30
CTG GTT GTT ACC TGT TAT CKT TTA TTA TTA CTC CAC AAA GAA ATA CTT 217
Leu Val Val Thr Cys Tyr Xaa Leu Leu Leu Leu His Lys Glu Ile Leu
 -25 -20 -15
GGA TGT TCG TCT GTT TGT CAG CTC TGC ACT GGG AGA CAA ATT AAC TGC 265
Gly Cys Ser Ser Val Cys Gln Leu Cys Thr Gly Arg Gln Ile Asn Cys
 -10 -5 1 5
CGT AAC TTA GGC CTT TCG AGT ATT CTA AGA ATT TTC CTG AAA GTA CAG 313
Arg Asn Leu Gly Leu Ser Ser Ile Leu Arg Ile Phe Leu Lys Val Gln
 10 15 20
TTT TTC TGT ATC
Phe Phe Cys Ile
 25

```

(2) INFORMATION FOR SEQ ID NO: 264:

(i). SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 176..352  
id W42809  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..129
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 50..165  
id W42809  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..242
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 116..218  
id N99674  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..129
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 34..105  
id N99674  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 243..285
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 218..260  
id N99674  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..57
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 2..32  
id N99674  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..272
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 78..210  
id R20073  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 267..364
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 206..303  
id R20073  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..129
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..67  
id R20073  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..105  
id N99685  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..242
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 105..207  
id N99685  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 251..231  
id N99685  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..134

id AA154228  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 140..206  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 134..200  
id AA154228  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 10..228  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.4  
seq ACCFLSAFSPILT/KS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATAATAAAA ATG AAC CCC GTT ACA GAG TCA CCA TCA TGT CTC TTC TCA CCA | 51  |
| Met Asn Pro Val Thr Glu Ser Pro Ser Cys Leu Phe Ser Pro           |     |
| -70 -65 -60                                                       |     |
| CCC TCT GAA TCT GCA TTA GCC AGT CAA CTA GCC CTT TCA GCG TCA TGT   | 99  |
| Pro Ser Glu Ser Ala Leu Ala Ser Gln Leu Ala Leu Ser Ala Ser Cys   |     |
| -55 -50 -45                                                       |     |
| GAC CAG CGC GCC CCA TTC AGC TTG GCT GGT GTC GKT TCA MMA KRA CCC   | 147 |
| Asp Gln Arg Ala Pro Phe Ser Leu Ala Gly Val Xaa Ser Xaa Xaa Pro   |     |
| -40 -35 -30                                                       |     |
| AGG CTG GCC AGT CGT CAG GTT GCA CCG CCC TTT GGT TCC CGA GCA TGC   | 195 |
| Arg Leu Ala Ser Arg Gln Val Ala Pro Pro Phe Gly Ser Arg Ala Cys   |     |
| -25 -20 -15                                                       |     |
| TGT TTT CTC TCA GCC TTC TCT CCA ACC TTA ACC AAA TCG GCA GCA GCC   | 243 |
| Cys Phe Leu Ser Ala Phe Ser Pro Thr Leu Thr Lys Ser Ala Ala Ala   |     |
| -10 -5 1 5                                                        |     |
| ACC TCG ACC GCC CAC ACA TTC CTG GCC AAT CAG CTC AGC TGT TTA TTT   | 291 |
| Thr Ser Thr Ala His Thr Phe Leu Ala Asn Gln Leu Ser Cys Leu Phe   |     |
| 10 15 20                                                          |     |
| ACC AAA TGT CTT CAC AAC AAC TAC AGC AGC AGC CTT CGG CTA ACA AAA   | 339 |
| Thr Lys Cys Leu His Asn Asn Tyr Ser Ser Ser Leu Arg Leu Thr Lys   |     |
| 25 30 35                                                          |     |
| AAG CAG GAA AAA TCC ACA ACA CCC CAG                               | 366 |
| Lys Gln Glu Lys Ser Thr Thr Pro Gln                               |     |
| 40 45                                                             |     |

## (2) INFORMATION FOR SEQ ID NO: 265:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 base pairs  
(B) TYPE: NUCLEIC ACID

- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..86
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 8..92  
id AA070287  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..80
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..66  
id T10748  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..88
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 17..83  
id N67981  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..85
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 17..81  
id AA069568  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 25..87
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq LGLSVLLTAATVA/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

```
AAGGCCGCGG CCGCCAGCGT GGGG ATG TCT AGG AGC TCG AAG GTG GTG CTG 51
 Met Ser Arg Ser Ser Lys Val Val Leu
 -20 -15

GGC CTC TCG GTG CTG CTG ACG GCG GCC ACA GTG GCC GGC GTA CAT GTG 99
Gly Leu Ser Val Leu Leu Thr Ala Ala Thr Val Ala Gly Val His Val
```



-10

-5

1

AAG CAG CAG TGG GAC  
Lys Gln Gln Trp Asp  
5

114

## (2) INFORMATION FOR SEQ ID NO: 266:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..197
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 8..204  
id H10448  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..197
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..193  
id AA127134  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..197
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..193  
id HUML13653  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..197
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 9..205  
id HSC18H071  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..197

(C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 13..176  
                           id AA194682  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 31..108  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.3  
                           seq GVGLVTLLGLAVG/SY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

```

GTCAGGTGGT GGAGGAAAAG GCGCTCCGTC ATG GGG ATC CAG ACG AGC CCC GTC 54
 Met Gly Ile Gln Thr Ser Pro Val
 -25 -20

CTG CTG GCC TCC CTG GGG GTG GGG CTG GTC ACT CTG CTC GGC CTG GCT 102
Leu Leu Ala Ser Leu Gly Val Gly Leu Val Thr Leu Leu Gly Leu Ala
 -15 -10 -5

GTG GGC TCC TAC TTG GTT CGG AGG TCC CGC CGG CCT CAG GTC ACT CTC 150
Val Gly Ser Tyr Leu Val Arg Arg Ser Arg Arg Pro Gln Val Thr Leu
 1 5 10

CTG GAC CCC AGT GAA AAG TAC CTG CTA CGA CTG CTA GAC AAG ACG ACC 198
Leu Asp Pro Ser Glu Lys Tyr Leu Leu Arg Leu Leu Asp Lys Thr Thr
 15 20 25 30

CCC GGG
Pro Gly
 204

```

## (2) INFORMATION FOR SEQ ID NO: 267:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 33..227  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 1..195  
                           id W00881  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 167..319  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.2  
 seq VLLLSSAXLVXXS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

```

CATTGCTCT TCTCTTAACT CCTACCTGAA AACCCCATTC CTAAATTATT CACTATATTT 60
CAGACTTCTT CACTCTTCTC CMAAACCTG AATCAGCTTG TGCTGATTTT TTCCTATCTG 120
CTATCCCTAA AAGGACTAGA CCTTCTTTCT ATCCTTACTC CCCTCA ATG TAT CCA 175
 Met Tyr Pro
 -50

TCT TAC CTC TTG ATT KKS CCT CCC ATT CCC TCA CAG TTC CTG AAA CAG 223
Ser Tyr Leu Leu Ile Xaa Pro Pro Ile Pro Ser Gln Phe Leu Lys Gln
 -45 -40 -35

TGC SCC CCC CCG ACC CTA AGC GAC CCC TTT CTG CCC CTG GCC TTG AGG 271
Cys Xaa Pro Pro Thr Leu Ser Asp Pro Phe Leu Pro Leu Ala Leu Arg
 -30 -25 -20

TCC CTT GAC GTG CTG CTC CTG TCT TCT GCT CNB YTA GTB VVC NAT TCC 319
Ser Leu Asp Val Leu Leu Leu Ser Ser Ala Xaa Leu Val Xaa Xaa Ser
 -15 -10 -5

TCT CCC TTG GAA TTC ATC AGA 340
Ser Pro Leu Glu Phe Ile Arg
1 5

```

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 368 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 253..332  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
 region 159..233  
 id AA114672  
 est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 195..293  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.2  
 seq ILLXTFQWCLR/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

```

AGGGGTACCT GGTCGTCATG GCAGGCGGTA TTGACCGAAG AGCTTGRTGA GGAAGAGCAG 60
CTGCTGAGAA GGCATCGCAA AKAGAAGAAG GAGTTGCAAS CCAAATTCA GGGCATGAAG 120
AATGCTGTTC CCAAGAATGA CAATGAAGAG GDAGGARGCA GCTCACCGRG GATGTGGCCA 180
AGTTGGA AAA AGAW ATG GAA CAG AAA CAY AGA GAS GAA CTG GAG CAA TTG 230
 Met Glu Gln Lys His Arg Xaa Glu Leu Glu Gln Leu
 -30 -25

AAG CTG RCT ACT AAG GAG AAT AAG ATT CTG TTG CTG YWA ACA TTT CAA 278
Lys Leu Xaa Thr Lys Glu Asn Lys Ile Leu Leu Leu Xaa Thr Phe Gln
-20 -15 -10

ACT TGG TGC TTG AGA ATC AGC CAC CTC GGA TAT CAR AAG CAC AWA AGA 326
Thr Trp Cys Leu Arg Ile Ser His Leu Gly Tyr Gln Lys His Xaa Arg
-5 1 5 10

GRC GGG TGC CTG GAT MSA AGG AGC ICT CTG TGT TGT CCT TGG 369
Xaa Gly Cys Leu Asp Xaa Arg Ser Ser Leu Cys Cys Pro Trp
 15 20 25

```

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (E) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(1..43)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
                           region 209..251  
                           id AA013573  
                           est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(1..43)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90

region 153..195  
id AA014924  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 54..122  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.9  
seq TLKFLTLQKSNA/KR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```

AGACGAAGCT CGATGAAGAT TTAGAGAGTT CCAGTGAATC CGATGTGAGT CTG ATG 56
 Met

ATG ACA GCA CCT GTT CTA GCA GCT CAG ACT CTG AAG TTT TTG ACG TTA 104
Met Thr Ala Pro Val Leu Ala Ala Gln Thr Leu Lys Phe Leu Thr Leu
 -20 -15 -10

TTG CAG AAA TCA AAC GCA AAA AGG SCC AAC CTT GAC CGA CTT CAT GAT 152
Leu Gln Lys Ser Asn Ala Lys Arg Xaa Asn Leu Asp Arg Leu His Asp
 -5 1 5 10

GAA CTT TGG TAC AAC GAT CCA GGC CAG ATG AAT GAT GGA CCA CTC TGC 200
Glu Leu Trp Tyr Asn Asp Pro Gly Gln Met Asn Asp Gly Pro Leu Cys
 15 20 25

AAA TGC AGC GCA AAG GCA AGA CGC ACA GGA ATT AGG CAC AGC ATT TAT 248
Lys Cys Ser Ala Lys Ala Arg Arg Thr Gly Ile Arg His Ser Ile Tyr
 30 35 40

CCT GGA GAA GAG GCC ATC AAG CCC TGT CGT CCT ATG ACC AAC AAT GCT 296
Pro Gly Glu Glu Ala Ile Lys Pro Cys Arg Pro Met Thr Asn Asn Ala
 45 50 55

GGC AGA CTT TTC CAC TAC CGG ATC ACA GTM TCC CCG CCT ACG AAC TTT 344
Gly Arg Leu Phe His Tyr Arg Ile Thr Val Ser Pro Pro Thr Asn Phe
 60 65 70

TTA ACT GAC AGG CCA ACT GTT ATA GAA TAC GAT GAT CAC GAG TAT ATC 392
Leu Thr Asp Arg Pro Thr Val Ile Glu Tyr Asp Asp His Glu Tyr Ile
 75 80 85 90

TTT GAA
Phe Glu
 398

```

## (2) INFORMATION FOR SEQ ID NO: 270:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 105..208  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 81..184  
                           id N51797  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 30..110  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 7..87  
                           id N51797  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 54..134  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.9  
                           seq ALALAXAPDLAQA/PL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

```

AGTGCGAAG GTTCTGGGAA GTAGGAGACC CCACTGGGCTT TGGTCCCCTA AGA ATG 56
 Met
GAC TCT GCT GCC TGT GCT GCT GCT GCC ACC CCT GTT CCA GCC CTG GCT 104
Asp Ser Ala Ala Cys Ala Ala Ala Ala Thr Pro Val Pro Ala Leu Ala
-25 -20 -15
TTG GCC HTA GCT CCA GAC CTA GCA CAA GCC CCA CTG GCA CTC CCT GGC 152
Leu Ala Xaa Ala Pro Asp Leu Ala Gln Ala Pro Leu Ala Leu Pro Gly
-10 -5 1 5
CTG TTA AGC CCA TCT TGC CTT CTC TCC TCT GGA CAA GAA GTA AAT GGG 200
Leu Leu Ser Pro Ser Cys Leu Leu Ser Ser Gly Gln Glu Val Asn Gly
10 15 20
AGT GAA AGA GGA ACT TGT CTC TGG AGG CCC TGG CTG TCT TCC ACA AAT 248
Ser Glu Arg Gly Thr Cys Leu Trp Arg Pro Trp Leu Ser Ser Thr Asn
25 30 35
GAC TCC CCA AGG CAG ATG AGG AAG CTG GTG GAT TTG GCT GCT GST GGG 296
Asp Ser Pro Arg Gln Met Arg Lys Leu Val Asp Leu Ala Ala Gly Gly
40 45 50
GCA ACG GCT GCT GAG GTC ACC AAG GCT GAA TCC ATR NTC CAT CAC CCT 344
Ala Thr Ala Ala Glu Val Thr Lys Ala Glu Ser Xaa Xaa His His Pro
55 60 65 70
GTC AGG CTC TTC TGG
Val Arg Leu Phe Trp
359

```

## (2) INFORMATION FOR SEQ ID NO: 271:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..304
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 15..317  
id T86266  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 64..135
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq ILGLLGLLGTLVA/ML

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

```

AAAGAGCTTC AGCCTGAAGA CAAGGGAGCA GTCCCTGAAG ACGCTTCTAC TGAGAGGTCT 60
GCC ATG GCC TCT CTT GGC CTC CAA CTT GTG GGC TAC ATC CTA GGC CTT 108
Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
 -20 -15 -10
CTG GGG CTT TTG GGS ACA CTG GTT GCC ATG CTG CTC CCC AGC TGG AAA 156
Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys
 -5 1 5
ACA AGT TCT TAT GTC GGT GCC AGC ATT GTG ACA GCA GTT GGC TTC TCC 204
Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser
 10 15 20
AAG GGC CTC TGG ATG GAA TGT GCC ACA YAC AGC ACA GGC ATC ACC CAG 252
Lys Gly Leu Trp Met Glu Cys Ala Thr Xaa Ser Thr Gly Ile Thr Gln
 25 30 35
TGT GAC ATC TAT AGC ACC CTT CTG GGC CTG CCC GCT GAC ATC CAG GCT 300
Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala Asp Ile Gln Ala
 40 45 50 55
GCC CAG GCC ATG ATG GTG ACA TCC AGT GCA ATC TCC TCC CTG GCC TGC 348

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gln | Ala | Met | Met | Val | Thr | Ser | Ser | Ala | Ile | Ser | Ser | Leu | Ala | Cys |     |
|     |     |     | 60  |     |     |     |     |     | 65  |     |     |     |     | 70  |     |     |
| ATT | ATC | TCT | GTG | GTG | GGC | ATG | AGA | TGC | ACA | GTC | TTC | TGC | CAG | GAA | TCC | 396 |
| Ile | Ile | Ser | Val | Val | Gly | Met | Arg | Cys | Thr | Val | Phe | Cys | Gln | Glu | Ser |     |
|     |     |     | 75  |     |     |     | 80  |     |     |     |     |     | 85  |     |     |     |
| CGA | GCC | AGG |     |     |     |     |     |     |     |     |     |     |     |     |     | 405 |
| Arg | Ala | Arg |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 90  |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 272:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 15..243  
id T86266  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 160..231
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq ILGLLGLLGTLVA/ML

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

|             |             |             |             |                     |            |     |
|-------------|-------------|-------------|-------------|---------------------|------------|-----|
| AGCTGCTTGT  | GGCCACCCAC  | AGACACTTGT  | AAGGAGGAGA  | GAAGTCAGCC          | TGGCAGAGAG | 60  |
| ACTCTGAAAT  | GASSGATTAG  | AGGTGTTCAA  | GGRAGCAAAG  | AGCTTCAGCC          | TGAAGACAAG | 120 |
| GGAGCAGTCC  | CTGAAGACGC  | TTCTACTGAG  | AGGTCTGCC   | ATG GCC TCT CTT GGC |            | 174 |
|             |             |             |             | Met Ala Ser Leu Gly |            |     |
|             |             |             |             | -20                 |            |     |
| CTC CAA CTT | GTG GGC TAC | ATC CTA GGC | CTT CTG GGG | CTT TTG GGC         | ACA        | 222 |
| Leu Gln Leu | Val Gly Tyr | Ile Leu Gly | Leu Leu Gly | Leu Leu Gly         | Thr        |     |
|             | -15         |             | -10         |                     | -5         |     |
| CTG GTT GCC | ATG CTG CTC | CCC AGC TGG | AAA ACA AGT | TCT TAT GTC         | GGT        | 270 |
| Leu Val Ala | Met Leu Leu | Pro Ser Trp | Lys Thr Ser | Ser Tyr Val         | Gly        |     |



|                                                                 |    |    |    |     |
|-----------------------------------------------------------------|----|----|----|-----|
|                                                                 | 1  | 5  | 10 |     |
| GCC AGC ATT GTG ACA GCA GTT GGC TTC TCC AAG GGC CTC TGG ATG GAA |    |    |    | 318 |
| Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys Gly Leu Trp Met Glu |    |    |    |     |
| 15                                                              | 20 | 25 |    |     |
| TGT GCC                                                         |    |    |    | 324 |
| Cys Ala                                                         |    |    |    |     |
| 30                                                              |    |    |    |     |

## (2) INFORMATION FOR SEQ ID NO: 273:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..260
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 19..184  
id AA132585  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 347..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 2..54  
id N57441  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 272..325
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq LLCECLLLVAGYA/HD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ACGCAGCCGT CAGCCGAACA ATTCGATGAC GAGGCCCAGG AAGCACGCTG AAACCCTGGG | 63  |
| CGGCGGCAAG CTGTGCGACC TCTTCTGCGG CCGGCCTGGA CTAGCTTTAT CGTCATCTGG | 126 |
| GAAATTGTTA AAAATGCAAA TTCGCAAGTT TGAGAGCCAT GGTTCGAAGA AACTGCATAA | 189 |

```

GCATACGAAA TAAGTTGCAG CCTCCCGWCT TATACCCTGG TACTTCTAGT CTAAACAGG 240
ATTGACTCT ACTAATCCAG CCTTATACAG G.ATG CTG TGT TCT TTG CTC CTT 292
 Met Leu Cys Ser Leu Leu Leu
 -15

TGT GAA TGT CTG TTG CTG GTA GCT GGT TAT GCT CAT GAT GAT GAC TGG 340
Cys Glu Cys Leu Leu Leu Val Ala Gly Tyr Ala His Asp Asp Asp Trp
-10 -5 1 5

ATT GAC CCC ACA GAC ATG CTT AAC TAT GAT GCT GCT TCA GGA ACA ATG 388
Ile Asp Pro Thr Asp Met Leu Asn Tyr Asp Ala Ala Ser Gly Thr Met
10 15 20

AGA AAA TCT 397
Arg Lys Ser

```

## (2) INFORMATION FOR SEQ ID NO: 274:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..42
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 14..55  
id H32593  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 22..87
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq LWYVCPCPSGAWM/VP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

```

AGACGCTGCC CTTCCGCAGC G ATG GCA TCC CGG CTC TGT GGA GGG GCC CTC 51
 Met Ala Ser Arg Leu Cys Gly Gly Ala Leu
 -20 -15

TGG TAT GTG TGT CCC TGT CCT TCT GGG GCG TGG ATG GTK CCT GGG 96
Trp Tyr Val Cys Pro Cys Pro Ser Gly Ala Trp Met Val Pro Gly
-10 -5 1

```

## (2) INFORMATION FOR SEQ ID NO: 275:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 15..250  
id H23844  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 25..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 8..237  
id AA036876  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 21..251  
id H22656  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..217
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..183  
id W05714  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 218..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 183..219  
id W05714  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 34..244  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 1..211  
                           id AA100765  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 69..152  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.5  
                           seq LGYLVLSEGAFLA/SS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

```

ACGTGACCGG GGCCTGAAGC CGGAAGCTAC CTATCTGGTA GGGAGCTCCC CCAGCACCGA 60
AGACTGCG ATG ACT TCT GCA CTG ACC CAG GGG CTG GAG CGA ATC CCA GAC 110
 Met Thr Ser Ala Leu Thr Gln Gly Leu Glu Arg Ile Pro Asp
 -25 -20 -15

CAG CTC GGC TAC CTG GTA CTG AGT GAA GGT GCA GTG CTG GCG TCA TCT 158
Gln Leu Gly Tyr Leu Val Leu Ser Glu Gly Ala Val Leu Ala Ser Ser
 -10 -5 1

GGG GAC CTG GAG AAT GAT GAG CAG GCA DCC AGT GCC ATC TCT GAG CTG 206
Gly Asp Leu Glu Asn Asp Glu Gln Ala Xaa Ser Ala Ile Ser Glu Leu
 5 10 15

GTC AGC ACA GCC TGC GGT TTC CGG CTG CAC CGC GGC ATG AAT GTG CCC 254
Val Ser Thr Ala Cys Gly Phe Arg Leu His Arg Gly Met Asn Val Pro
 20 25 30

ASG 257
Arg
35

```

## (2) INFORMATION FOR SEQ ID NO: 276:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 9..243

(C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 6..245  
                           id H64050  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 15..248  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 1..234  
                           id R17172  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 14..248  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 1..235  
                           id HSC15C081  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 22..248  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 1..227  
                           id AA149663  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 43..248  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 29..234  
                           id HSU46380  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 24..149  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.4  
                           seq ITGVILLAVGIWG/KV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

```

AGGTGCAGGG TCTCGGGCTA GTC ATG GCG TCC CCG TCT CGG AGA CTG CAG ACT 53
 Met Ala Ser Pro Ser Arg Arg Leu Gln Thr
 -40 -35

AAA CCA GTC ATT ACT TGT TTC AAG AGC GTT CTG CTA ATC KAC ACT NTK 101
Lys Pro Val Ile Thr Cys Phe Lys Ser Val Leu Leu Ile Xaa Thr Xaa
 -30 -25 -20

ATT TKC TGG ATC ACT GGC GTC ATC CTT CTT GCA GTT GGC ATT TGG GGC 149

```

```

Ile Xaa Trp Ile Thr Gly Val Ile Leu Leu Ala Val Gly Ile Trp Gly
-15 -10 -5

AAG GTG AGC CTG GAG AAT TAC TTT KCK CTT TTA AAT GAG AAG GCC ACC 197
Lys Val Ser Leu Glu Asn Tyr Phe Xaa Leu Leu Asn Glu Lys Ala Thr
 1 5 10 15

AAT GTC CCC TTC GKG CTC ATT GCT ACT GGT ACC GTC ATK ATT CTT TTG 245
Asn Val Pro Phe Xaa Leu Ile Ala Thr Gly Thr Val Xaa Ile Leu Leu
 20 25 30

GGC TAC CGG
Gly Tyr Arg
 35

```

## (2) INFORMATION FOR SEQ ID NO: 277:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..228
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 19..246  
id HUMHG1206  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..222  
id C15962  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 35..220  
id HUM417F07B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 2..33  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 1..32  
                           id HUM417F07B  
                           est

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 59..228  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 18..187  
                           id AA139623  
                           est

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 94..173  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 1..85  
                           id N88476  
                           est

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 177..228  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 82..133  
                           id N88476  
                           est

(ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 49..108  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.3  
                           seq VLLGSGLTILSQP/LM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

|                                                                  |     |
|------------------------------------------------------------------|-----|
| GTGCGTTGGT GGCTCCGTCT GTCTGTCCGT CCGCCCGCGG GTGCCATC ATG GCG GAC | 57  |
| Met Ala Asp                                                      |     |
| -20                                                              |     |
| GCG GCC AGT CAG GTG CTC CTG GGC TCC GGT CTC ACC ATC CTG TCC CAG  | 105 |
| Ala Ala Ser Gln Val Leu Leu Gly Ser Gly Leu Thr Ile Leu Ser Gln  |     |
| -15 -10 -5                                                       |     |
| CCG CTC ATG TAC GTG AAA GTG CTC ATC CAG GTG GGA TAT GAG CCT CTT  | 153 |
| Pro Leu Met Tyr Val Lys Val Leu Ile Gln Val Gly Tyr Glu Pro Leu  |     |
| 1 5 10 15                                                        |     |
| CCT CCA ACA ATA GGA CGA AAT ATT TTT GGG CGG CAA GTG TGN YAG CTT  | 201 |
| Pro Pro Thr Ile Gly Arg Asn Ile Phe Gly Arg Gln Val Xaa Xaa Leu  |     |
| 20 25 30                                                         |     |
| CCT NGT CTC TTT AGT TAT GCT CAG CAC GGG                          | 231 |

Pro Xaa Leu Phe Ser Tyr Ala Gln His Gly  
35 40

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..185)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 93..276  
id AA136898  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..89
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 30..76  
id W96077  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..161
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 110..146  
id W96077  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 83..119
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 69..105  
id W96077  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..49
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 1..35



id W96077  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 126..161  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 129..164  
id N41630  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 58..89  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 63..94  
id N41630  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..31  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 7..36  
id N41630  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 38..161  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 19..142  
id AA043148  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 121..185  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 61..125  
id HUM430A04B  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 60..119  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..60  
id HUM430A04B  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 93..157  
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.3  
seq ALIFGGFISLIGA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

```

AACCTCTTCC GAGCGGGGTC ACGGCCCCGGC CGTCGGTAAC CTGGTTTCCG AGAGTGCCGG 60
CGGGTCGGCG GGTCAAGGCA GCGCGGGGCC TGACGCC ATG TCC CGG AAC CTG CGC 115
 Met Ser Arg Asn Leu Arg
 -20 -15

ACC GCG CTC ATT TTC GGC GGC TTC ATC TCC CTG ATC GGC GCC GCC TTC 163
Thr Ala Leu Ile Phe Gly Gly Phe Ile Ser Leu Ile Gly Ala Ala Phe
 -10 -5 1

TAT CCC ATC TAC TTC CGA CCC CAT GGG 190
Tyr Pro Ile Tyr Phe Arg Pro His Gly
 5 10

```

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(97..229)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 10..142  
id H62783  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 80..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 54..192  
id T71240  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 148..221
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 356..429

id AA075451  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 80..140  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 288..348  
id AA075451  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 135..222  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 350..437  
id AA009954  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 105..140  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 319..354  
id AA009954  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 148..216  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 384..452  
id W15396  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 80..117  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 315..352  
id W15396  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 206..256  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.1  
seq LWCFHLVVLSLYS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

ATGAGTGTG ATGTTTTTCT GCACTAGAAG GCACTATGTT GAACTATTAA ACTTACCAGC 60  
ACTTTCTTTT TCCACICCAT AGTTCATTG TACTGACAAC CTCAGCTGGC ATCATGGACC 120

```

ATGAAGAAGC AAGACGAAAA CACACAGGRA GGGAAATCC TGGGATTCTT TTTCTAGGGA 180
TGTAATACAT ATATTACAA ATAAA ATG CCT CAT GGA CTC TGG TGC TTC CAC 232
 Met Pro His Gly Leu Trp Cys Phe His
 -15 -10

TTG GTC GTT TTG AGC CTT TAC AGC AGT GTA GCC ACA GCC CGG 274
Leu Val Val Leu Ser Leu Tyr Ser Ser Val Ala Thr Ala Arg
 -5 1 5

```

## (2) INFORMATION FOR SEQ ID NO: 280:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..124)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 104..226  
id W94087  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..124
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 12..134  
id R37206  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..124
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 19..141  
id N42384  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..92)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 177..267

id H84930  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(81..124)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 144..187  
id H84930  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(2..124)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 148..270  
id H82795  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 21..62  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5  
seq SLVAVFLSCGLIS/KN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

```
ATAAATTAGC AGTATTAGTT ATG AGT TTG GTT GCA GTG TTC TTA TCT TGT GGG 53
 Met Ser Leu Val Ala Val Phe Leu Ser Cys Gly
 -10 -5

CTG ATT TCC AAA AAC CAC ATG CTG CTG AAT TTA CCA GGG ATC CTC ATA 101
Leu Ile Ser Lys Asn His Met Leu Leu Asn Leu Pro Gly Ile Leu Ile
 1 5 10

CCT CAC AAT GCA AAC CAC TTA CTG 125
Pro His Asn Ala Asn His Leu Leu
 15 20
```

## (2) INFORMATION FOR SEQ ID NO: 281:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Kidney

## (ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 2..85  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 91  
                           region 4..87  
                           id HUML1521  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 85..120  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 86..121  
                           id HUML1521  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 89..148  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                           region 123..182  
                           id W52706  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 34..84  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 69..119  
                           id W52706  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(75..148)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 91  
                           region 324..397  
                           id AAL32959  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 27..98  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5  
                           seq GALAVGAVPVVLS/AM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

```

AAGTTGNSA CCCGGACGGC CTCACC ATG ATG AAA CGG GCA GCT GCT GCT GCA 53
 Met Met Lys Arg Ala Ala Ala Ala
 -20

GTC GGA GGA GCC CTG GCA GTG GGG GCT GTG CCC GTG GTG CTC AGT GCC 101
Val Gly Gly Ala Leu Ala Val Gly Ala Val Pro Val Val Leu Ser Ala
-15 -10 -5 1

```

ATG GGC TTC ACT GGG GCA GGA ATC GCC GCG TCC TCC ATA GCA GCC CAT 149  
 Met Gly Phe Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile Ala Ala His  
                   5                  10                  15

GGG 152  
 Gly

## (2) INFORMATION FOR SEQ ID NO: 282:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 232..430
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
                           region 14..212  
                           id H14129  
                           est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 19..261
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
                           seq LISFSWFANYIRA/GT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

ATTGCGTTCA TTGCCGGC ATG GCC GTC ATT GTG GAT AAA CCC TGG TTC TAT 51  
                   Met Ala Val Ile Val Asp Lys Pro Trp Phe Tyr  
                   -80                  -75

GAC ATG AAG AAA GTT TGG GAG GGA TAT CCC ATA CAG AGC ACT ATC CCT 99  
 Asp Met Lys Lys Val Trp Glu Gly Tyr Pro Ile Gln Ser Thr Ile Pro  
 -70                  -65                  -60                  -55

TCC CAG TAT TGG TAC TAC ATG ATT GAA CTT TCC TTC TAC TGG TCC CTG 147  
 Ser Gln Tyr Trp Tyr Tyr Met Ile Glu Leu Ser Phe Tyr Trp Ser Leu  
                   -50                  -45                  -40

CTC TTC AGC ATT GCC TCT GAT GTC AAG CGA AAG GAT TTC AAG GAA CAG 195  
 Leu Phe Ser Ile Ala Ser Asp Val Lys Arg Lys Asp Phe Lys Glu Gln  
                   -35                  -30                  -25

ATC ATC CAC CAT GTG GCC ACC ATC ATT CTC ATC AGC TTT TCC TGG TTT 243  
 Ile Ile His His Val Ala Thr Ile Ile Leu Ile Ser Phe Ser Trp Phe

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| -20                                                             | -15 | -10 |     |
| GCC AAT TAC ATC CGA GCT GGG ACT CTA ATC ATG GCT CTG CAT GAC TCT |     |     | 291 |
| Ala Asn Tyr Ile Arg Ala Gly Thr Leu Ile Met Ala Leu His Asp Ser |     |     |     |
| -5                                                              | 1   | 5   | 10  |
|                                                                 |     |     |     |
| TCC GAT TAC CTG CTG GAG TCA GCC AAG ATG TTT AAC TAC GCG GGA TGG |     |     | 339 |
| Ser Asp Tyr Leu Leu Glu Ser Ala Lys Met Phe Asn Tyr Ala Gly Trp |     |     |     |
| 15                                                              | 20  | 25  |     |
|                                                                 |     |     |     |
| AAG AAC ACC TGC AAC AAC ATC TTC ACC GTC TTC GCC ATT GTT TTT ATC |     |     | 387 |
| Lys Asn Thr Cys Asn Asn Ile Phe Thr Val Phe Ala Ile Val Phe Ile |     |     |     |
| 30                                                              | 35  | 40  |     |
|                                                                 |     |     |     |
| ATC ACC CGA CTG GTC ATC CTG CCC TTC TGG ATC CTG CAT TGC         |     |     | 429 |
| Ile Thr Arg Leu Val Ile Leu Pro Phe Trp Ile Leu His Cys         |     |     |     |
| 45                                                              | 50  | 55  |     |

## (2) INFORMATION FOR SEQ ID NO: 283:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..221
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 37..147  
id T82645  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 35..82
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq SLFIYIFLTCSNT/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATAGTATCTA TTGAAAAGGA AGCAGTGTGT ATCT ATG ATT ATA TCT CTG TTC ATC | 55  |
| Met Ile Ile Ser Leu Phe Ile                                       |     |
| -15                                                               | -10 |
|                                                                   |     |
| TAT ATA TTT TTG ACA TGT AGC AAC ACC TCT CCA TCT TAT CAA GGA ACT   | 103 |
| Tyr Ile Phe Leu Thr Cys Ser Asn Thr Ser Pro Ser Tyr Gln Gly Thr   |     |
| -5                                                                | 1   |
| 5                                                                 |     |



|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CAA CTC GGT CTG GGT CTC CCC AGT GCC CAG TGG TGG CCT TTG ACA GGT | 151 |
| Gln Leu Gly Leu Gly Leu Pro Ser Ala Gln Trp Trp Pro Leu Thr Gly |     |
| 10 15 20                                                        |     |
| AGG AGG ATG CAG TGC TGC AGG CTA TTT TGT TTT TTG TTA CAA AAC TGT | 199 |
| Arg Arg Met Gln Cys Cys Arg Leu Phe Cys Phe Leu Leu Gln Asn Cys |     |
| 25 30 35                                                        |     |
| CTT TTC CCT TTT CCC CTC CAC CTG ATT CAG CAT GAT CCC TGT GAG CTG | 247 |
| Leu Phe Pro Phe Pro Leu His Leu Ile Gln His Asp Pro Cys Glu Leu |     |
| 40 45 50 55                                                     |     |
| GTT CTC ACA ATC TCT GGG ACT                                     | 268 |
| Val Leu Thr Ile Ser Gly Thr                                     |     |
| 60                                                              |     |

## (2) INFORMATION FOR SEQ ID NO: 284:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (E) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..250
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 7..248  
id HSC2OD111  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 122..257
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..136  
id T77096  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..146
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 19..147  
id N32450  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 9..104  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.7  
 seq LQMLLG FVGRSKS/GL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

```

AGACCAAG ATG GCG GCG GAG CTG GTG GAG GCC AAA AAC ATG GTG ATG AGT 50
 Met Ala Ala Glu Leu Val Glu Ala Lys Asn Met Val Met Ser
 -30 -25 -20

TTT CGA GTC TCC GAC CTT CAG ATG CTC CTG GGT TTC GTG GGC CGG AGT 98
Phe Arg Val Ser Asp Leu Gln Met Leu Leu Gly Phe Val Gly Arg Ser
 -15 -10 -5

AAG AGT GGA CTG AAG CAC GAG CTC GTC ACC AGG GCC CTC CAG CTG GTG 146
Lys Ser Gly Leu Lys His Glu Leu Val Thr Arg Ala Leu Gln Leu Val
 1 5 10

CAG TTT GAC TGT AGC CCT GAG CTG TTC AAG AAG ATC AAG GAG CTG TAC 194
Gln Phe Asp Cys Ser Pro Glu Leu Phe Lys Lys Ile Lys Glu Leu Tyr
 15 20 25 30

GAG ACC CGC TAC GCC AAG AAG AAC TCG GAG CCT GCC CCA CAG CCG CAC 242
Glu Thr Arg Tyr Ala Lys Lys Asn Ser Glu Pro Ala Pro Gln Pro His
 35 40 45

CGG CCC CTG GAC CCC CTG ACC GGG 266
Arg Pro Leu Asp Pro Leu Thr Gly
 50

```

## (2) INFORMATION FOR SEQ ID NO: 285:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 10..105  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
 region 1..96  
 id R05622  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 24..92  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 2..70  
                           id H94933  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 64..243  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.7  
                           seq VHALCPLSPLVTT/GC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

```

AACTCTCCAA AAAGCAGAGA CAGCAGGAAG AGGGGAGTGG AGGCAGCCCA TTCACCTGGG 60
GAA ATG ACT GGG TTG TCG ATG GMC GGT GGC GGB AGC CSA AMG GGG GAY 108
 Met Thr Gly Leu Ser Met Xaa Gly Gly Gly Ser Xaa Xaa Gly Asp
 -60 -55 -50

GTG GAS CCG TDC TAC TAT GGT AAR CVI GGG CCC CTG CGC RCC CTT CCT 156
Val Xaa Pro Xaa Tyr Tyr Gly Lys Xaa Gly Pro Leu Arg Xaa Leu Pro
-45 -40 -35 -30

GAG CCC TCA GGA CCC CTT CCA CCA AGC AGC GGC CTC TCC CAG CCC CAG 204
Glu Pro Ser Gly Pro Leu Pro Pro Ser Ser Gly Leu Ser Gln Pro Gln
 -25 -20 -15

GTC CAT GCT CTG TGC CCC TTA TCT CCC CTG GTT ACC ACG GGC TGC TGC 252
Val His Ala Leu Cys Pro Leu Ser Pro Leu Val Thr Thr Gly Cys Cys
 -10 -5 1

GGG CAG GCT GCG
Gly Gln Ala Ala
 5

```

## (2) INFORMATION FOR SEQ ID NO: 286:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 157..269  
 (C) IDENTIFICATION METHOD: blastn

- (D) OTHER INFORMATION: identity 97  
region 95..207  
id N41379  
est
- (ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 62..173  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 1..112  
id N41379  
est
- (ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 275..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 213..257  
id N41379  
est
- (ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 8..173  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 1..166  
id AA044371  
est
- (ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 157..219  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 149..211  
id AA044371  
est
- (ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: complement(272..319)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 423..470  
id N30852  
est
- (ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: complement(225..264)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 478..517  
id N30852  
est
- (ix) FEATURE:  
(A) NAME/KEY: other

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| AAAGTCTCTAG AGGGGGTCGG GGTMTGGGTG GACAAGCTTT CCTCGTCTC TCCCNACAGA  | 60  |
| GCTGACGTGT CCTGGGTTCC ACCGGGAGCG GGCATTTCCA CCGGACGGGA GGGTTCGGGG  | 120 |
| TGTCCGGGGC TGGGGAATAC GTARGGGKTG CSGCGCCGGT GTGGGAAGTT GGGGCGTGTG  | 180 |
| GGTGCAGTCC CGGGAGTTCT TGGAGGGGGT CGGCCACCG AGCTTCCGGA CCGGCTGATC   | 240 |
| TGCCCCGTAGC TTGCCGGAGG GAGGGCGGAG CTGACTCTCC GTCCCTTCTC CCATCCCCTC | 300 |
| SAGTGGTGGG TACGGGCACC TCGCTGGCGC TCTCCTCCCT CCTGTCCCTN GNNSNTCTTT  | 360 |
| GCTGGG ATG CAG ATG TAC AGC CGT CAG CTG GCC TCC AMC GAG TGG CTC     | 408 |
| Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Xaa Glu Trp Leu            |     |
| -30 -25 -20                                                        |     |
| ACC ATC CAG GGC GGC CTG CTT GGW KCG GGT CTC TTS KRG TYC TCG CTC    | 456 |
| Thr Ile Gln Gly Gly Leu Leu Gly Xaa Gly Leu Xaa Xaa Xaa Ser Leu    |     |
| -15 -10 -5                                                         |     |
| ACT GCG GGG                                                        | 465 |
| Thr Ala Gly                                                        |     |
| 1                                                                  |     |

## (2) INFORMATION FOR SEQ ID NO: 287:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..344
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 56..337  
id AA203498  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 7..63
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..59  
id AA203498  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 344..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 338..379  
id AA203498  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..292
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 44..273  
id W87295  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 292..344
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 274..326  
id W87295  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 20..65  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 2..47  
id W87295  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 344..385  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 327..368  
id W87295  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 33..344  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..312  
id AA248429  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 344..385  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 313..354  
id AA248429  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 76..344  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..269  
id W01758  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 344..385  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 270..311  
id W01758  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 63..234  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 30..201  
id AA249697  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 33..65  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 1..33  
 id AA249697  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 257..289  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 222..254  
 id AA249697  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 227..256  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 193..222  
 id AA249697  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 19..180  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.3  
 seq LIVWLLVKSFSSES/GI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATCTGGCTCA GTTCCGCC ATG GCC TCC TTG GAA GTC AGT CST AGT CCT CGC | 51  |
| Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg                     |     |
| -50 -45                                                         |     |
| AGG TCT CGG CGG GAG CTG GAA GTG CGC AGT CCA CGA CAG AAC AAA TAT | 99  |
| Arg Ser Arg Arg Glu Leu Glu Val Arg Ser Pro Arg Gln Asn Lys Tyr |     |
| -40 -35 -30                                                     |     |
| TCG GTG CTT TTA CCT ACC TAC AAC GAG CGC GAG AAC CTG CCG CTC ATC | 147 |
| Ser Val Leu Leu Pro Thr Tyr Asn Glu Arg Glu Asn Leu Pro Leu Ile |     |
| -25 -20 -15                                                     |     |
| GTG TGG CTG CTG GTG AAA AGC TTC TCC GAG AGT GGA ATC AAC TAT GAA | 195 |
| Val Trp Leu Leu Val Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu |     |
| -10 -5 1 5                                                      |     |
| ATT ATA ATC ATA GAT GAT GGA AGC CCA GAT GGA ACA AGG GAT GTT GCT | 243 |
| Ile Ile Ile Ile Asp Asp Gly Ser Pro Asp Gly Thr Arg Asp Val Ala |     |
| 10 15 20                                                        |     |
| GAA CAG TTG GAG AAG ATC TAT GGG TCA GAC AGA ATT CTT CTA AGA CCA | 291 |
| Glu Gln Leu Glu Lys Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro |     |
| 25 30 35                                                        |     |



CGA GAG AAA AAG TTG GGA CTA GGA ACT GCA TAT ATT CDY SRA ATG AAA 339  
Arg Glu Lys Lys Leu Gly Leu Gly Thr Ala Tyr Ile Xaa Xaa Met Lys  
40 45 50

CAT GCA CAG GAA ACT ACA TCA TTA TTA TGG ATS CTG ATC TCT CAC 384  
His Ala Gln Glu Thr Thr Ser Leu Leu Trp Xaa Leu Ile Ser His  
55 60 65

## (2) INFORMATION FOR SEQ ID NO: 288:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 36..268
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 13..245  
id AA134651  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 266..303
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 244..281  
id AA134651  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..272
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 95..353  
id W26888  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..262
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 7..208  
id T66207  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 263..325.  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
 region 208..270  
 id T66207  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 39..267  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 1..229  
 id W00383  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 35..304  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 13..282  
 id HSC36A071  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 207..266  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.3  
 seq LLDSSLMASGTAS/RS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

```

AAACCGGGKG TAGACGTACC TCACGGAAGC CGGCTTTGGC CCTGCGGCTK YTACCGTCCG 60
CGCGGAGAAA TTGTGGATC TGGCAGTCTA GGAATGAATC TCCTCTCAGC CTTTAAGCTC 120
ACCTGGTCAG AATCCTTGA TGAGCCTGTG GGACCGTTCC TCCTAGCCCG GTGGTTTGA 180
ACCAGTGGCT TTGGGACTGT AAGAGG ATG GAC AAA GAT TCT CAG GGG CTG CTA 233
 Met Asp Lys Asp Ser Gln Gly Leu Leu
 -20 -15

GAT TCA TCC CTG ATG GCA TCA GGC ACT GCC AGC CGC TCA GAG GAT GAG 281
Asp Ser Ser Leu Met Ala Ser Gly Thr Ala Ser Arg Ser Glu Asp Glu
-10 -5 1 5

GAG TCA CTG GCA GGG CAG AAG CGA GCC TCC TCC CAG GCC CTG GGC ACC 329
Glu Ser Leu Ala Gly Gln Lys Arg Ala Ser Ser Gln Ala Leu Gly Thr
 10 15 20

GGG 332
Gly

```

## (2) INFORMATION FOR SEQ ID NO: 289:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 126..226
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 38..138  
id AA009514  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 252..343
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 161..252  
id AA009514  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..131
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 15..44  
id AA009514  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 100..207
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq CLAVSWEAAGCHG/AG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

```

AAAGGAATAC TGACAGATAA GGCCGGAAAC AAAACTGATG GCTTGAAAAA CATTTTATG 60
GAATGTATTT ACTATCATTT TGTTTTACTA TAGAGGTAG ATG GGA CTC TTA ACT 114
 Met Gly Leu Leu Thr
 -35

TTT GGG TAC ATT GAA AMC AKG CKG AAA ACT GAA CAC AAT CCT GAT CAT 162
Phe Gly Tyr Ile Glu Xaa Xaa Xaa Lys Thr Glu His Asn Pro Asp His
-30 -25 -20

```

(2) INFORMATION FOR SEQ ID NO: 290:

(A) LENGTH: 206 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle .

(A) NAME/KEY: other  
(B) LOCATION: 73..208  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 53..188  
id T06781  
est

(A) NAME/KEY: other  
(B) LOCATION: 20..80  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 1..61  
id T06781  
est

[illegible]

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 12..59  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.1  
 seq YAAVAGVLAVES/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

```

AGCGCGGGAA C ATG GGG CTG TAC GCT GCG GTG GCA GGC GTG CTG GCC GGC 50
 Met Gly Leu Tyr Ala Ala Val Ala Gly Val Leu Ala Gly
 -15 -10 -5

GTG GAG AGC CGC CAG GGC TCT AAT CAA GGG GCT GGT GTA CTC CAG CAA 98
Val Glu Ser Arg Gln Gly Ser Asn Gln Gly Ala Gly Val Leu Gln Gln
 1 5 10

CTT CCA GAA CGT GAA RCA GCT GTA CGC GCT GGT GTG CGA AAS GCA GCG 146
Leu Pro Glu Arg Glu Xaa Ala Val Arg Ala Gly Val Arg Xaa Ala Ala
 15 20 25

CTA CTC CGC CGT GCT GGA TRC CGT GAT CTC CAR CGC CGG CCT CCT CAG 194
Leu Leu Arg Arg Ala Gly Xaa Arg Asp Leu Gln Arg Arg Pro Pro Gln
 30 35 40 45

TGC GAA GAA GCT 206
Cys Glu Glu Ala

```

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 26..219  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 91  
                           region 1..194  
                           id T06781  
                           est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 204..234  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 176..206  
                           id T06781  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 22..74  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
                           region 1..53  
                           id AA101354  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 71..110  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 51..90  
                           id AA101354  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 18..203  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.1  
                           seq LDAVIASAGLLRA/EK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

```

AAAAGGCGCG CGGGAAC ATG GGG CTG TAT GCT GCA GCT GCA GGC GTG TTG 50
 Met Gly Leu Tyr Ala Ala Ala Gly Val Leu
 -60 -55

GCC GGC GTG GAG AGC CGC CAG GGC TCT ATC AAG GGC TTG GTG TAC TCC 98
Ala Gly Val Glu Ser Arg Gln Gly Ser Ile Lys Gly Leu Val Tyr Ser
-50 -45 -40

AGC AAC TTC CAG AAC GTG AAG CAG CTG TAC GCG CTG GTG TGC GAA ACG 146
Ser Asn Phe Gln Asn Val Lys Gln Leu Tyr Ala Leu Val Cys Glu Thr
-35 -30 -25 -20

CAG CGC TAC TCC GCC GTG CTG GAT GCT GTG ATC GCC AGC GCC GGC CTC 194
Gln Arg Tyr Ser Ala Val Leu Asp Ala Val Ile Ala Ser Ala Gly Leu
-15 -10 -5

CTC CGT GCG GAG AAG AAG CTG CGG CCG CAC CTG GCC AAG GTG CTA GTG 242
Leu Arg Ala Glu Lys Lys Leu Arg Pro His Leu Ala Lys Val Leu Val
 1 5 10

TAT GAG TTG TTG TTG GGA AAG GGC TTT CGA GGG GGT GGG GGC CGA TGG 290
Tyr Glu Leu Leu Leu Gly Lys Gly Phe Arg Gly Gly Gly Gly Arg Trp
 15 20 25

AAG GCC CGG
Lys Ala Arg
 30 299

```

## (2) INFORMATION FOR SEQ ID NO: 292:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 457 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 296..458  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 1..163  
                           id R50658  
                           est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(413..458)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 442..487  
                           id AA016001  
                           est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 5..196  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.1  
                           seq WLLRLAYLADIFT/KL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

|                                                                                      |     |
|--------------------------------------------------------------------------------------|-----|
| AGAA ATG GGT GCT CAG CAC ACA GCA CTT CTT CTA AAT ACA GAG GTG AGG                     | 49  |
| Met Gly Ala Gln His Thr Ala Leu Leu Leu Asn Thr Glu Val Arg                          |     |
| -60                          -55                          -50                        |     |
| TGG CTT TCT CGA GGT AAA GTT CTT GTA AGA CTT TTT GAA CTT CGT CGT                      | 97  |
| Trp Leu Ser Arg Gly Lys Val Leu Val Arg Leu Phe Glu Leu Arg Arg                      |     |
| -45                          -40                          -35                        |     |
| GAA CTT TTG GTT TTC ATG GAT TCT GCT TTT CGA CTA TCT GAT TGT TTA                      | 145 |
| Glu Leu Leu Val Phe Met Asp Ser Ala Phe Arg Leu Ser Asp Cys Leu                      |     |
| -30                          -25                          -20                        |     |
| ACA AAT TCA TCT TGG CTG CTA AGA CTT GCA TAT CTT GCA GAT ATT TTT                      | 193 |
| Thr Asn Ser Ser Trp Leu Leu Arg Leu Ala Tyr Leu Ala Asp Ile Phe                      |     |
| -15                          -10                          -5                         |     |
| ACT AAA TTA AAT GAA GTT AAT TTG TCA ATG CAA GGA AAA AAT GTG ACC                      | 241 |
| Thr Lys Leu Asn Glu Val Asn Leu Ser Met Gln Gly Lys Asn Val Thr                      |     |
| 1                          5                          10                          15 |     |
| GTT TTT ACA GTA TTT GAT AAA ATG TCG TCA TTG TTA AGA AAA TTG GAA                      | 239 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Phe | Thr | Val | Phe | Asp | Lys | Met | Ser | Ser | Leu | Leu | Arg | Lys | Leu | Glu |     |  |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| TTT | TGG | GCC | TCA | TCT | GTA | GAA | GAA | GAA | AAC | TTT | GAT | TGT | TTT | CCT | ACA | 337 |  |
| Phe | Trp | Ala | Ser | Ser | Val | Glu | Glu | Glu | Asn | Phe | Asp | Cys | Phe | Pro | Thr |     |  |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| CTC | AGT | GAT | TTT | TTG | ACT | GAA | ATT | AAT | TCT | ACA | GTT | GAT | AAA | GAT | ATT | 385 |  |
| Leu | Ser | Asp | Phe | Leu | Thr | Glu | Ile | Asn | Ser | Thr | Val | Asp | Lys | Asp | Ile |     |  |
|     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| TGC | AGT | GCC | ATT | GTG | CAG | CAC | CTA | AGG | GGT | TTG | CGC | GCT | ACT | CTG | TTA | 433 |  |
| Cys | Ser | Ala | Ile | Val | Gln | His | Leu | Arg | Gly | Leu | Arg | Ala | Thr | Leu | Leu |     |  |
|     |     |     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |  |
| AAA | TAC | TTT | CCT | GTA | ACA | AAT | GAC |     |     |     |     |     |     |     |     | 457 |  |
| Lys | Tyr | Phe | Pro | Val | Thr | Asn | Asp |     |     |     |     |     |     |     |     |     |  |
|     |     |     | 80  |     |     | 85  |     |     |     |     |     |     |     |     |     |     |  |

## (2) INFORMATION FOR SEQ ID NO: 293:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 19..206  
id AA044042  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 6..183  
id AA127902  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..150  
id AA056679  
est



## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(99..247)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 302..450  
                           id W93399  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 90..237  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 11..158  
                           id R29154  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 117..191  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4  
                           seq LVVMVPLVGLIHL/GW

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

```

AATCCGCGGC AGAGCGGCTG CTTGAGATCT GTTCTGGGG CCTCTGGCGG TGGCGGCCTG 60
TGGCGGCCTG GGGCGGCGCG ACGGCTGGTG CGCAGGTACA CTGATGCTGA AGTACT ATG 119
 Met
 -25

AGC CTT CGG AAC TTG TGG AGA GAC TAC AAA GTT TTG GTT GTT ATG GTC 167
Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Val Met Val
 -20 -15 -10

CCT TTA GTT GGG CTC ATA CAT TTG GGG TGG TAC AGA ATC AAA AGC AGC 215
Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser Ser
 -5 1 5

CCT GTT TTC CAA ATA CCT AAA AAC GAC AAC ATG 248
Pro Val Phe Gln Ile Pro Lys Asn Asp Asn Met
 10 15

```

## (2) INFORMATION FOR SEQ ID NO: 294:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 389 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 245..374  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 20..149  
 id T41381  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 75..227  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
 seq GKLLQLVLGCAIS/CE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

```

AAAAATAAAA TGTAGGCAGC AAAAGTGGAA GAGGAGAGGC AGCTGGTGCA CTAATCCAGG 60
TCAGCAATCT GAAG ATG GTC TTA CGG AGC CTA GTA GAG TAC TCC CAG GAT 110
 Met Val Leu Arg Ser Leu Val Glu Tyr Ser Gln Asp
 -50 -45 -40

GTC CTG GCG CAT CCT GTG TCA GAA GAG CAT CTC CCA GAT GTG AGC CTC 158
Val Leu Ala His Pro Val Ser Glu Glu His Leu Pro Asp Val Ser Leu
 -35 -30 -25

ATT GGA GAG TTC TCA GAC CCG GCA GAG CTC GGC AAG CTG CTT CAG CTG 206
Ile Gly Glu Phe Ser Asp Pro Ala Glu Leu Gly Lys Leu Leu Gln Leu
 -20 -15 -10

GTG CTG GGC TGT GCC ATC AGT TGC GAG AAA AAG CAG GAC CAC ATC CAG 254
Val Leu Gly Cys Ala Ile Ser Cys Glu Lys Lys Gln Asp His Ile Gln
 -5 1 5

AGA ATC ATG ACG CTG GAA GAA TCG GTT CAG CAT GTG GTG ATG GAA GCC 302
Arg Ile Met Thr Leu Glu Glu Ser Val Gln His Val Val Met Glu Ala
 10 15 20 25

ATC CAA GAG CTC ATG ACC AAA GAC ACT CCT GAC TCC CTG TCA CCA GAG 350
Ile Gln Glu Leu Met Thr Lys Asp Thr Pro Asp Ser Leu Ser Pro Glu
 30 35 40

ACG TAT GGC AAC TTT GAC AGC CAG TCC CGC AGT ACT GGG 389
Thr Tyr Gly Asn Phe Asp Ser Gln Ser Arg Ser Thr Gly
 45 50

```

## (2) INFORMATION FOR SEQ ID NO: 295:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 105..270  
id AA084830  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 200..229
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 64..93  
id AA084830  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 66..231  
id W01570  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 200..229
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 26..55  
id W01570  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 296..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..111  
id H82170  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 296..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 7..115  
id N71014  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(147..201)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 238..292  
id N35296  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 358..396
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq MIHGFLAPTTS/KN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

```
ATGGGGGCGG ASTAGCCGGA GCCGCGAGTC CATTTTGGGG CTGTGCTTGG CGCGTACCGT 60
GCGGTCCCTG TAGTTGGAGG ACGGGCGGTC GCGCSGGCCT TTCCCACTAG CCGGAGGTCTG 120
GAGATAAGTA CCCGCCGCCG GGCTTCTCTC GGGAAAGCGG GGTGGTCCTC GAACCTTCAG 180
CGAGGGTGGG GAGTTGCCCA GTAGCCTCTA GTTCGITAGT CAAAACGTGA AAAAAAAGA 240
CCTGCTTTGC CVTGGGAAAT AGTAACCCTG CCAAATACAT CAGCTTGTAG GAGACAGAGG 300
ATGTGATGGA GCTGCTTGAA GAAGATCTCA CATGCCCTAT TTGTGTAGT CTGTTTG 357
ATG ATC CAC GGG TTT TGC CTT GCT CCC ACA ACT TCT GCA AAA AAT GCT 405
Met Ile His Gly Phe Cys Leu Ala Pro Thr Thr Ser Ala Lys Asn Ala
 -10 -5 1
```

## (2) INFORMATION FOR SEQ ID NO: 296:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..86
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 1..63  
id C16693  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 25..86  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 9..70  
                           id H48377  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 38..86  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 36..84  
                           id R17245  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 38..86  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 7..55  
                           id H19182  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(19..54)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 91  
                           region 181..216  
                           id T12463  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 90..140  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
                           seq RTWCLACVEASPG/QP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

```

AAGCCTGGGA CACCGCCGGC GGGGAGAGAA GCGGATCCCG TCCGAGCCCC GGCCCCAAGT 60
AACGCCGCCG CCCCGGAGCC GCCGTGAGT ATG CYT TGT CCC AGG ACC TGG TGT 113
 Met Xaa Cys Pro Arg Thr Trp Cys
 -15 -10
CTC GCC TGC GTT GAA GCA TCT CCA GGG CAG CCC TTC CTC CCG CCC CGC 161
Leu Ala Cys Val Glu Ala Ser Pro Gly Gln Pro Phe Leu Pro Pro Arg
 -5 1 5
CCC GGG
Pro Gly

```

167

## (2) INFORMATION FOR SEQ ID NO: 297:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 93..226  
id W81645  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..90
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 31..95  
id W81645  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 62..195  
id W06951  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..90
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 7..64  
id W06951  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 2..179  
id W38711  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

(B) LOCATION: 24..86  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
 seq ETCALASHSGSSG/SK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

```

GCNGTCGGCT CCGCGGCGCC GCC ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC 53
 Met Ala Asp Val Glu Asp Gly Glu Glu Thr
 -20 -15

TGC GCC CTG GCC TCT CAC TCC GGG AGC TCA GGC TCC AAG TCG GGA GGC 101
Cys Ala Leu Ala Ser His Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly
-10 -5 1 5

GAC AAG ATG TTC TCC CTC AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC 149
Asp Lys Met Phe Ser Leu Lys Lys Trp Asn Ala Val Ala Met Trp Ser
 10 15 20

TGG GAC GTG GAG TGC GAT ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG 197
Trp Asp Val Glu Cys Asp Thr Cys Ala Ile Cys Arg Val Gln Val Met
 25 30 35

GAT GCC TGT MTT AGA TGT CAA GCG GGC 224
Asp Ala Cys Xaa Arg Cys Gln Ala Gly
 40 45

```

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 122..188
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 198..264  
id R58050  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(122..188)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 193..259  
id H98670

est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(122..188)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 194..260  
id N66980  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(122..188)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 198..264  
id AA159781  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(122..188)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 161..227  
id H45410  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 273..350  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq IIMFLLIIVCGSP/RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

TAGAAGTAGC AGGATCGCCT TAATAATAAT AATAGTTTGT TAGCATGAAG CCTGAGCATT 60  
GTCCAAAGTT TGGAAATGTG AACGCTGATA GTCACATCTG TCCATCTTTC CACATTTCTA 120  
GGATGCTGAC AGACAGCACC AAGAAGTAAT TGCAATTTAT CGGACACACC TTCTTAGTGC 180  
TGCACAGGTA AAGAACTACT TCTCCTTTGG AAAGAATATT GCTTTAGAGA TAATAATTTT 240  
TATTTTCAAA TAAATTTATG TGAAAGTAAT TG ATG TTT AAA GTA GCT GCA CCC 293  
Met Phe Lys Val Ala Ala Pro  
-25 -20  
CCT ATG CTT ATT TAA KAA ATA ATT ATG TTT CTT TTA ATC ATT GTT TGT 341  
Pro Met Leu Ile Xaa Xaa Ile Ile Met Phe Leu Leu Ile Ile Val Cys  
-15 -10 -5  
GGA TCT CCC AGG CCG 356  
Gly Ser Pro Arg Pro  
1



## (2) INFORMATION FOR SEQ ID NO: 299:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(87..181)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 228..322  
id N29854  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..46)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 363..408  
id N29854  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(44..93)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 315..364  
id N29854  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(87..181)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 67..161  
id T32629  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..93)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 154..246  
id T32629  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: complement(87..181)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 230..324  
id W61289  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(6..93)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 317..404  
id W61289  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(87..181)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 232..326  
id N53422  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(3..93)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 319..409  
id N53422  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 87..181  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 78..172  
id N50275  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 9..93  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..85  
id N50275  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 64..126  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.6  
seq FXMCLWSLRNLF/RC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

```

AGCTATTTGG ATAGTGTAGC TTTAATGTGC TGCACATGAT ACTGGCAGCC CTAGAGTTCA 60
TAG ATG GAC TTT TGG GAC CCA GCA GTT TTT RAA ATG TGT TTA TGG AGT 108
 Met Asp Phe Trp Asp Pro Ala Val Phe Xaa Met Cys Leu Trp Ser
 -20 -15 -10

TTA AGA AAT TTA TTT TCC AGG TGC AGC CCC TGT CTA ACT GAA ATT TCT 156
Leu Arg Asn Leu Phe Ser Arg Cys Ser Pro Cys Leu Thr Glu Ile Ser
 -5 1 5 10

CTT CAC CTT GTA CAC TTG ACA GCT GAA AAA AAA CAA CAT GGG AGT AAT 204
Leu His Leu Val His Leu Thr Ala Glu Lys Lys Gln His Gly Ser Asn
 15 20 25

AAT GGG TCG GCG 216
Asn Gly Ser Ala
 30

```

## (2) INFORMATION FOR SEQ ID NO: 300:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..122
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 1..114  
id R56502  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 173..269
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 162..258  
id R56502  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 129..172
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 119..162  
id R56502

est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 160..261
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq SVPLLSLSHSIGI/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

```
AGTGACCAAA TGACTTAACC ACAGATGGAG TGAAGACAGG GGTAAGTCTGCT TGGTCTGGTC 60
CCCAGTAGAG CATTEGCTCAC TATAAACCAC AAGCTGCTTC TAATTTATTT GAGRTGKTAW 120
TAAYCGTGGG CCTTKATATT CTGGTCTCTC TTGCTGCAA ATG AGT CCG GCA GGC 174
 Met Ser Pro Ala Gly
 -30
AAG CAC AAC TCA GAA AGC AAA TTC ACC TTC TTT GTA GCC CTT GAT GGG 222
Lys His Asn Ser Glu Ser Lys Phe Thr Phe Phe Val Ala Leu Asp Gly
 -25 -20 -15
TCG GTC CCC CTG TIG TCT CTT TCT CAT TCC ATA GGC ATT TCC CCC ACA 270
Ser Val Pro Leu Leu Ser Leu Ser His Ser Ile Gly Ile Ser Pro Thr
 -10 -5 1
AGG 273
Arg
```

## (2) INFORMATION FOR SEQ ID NO: 301:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(78..160)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 149..231  
id H15081  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..71)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 238..308  
id H15081  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(2..71)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 234..303  
id H16744  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(78..160)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 148..230  
id R61691  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(2..72)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 236..306  
id R61691  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(2..85)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 223..306  
id H17833  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(109..160)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 148..199  
id H17833  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 23..73  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq LVCVGLHTEGPWG/RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

ATGTGGTGCT TGTGCTCTAA CT ATG CAC TGG GCC CTT GTC TGC GTC GGC TTG 52  
Met His Trp Ala Leu Val Cys Val Gly Leu

-15

-10

```

CAT ACA GAG GGC CCC TGG GGT CGG CCC TCC GGC CTG GCC TCA GCC AGT 100
His Thr Glu Gly Pro Trp Gly Arg Pro Ser Gly Leu Ala Ser Ala Ser
 -5 1 5

GGG ATG GAC AGG GCC AGG CAG GCC TCT GAA CTT CCA CCT CCT GGG GCC 148
Gly Met Asp Arg Ala Arg Gln Ala Ser Glu Leu Pro Pro Pro Gly Ala
 10 15 20 25

TCC CAG ACC CCC CAG 163
Ser Gln Thr Pro Gln
 30

```

## (2) INFORMATION FOR SEQ ID NO: 302:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 155..325  
id H16532  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..62
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..58  
id H16532  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 170..340  
id H17763  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..62

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..55  
id H17763  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 86..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 168..247  
id R21494  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 11..62  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..52  
id R21494  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 183..222  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 268..307  
id R21494  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 86..238  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 111..263  
id AA084554  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 86..256  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 136..306  
id R52491  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 20..235  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq WFYIGSSLNGTRG/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

```

AGAGCTCGCT .GTGGCCCGG ATG TTC GGT GCA GCT GCC AGA TCC GCT GAT CTA 52
 Met Phe Gly Ala Ala Ala Arg Ser Ala Asp Leu
 -70 -65

GTG CTT CTC GAA AAA AAC CTT CAG GCG GCC CAT GGG TAT GCC CAA GAG 100
Val Leu Leu Glu Lys Asn Leu Gln Ala Ala His Gly Tyr Ala Gln Glu
-60 -55 -50

GAC AGA GAA CGA ATG CAC AGA DRT ATT GTC AGC CTT GSA CAG AAT CTC 148
Asp Arg Glu Arg Met His Arg Xaa Ile Val Ser Leu Xaa Gln Asn Leu
-45 -40 -35 -30

CTG AAC TTT ATG ATT GGC TCT ATC TTG GAT TTA TGG CAA TGC TTC CTC 196
Leu Asn Phe Met Ile Gly Ser Ile Leu Asp Leu Trp Gln Cys Phe Leu
 -25 -20 -15

TGG TTT TAC ATT GGT TCT TCA TTG AAT GGT ACT CGG GSA AAA AGA GTT 244
Trp Phe Tyr Ile Gly Ser Ser Leu Asn Gly Thr Arg Gly Lys Arg Val
 -10 -5 1

CCA GCG CAC TTT
Pro Ala His Phe
5
256

```

## (2) INFORMATION FOR SEQ ID NO: 303:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 3..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..114  
id N87112  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..81  
id AA094982  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..130



(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..79  
id T68050  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 47..130  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..84  
id AA157180  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 50..130  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..81  
id AA186993  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 43..123  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq VVALLIVCDVPSA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

```
AGCCGGAGCA AAGTTTCACT TATAGAAGGG AGAGGAGCGA AC ATG GCA GCG CGT 54
 Met Ala Ala Arg
 -25

TGG CGG TTT TGG TGT GTC TCT GTG ACC ATG GTG GTG GCG CTG CTC ATC 102
Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val Ala Leu Leu Ile
-20 -15 -10

GTT TGC GAC GTT CCC TCA GCC TCT GCC CGG 132
Val Cys Asp Val Pro Ser Ala Ser Ala Arg
-5 1
```

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 436 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 73..238  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 16..181  
id W32979  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 316..394  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 260..338  
id W32979  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 251..322  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 194..265  
id W32979  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 251..437  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 107..293  
id AA128556  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 145..238  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..94  
id AA128556  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 251..381  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 104..234  
id T20234  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 153..238  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98

region 6..91  
id T20234  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 383..437  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 235..289  
id T20234  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 115..238  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 65..188  
id T32594  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 251..318  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 201..268  
id T32594  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 52..115  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..64  
id T32594  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 245..292  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq LLLQPSMIQEVWT/XY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

```
ATCAGACGCC AGTATAAGCC TTTGAGTCTC AATAGACTGC AGTATCTTAT TGATTTGGGT 60
CGTGTGATC CTAGTCAACC TAITGACTTA ACCCAGCTTG TCAATGGGAG AGGTGTGACC 120
ATCCAGCCAC TTAAAAGGGA TTATGGTGTC CAGCTGGTTG AGGAGGGTGC TGACACCTTT 180
ACGGCAAAAG TTAATATTGA AGTACAGTTG GCTTCAGAAC TAGCTATTGC TGCCATTGAA 240
AAAA ATG GTG GTG TTG TTA CTA CAG CCT TCT ATG ATC CAA GAA GTC TGG 289
Met Val Val Leu Leu Leu Gln Pro Ser Met Ile Gln Glu Val Trp
```

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ACA THG TAT GCA AAC CTG TTC CAT TCT TTC TTC GTG GAC AAC CCA TTC | 337 |
| Thr Xaa Tyr Ala Asn Leu Phe His Ser Phe Phe Val Asp Asn Pro Phe |     |
| 1 5 10 15                                                       |     |
| CAA AAA GAA TGC TTC CAC CAG AAG AAC TGG TAC CAT ATT ACA CTG ATG | 385 |
| Gln Lys Glu Cys Phe His Gln Lys Asn Trp Tyr His Ile Thr Leu Met |     |
| 20 25 30                                                        |     |
| CAA AGA ACC GTG GGT ACC TGG CGG ATC CTG CCA AAT TTC CTG AAG CAC | 433 |
| Gln Arg Thr Val Gly Thr Trp Arg Ile Leu Pro Asn Phe Leu Lys His |     |
| 35 40 45                                                        |     |
| GAC                                                             | 436 |
| Asp                                                             |     |

## (2) INFORMATION FOR SEQ ID NO: 305:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 82..407
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 98.5  
region 1..326  
id HSARSE  
vrt

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..171
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..84  
id AA160312  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 149..241
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5  
seq LAVLLSLAPSASS/DI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

```

AAACTCGAA GTTAATCATT CCCAGCTCAA AGCCTTGTGC AAGTGCTCTC TGCCTTCACG 60
CTTGCTTCCT TTGGGAGAGA ACCTTCCTCT TCTTGATCGG GGATTCAGGA AGGAGCCCAG 120
GRGCAGAGGA AGTAGAGAGA GAGRCAAC ATG TTA CAT CTG CAC CMT TCT TGT 172
 Met Leu His Leu His Xaa Ser Cys
 -30 -25

TTG TGT TTC AGG AGC TGG CTG CCA GCG ATG CTC GCT GTA CTG CTA AGT 220
Leu Cys Phe Arg Ser Trp Leu Pro Ala Met Leu Ala Val Leu Leu Ser
 -20 -15 -10

TTG GCA CCA TCA GCT TCC AGC GAC ATT TCC GCC TCC CGA CCG AAC ATC 268
Leu Ala Pro Ser Ala Ser Ser Asp Ile Ser Ala Ser Arg Pro Asn Ile
 -5 1 5

CTT CTT CTG ATG GCG GAC GAC CTT GGC ATT GGG GAC ATT GGC TGC TAT 316
Leu Leu Leu Met Ala Asp Asp Leu Gly Ile Gly Asp Ile Gly Cys Tyr
 10 15 20 25

GGC AAC AAC ACC ATG AGG ACT CCG ARN ATT GAC CGC CTT GCA GAG GAC 364
Gly Asn Asn Thr Met Arg Thr Pro Xaa Ile Asp Arg Leu Ala Glu Asp
 30 35 40

GGC GTG AAG CTG ACC CAA CAC ATC TCT GCC GCA TCT TTG TGC 406
Gly Val Lys Leu Thr Gln His Ile Ser Ala Ala Ser Leu Cys
 45 50 55

```

## (2) INFORMATION FOR SEQ ID NO: 306:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 15.8  
seq LLLLLLLRHGAQG/KP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

```

Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His
-20 -15 -10 -5

Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala
 1 5

```

## (2) INFORMATION FOR SEQ ID NO: 307:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 14  
seq LAMLALLSPLSLA/QY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

Met Glu Arg Pro Leu Cys Ser His Leu Cys Ser Cys Leu Ala Met Leu  
-25                      -20                      -15                      -10

Ala Leu Leu Ser Pro Leu Ser Leu Ala Gln Tyr Asp Ser Trp Pro Xaa  
                    -5                      1                      5

Xaa Pro Glu Tyr Phe Gln Gln Pro  
                    10                      15

## (2) INFORMATION FOR SEQ ID NO: 308:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12.3  
seq HILFLLLLPVAAA/QT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro Val Ala  
                    -15                      -10                      -5

Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe Tyr  
1 5 10

Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu Pro  
15 20 25 30

Leu Leu Ala Gly Leu Val Ala  
35

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: -22..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 12.2  
seq LALALGLAQPASA/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

Met Ala Val Lys Leu Gly Thr Leu Leu Leu Ala Leu Ala Leu Gly Leu  
-20 -15 -10

Ala Gln Pro Ala Ser Ala Arg Arg Lys Leu Leu Val Phe Leu Leu  
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Kidney

(1x) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: -20..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix.

(D) OTHER INFORMATION: score 11.9

seq LVLEFLLSPVEA/QQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

```

Met Glu Thr Leu Gly Ala Leu Leu Val Leu Glu Phe Leu Leu Leu Ser
-20 -15 -10 -5

Pro Val Glu Ala Gln Gln Ala Thr Glu His Arg Leu Lys Pro Trp Leu
 1 5 10

Val Gly Leu Ala Ala Val Val Gly Phe Leu Phe Ile Val Tyr Leu Val
 15 20 25

Leu Leu Ala Asn Arg Leu Trp Cys Ser Lys Ala Arg Ala Glu Asp Glu
 30 35 40

Glu Glu Thr Thr Phe Arg Met Glu Ser Gly
45 50

```

## (2) INFORMATION FOR SEQ ID NO: 311:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.3  
seq PLLSSLLGGSQA/MD

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

```

Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln Ala
-15 -10 -5

Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val Pro
1 5 10 15

Glu Gly Leu Cys Ile Ser Val Xaa Leu Leu Phe Leu Leu Pro Pro Thr
 20 25 30

Arg Leu Asp Arg Val Tyr Pro Ser Arg
 35 40

```

## (2) INFORMATION FOR SEQ ID NO: 312:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7  
seq LWLLFFLVTAIHA/EL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

```

Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala Glu Leu
 -10 -5 1
Cys Gln Pro Gly Ala Glu Asn Ala Phe Lys Val Arg Leu Ser Ile Arg
 5 10 15
Thr Ala Leu Gly Asp Lys Ala Tyr Ala Trp Asp Thr Asn Glu Glu Tyr
 20 25 30
Leu Phe Lys Ala Met Val Ala Phe Ser Met Arg Lys Val Pro Asn Arg
 35 40 45 50
Glu Ala Thr Glu Ile Ser His Val Leu Leu Cys Asn Val Thr Gln Arg
 55 60 65
Val Ser Phe Trp Phe Val Val Thr Asp Pro Ser Lys Asn His Thr Leu
 70 75 80
Pro Ala Val Glu Val Gln Ser Ala Ile Arg Met Asn Lys Asn Arg Ile
 85 90 95
Asn Asn Ala Phe Phe Leu Asn Asp Gln Thr Leu Glu Phe Leu Lys Ile
 100 105 110
Pro Ser Thr Leu Ala Pro Thr Arg
 115 120

```

## (2) INFORMATION FOR SEQ ID NO: 313:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7  
seq LPLLCLFLQGATA/VL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

```

Met Ala Gly Ser Pro Ser Arg Ala Ala Gly Arg Arg Leu Gln Leu Pro
 -25 -20 -15

Leu Leu Cys Leu Phe Leu Gln Gly Ala Thr Ala Val Leu Phe Ala Val
 -10 -5 1 5

Phe Val Arg Tyr Asn His Lys Thr Asp Ala Ala Leu Trp Xaa Arg Lys
 10 15 20

Leu Gly

```

## (2) INFORMATION FOR SEQ ID NO: 314:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -39...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.6  
seq ALALLLVLP LLWP/CS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

```

Met Lys Trp Pro Trp Thr Cys Leu Ala Ile Leu Cys Pro Gly Pro Val
 -35 -30 -25

Leu Ser Pro Pro Cys Ser Gly Pro Xaa Leu Ala Leu Ala Leu Leu Leu
 -20 -15 -10

Val Leu Pro Leu Leu Trp Pro Cys Ser Val Phe Gly His Ala Leu Cys
 -5 1 5

Xaa Pro Ser Pro Ala Arg Arg

```

10

15

## (2) INFORMATION FOR SEQ ID NO: 315:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10  
seq PLLGLLLSLPAGA/DV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

```

Met Pro Ser Trp Ile Gly Ala Val Ile Leu Pro Leu Leu Gly Leu Leu
 -20 -15 -10

Leu Ser Leu Pro Ala Gly Ala Asp Val Lys Ala Arg Ser Cys Gly Glu
 -5 1 5

Val Arg Gln Ala Tyr Gly Ala Lys Gly Phe Ser Leu Ala Asp Ile Pro
 10 15 20 25

Tyr Gln Glu Ile Ala Xaa Glu His Leu Arg Ile Cys Pro Gln Glu Tyr
 30 35 40

Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu Ser Gln Gln Ser Lys
 45 50 55

Leu Glu Phe Glu Asn Leu Val Glu Glu Thr Ser His Phe Val Arg Thr
 60 65 70

Thr Phe Val Ser Arg His Lys Lys Phe Asp Gly Arg
 75 80 85

```

## (2) INFORMATION FOR SEQ ID NO: 316:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10  
seq LWLSLLVPSC/LCA/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

```

Met Leu Leu His Trp Val Arg Ser Gln Xaa Xaa Ser Asp Xaa Lys Leu
 -25 -20 -15

Trp Leu Ser Leu Leu Val Pro Ser Cys Leu Cys Ala Ser Pro Trp Pro
 -10 -5 1

Leu Pro Ser Leu Pro Leu Leu Pro Pro Ser Leu Leu Ser Leu Leu
 5 10 15 20

```

## (2) INFORMATION FOR SEQ ID NO: 317:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.6  
seq LLLFSLVSPPTC/KV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

```

Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala
 -30 -25 -20

Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro
 -15 -10 -5

Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala
 1 5 10

Trp Xaa Thr Pro Pro Thr Arg Trp
 15 20

```

## (2) INFORMATION FOR SEQ ID NO: 318:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -35...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5  
seq AMWWLLWGVQLQA/WP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

```

Met Pro Gly Pro Arg Val Trp Gly Lys Tyr Leu Trp Arg Ser Pro His
-35 -30 -25 -20

Ser Lys Gly Cys Pro Gly Ala Met Trp Trp Leu Leu Leu Trp Gly Val
 -15 -10 -5

Leu Gln Ala Trp Pro Xaa Pro Gly Leu Arg Pro Leu Gly Pro Arg Ala
 1 5 10

Thr Pro Ala Ala Asp Ile Pro Arg Val Pro Arg Ala Val Trp Gln Arg
15 20 25

Pro Arg Glu Gln His Gly His Gln Gly Ser Arg Gly Leu Cys Cys Glu
30 35 40 45

Ala Arg Leu Pro Gly Leu Arg Pro Gly Ala Val Pro Gly Leu Cys Arg
 50 55 60

Gly Leu Xaa Xaa Asn Leu Ile Arg Arg Phe Gly Ser Lys Pro Val Leu
65 70 75

Trp Ser Ala Arg Leu Pro Ser Gly Gln Ala Pro Trp Ser Glu Gly
80 85 90

```

## (2) INFORMATION FOR SEQ ID NO: 319:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -37..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 9.2  
seq LLAVLLASWRLWA/IK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

```

Met Cys Gly Pro Ala Met Phe Pro Ala Gly Pro Pro Trp Pro Arg Val
 -35 -30 -25

Arg Val Val Gln Val Leu Trp Ala Leu Leu Ala Val Leu Leu Ala Ser
 -20 -15 -10

Trp Arg Leu Trp Ala Ile Lys Asp Phe Gln Glu Cys Thr Trp Gln Val
 -5 1 5 10

Val Leu Asn Glu Phe Lys Arg Val Gly Glu Ser Gly Val Ser Asp Xaa
 15 20 25

Ser Leu Ser Lys Ser Pro Gly
 30

```

## (2) INFORMATION FOR SEQ ID NO: 320:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -55..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 9.2  
seq SLLLLSTALNILA/CQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

```

Met His Arg Arg Lys Leu Pro Leu Thr Asn Lys Arg Gln Leu Gln Lys
-55 -50 -45 -40

Kaa Leu Ser Lys Phe Ile Phe Ser Asp Glu Leu Phe Arg Asn Ile Leu
 -35 -30 -25

Phe Ser Leu Arg Thr Leu Arg Met Ile Leu Ser Leu Leu Leu Ser

```

-20                                  -15                                  -10  
Thr Ala Leu Asn Ile Leu Ala Cys Gln Ile Asn Glu Glu Leu Gly  
          -5                                          1                                  5

## (2) INFORMATION FOR SEQ ID NO: 321:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3  
seq VSALLMAWFGVLS/CV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val Leu  
          -15                                          -10                                  -5  
  
Ser Cys Val Gln Ala Xaa Xaa  
          1                                          5

## (2) INFORMATION FOR SEQ ID NO: 322:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.1  
seq LCLVCLLVHTAFR/VV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

Met Gln Leu Pro Leu Ala Leu Cys Leu Val Cys Leu Leu Val His Thr  
                   -15                  -10                  -5

Ala Phe Arg Val Val Glu Gly Gln Gly Trp Gln Ala Phe Lys Asn Asp  
                   1                  5                  10

Ala Thr Glu Ile Ile Pro Glu Leu Gly Glu Tyr Pro Glu Pro Pro Pro  
           15                  20                  25

Glu Arg  
       30

## (2) INFORMATION FOR SEQ ID NO: 323:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8  
seq ILLCSVAVXLSPS/EP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

Met Leu Cys Ile His Xaa Xaa Arg Ile Ile Gln Asp Ser Phe Ile Ala  
       -30                  -25                  -20

Leu Lys Ile Leu Leu Cys Ser Val Ala Val Xaa Leu Ser Pro Ser Glu  
       -15                  -10                  -5                  1

Pro Leu Ala Pro  
               5

## (2) INFORMATION FOR SEQ ID NO: 324:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal



(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -38..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.9  
seq LPFLSLFWPWAPG/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

Met Gly Gly Phe Phe Pro Pro Thr Glu Val Arg Glu Val Cys Ala Asn  
-35 -30 -25

Gln Gly Ala Ala His Asn Arg Asp Arg Leu Pro Phe Leu Ser Leu Phe  
-20 -15 -10

Trp Pro Trp Ala Pro Gly Ala Val Ser Val Gly Gln Ala Arg Tyr Arg  
-5 1 5 10

Thr Pro Thr Thr Xaa Ala Pro Ser Ala Ser Val Pro Trp Pro Arg Ala  
15 20 25

Gly Thr Cys Arg Thr Pro Thr  
30

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: -30..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.9  
seq HLWILLLFSEFCWM/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

Met Lys Leu Phe Tyr Asn Gln Leu Val Ser Glu Thr Lys His Asp Phe  
-30 -25 -20 -15

Ala His Leu Trp Ile Leu Leu Leu Phe Ser Phe Cys Trp Met Ser Arg  
-10 -5 1

Ser Phe Phe<sup>1</sup> Phe Phe  
5

## (2) INFORMATION FOR SEQ ID NO: 326:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLFFHILFHSCFS/HL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

Met Pro Ser Glu Ser Pro Pro Leu Leu Phe Phe His Ile Leu Phe His  
-20 -15 -10 -5  
Ser Cys Phe Ser His Leu Leu  
1

## (2) INFORMATION FOR SEQ ID NO: 327:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -68..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLCSALAWQQSLS/GK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met Ser Ser Met Trp Ser Glu Tyr Thr Ile Gly Gly Val Lys Ile Tyr  
-65 -60 -55  
Phe Pro Tyr Lys Ala Tyr Pro Ser Gln Leu Ala Met Met Asn Ser Ile

-50                      -45                      -40  
 Leu Arg Gly Leu Asn Ser Lys Gln His Cys Leu Leu Glu Ser Pro Thr  
   -35                      -30                      -25  
 Gly Ser Gly Lys Ser Leu Ala Leu Leu Cys Ser Ala Leu Ala Trp Gln  
  -20                      -15                      -10                      -5  
 Gln Ser Leu Ser Gly Lys Pro Ala Asp Glu Gly Val Ser Glu Lys Ala  
                           1                      5                      10  
 Glu Val Gln Leu Ser Cys Cys Cys Ala Cys His Ser Lys Asp Phe Thr  
           15                      20                      25  
 Asn Asn Asp Met Asn Gln Gly Thr Ser Arg His Phe Asn Tyr Pro Ser  
       30                      35                      40  
 Thr Pro Arg  
   45

## (2) INFORMATION FOR SEQ ID NO: 328:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8  
seq FVRFLGFVSLQS/DP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

Met Ala Leu Phe Leu Glu Leu Phe Leu Asn Ser Tyr Ser Leu Leu Phe  
       -25                      -20                      -15  
 Val Arg Phe Leu Gly Phe Val Ser Cys Leu Gln Ser Asp Pro Ile Cys  
       -10                      -5                      1  
 Ser Phe Phe Phe Phe  
   5

## (2) INFORMATION FOR SEQ ID NO: 329:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids

- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8  
seq LMAGSSLSAGVSG/ED

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

Met Asn Glu Asp Glu Lys Glu Met Lys Glu Ile Leu Met Ala Gly Ser  
                  -20                  -15                  -10

Ser Leu Ser Ala Gly Val Ser Gly Glu Asp Lys Thr Glu Ile Leu Asn  
                  -5                  1                  5

Pro Thr Pro Xaa Met Ala Lys Ser Leu Thr Ile Asp Cys Leu Glu Leu  
          10                  15                  20

Ala Leu Pro Pro Glu Leu Ala Phe Gln Leu Asn Glu Leu Phe Gly Pro  
  25                  30                  35                  40

Val Gly Ile Asp Ser Gly Ser Leu  
                  45

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8  
seq IIPLIXXLSLCLC/LW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

Met Gly Ser Phe Leu Leu Gly Gly Ile Ile Pro Leu Ile Xaa Xaa Leu

-20                      -15                      -10  
Ser Leu Cys Leu Cys Leu Trp Trp Arg Ile Ile  
-5                                      1                                      5

## (2) INFORMATION FOR SEQ ID NO: 331:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8  
seq VCLLCSCGSCAWS/VG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

Met Leu Gln Val Ala Thr Thr Asn Tyr Leu Glu Leu Ala Arg Glu Val  
-30                                      -25                                      -20  
Lys Pro Val Cys Leu Leu Cys Ser Gly Cys Ser Cys Ala Trp Ser Val  
-15                                      -10                                      -5                                      1  
Gly Cys Val Xaa Glu Ser Glu Ser Glu  
                                    5                                      10

## (2) INFORMATION FOR SEQ ID NO: 332:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

(2) INFORMATION FOR SEQ ID NO: 333:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

(2) INFORMATION FOR SEQ ID NO: 334:

(A) LENGTH: 50 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -23..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.3  
seq SSCLLGLLHLSSQ/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

```

Met Pro Lys His Cys His Ser Phe Ile Thr Ser Ser Cys Leu Leu Gly
 -20 -15 -10

Leu Leu His Leu Ser Ser Gln Phe Ser Cys Pro Gly Arg Lys Leu His
 -5 1 5

Pro Ala Gln Arg His Thr Glu Ala Glu Thr Gln Gly Arg Pro Leu Ser
 10 15 20 25

Asp Arg

```

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.2  
seq FIXFPFLFPFSFS/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

```

Met Cys Leu Leu Phe Xaa Phe Ile Xaa Phe Pro Phe Leu Phe Pro Phe
 -15 -10 -5

Ser Phe Ser Gln Thr Phe Ser Phe Ser Gln His Trp Asn Thr Gly Gly
 1 5 10

Ser His Pro Glu Glu Leu Glu Arg Pro Gly Ala His Pro Arg Leu Lys
 15 20 25

```

Ala Arg Pro Gln Pro Pro Leu Phe His Pro Phe Ile Ser Ser  
 30 35 40

## (2) INFORMATION FOR SEQ ID NO: 336:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1  
seq LLVASGXAEGVSA/QS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

Met Ala Ser Glu Arg Xaa Pro Asn Arg Pro Xaa Cys Leu Leu Val Ala  
 -25 -20 -15 -10

Ser Gly Xaa Ala Glu Gly Val Ser Ala Gln Ser Phe Leu Xaa Cys Phe  
 -5 1 5

Thr Met Ala Ser Thr Xaa Phe Asn Leu Gln Val Ala Xaa Pro Gly Gly  
 10 15 20

Lys Ala Met Glu Phe Val Asp Val Thr Xaa Ser Asn Ala Arg Trp Val  
 25 30 35

Gln Asp  
 40

## (2) INFORMATION FOR SEQ ID NO: 337:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:



(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -25..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.1  
 seq LAFQLVFLRATSG/SC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

```

Met Phe Pro Asp Tyr Lys Leu Gly Gly Ser Tyr Leu Leu Ala Phe Gln
-25 -20 -15 -10

Leu Val Phe Leu Arg Ala Thr Ser Gly Ser Cys Ser Lys Tyr Arg Arg
 -5 1 5

His Leu His Asn Ile Asn Val Arg Pro Gly Leu Val Arg Leu Leu Gly
 10 15 20

Ser Cys Ile Gln Lys Gln Pro Gly
 25 30

```

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 109 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens.  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -25..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.1  
 seq LLLXLXLLLIAlE/IM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

```

Met Arg Arg Ile Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Leu Xaa
-25 -20 -15 -10

Leu Xaa Leu Leu Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser
 -5 1 5

Leu Cys Phe Asn Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro
 10 15 20

Trp Cys Glu Ala His Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr
 25 30 35

Asn Ser Asp Asn Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys
 40 45 50 55

```

Val Tyr Ala Thr Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu Gly Glu  
60 65 70  
Val Gly Arg Asp Leu Arg Met Leu Leu Cys Asp Ile Lys  
75 80

## (2) INFORMATION FOR SEQ ID NO: 339:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq TFLLLLFYNAGRS/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

Met Thr Phe Leu Leu Leu Phe Xaa Asn Ala Gly Arg Ser Leu Arg  
-10 -5 1  
Met Cys

## (2) INFORMATION FOR SEQ ID NO: 340:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq EMFLVLLVTGVHS/NK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

Met Arg Thr Val Val Leu Thr Met Lys Ala Ser Val Ile Glu Met Phe  
 -25 -20 -15

Leu Val Leu Leu Val Thr Gly Val His Ser Asn Lys Glu Thr Ala Lys  
 -10 -5 1 5

Lys Ile Lys Arg Pro Gly  
 10

## (2) INFORMATION FOR SEQ ID NO: 341:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq ISLLFIFFSIANS/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

Met Ser Ser Pro Leu Leu Val Glu Gln Ser Ser Thr Lys Ser Pro Lys  
 -40 -35 -30 -25

Ser Trp Ser Trp Ser Phe Leu Ala Phe Ser Cys Ile Ser Leu Leu Phe  
 -20 -15 -10

Ile Phe Phe Ser Ile Ala Asn Ser Ser Pro Cys Gly  
 -5 1

## (2) INFORMATION FOR SEQ ID NO: 342:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq IPLLLFFHLSFL/NS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

Met Tyr Leu Phe Cys Leu Phe Ser Val Ser Lys Thr Ile Pro Leu Leu  
-25 -20 -15 -10

Leu Leu Phe Phe His Leu Ser Phe Leu Asn Ser Leu  
-5 1

## (2) INFORMATION FOR SEQ ID NO: 343:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9  
seq CLLILKFLSPAET/SI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

Met Ile Val Cys Leu Leu Ile Leu Lys Phe Leu Ser Pro Ala Glu Thr  
-15 -10 -5

Ser Ile Leu Ser Ser Ile Ala Thr Tyr Gly Ala Phe Tyr Phe Ile Val  
1 5 10 15

Pro Leu Glu Val Ser Gln Ile Leu Gln Thr Gln  
20 25

## (2) INFORMATION FOR SEQ ID NO: 344:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -25..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.7  
seq LILCFLFILHTHT/HT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

```
Met Asp Lys Ser Ile Lys Ser Ser Ile Ile Trp Ser Leu Ile Leu Cys
-25 -20 -15 -10
Phe Leu Phe Ile Leu His Thr His Thr His Thr His Thr His Thr His
 -5 1 5
```

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -36..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.7  
seq IFDLLLLLXXSNQ/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

```
Met Phe Phe Ile Phe Ile Asn Gly Phe Thr Leu Leu Leu Met Thr Leu
-35 -30 -25
Ala Met Lys Pro Arg His Pro Ile Phe Asp Leu Leu Leu Leu Xaa
-20 -15 -10 -5
Xaa Ser Asn Gln Leu Pro Val Thr Gly
 1 5
```

(2) INFORMATION FOR SEQ ID NO: 346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq LWPFLTWINPALS/IC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

Met Cys Pro Ser Leu Glu Glu Ala Pro Ser Val Lys Gly Thr Leu Pro  
-60 -55 -50 -45  
Cys Ser Gly Gln Gln Gln Pro Phe Pro Phe Gly Ala Ser Asn Ile Pro  
-40 -35 -30  
Leu Leu Leu Gly Arg Ser Arg Lys Val Ala Arg Gly Ala Pro Val Leu  
-25 -20 -15  
Trp Pro Phe Leu Thr Trp Ile Asn Pro Ala Leu Ser Ile Cys Asp Pro  
-10 -5 1  
Leu Gly Ser Cys Gly Trp Gln  
5 10

## (2) INFORMATION FOR SEQ ID NO: 347:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6  
seq LLSALWFCHPCCL/CC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

```

Met Leu Gln Asp Leu Leu Ser Ala Leu Trp Phe Cys His Pro Cys Cys
 -15 -10 -5

Leu Cys Cys Gly Leu Cys Trp Leu Gly Val Asp Ala Gly Cys Ser Gln
 1 5 10 15

Gly Gly Ser Gly Cys Pro
 20

```

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (E) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6  
seq LLSLAAYLSGPHQ/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

```

Met Met Asp Leu Arg Pro Leu Leu Ser Leu Ala Ala Tyr Leu Ser Gly
 -15 -10 -5

Pro His Gln Glu Pro Ser Val Pro Thr Arg Asp Gly Asp Val Asn Asn
 1 5 10

Leu Pro Lys Pro Asn Pro Ala Arg Ser Val Lys Gln Gly Gly Ile Trp
 15 20 25

Lys Ala Glu Gln Glu Arg Val Glu Val Glu
 30 35

```

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Heart

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.6  
seq LLPGLPLVRTSFS/HF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Met Glu Met Pro Pro Cys Leu Leu Pro Gly Leu Pro Leu Val Arg Thr  
                  -15                  -10                  -5  
Ser Phe Ser His Phe Phe Ser Leu Ser Gly Gly Thr Thr Thr Ala Arg  
                  1                  5                  10  
Gly

## (2) INFORMATION FOR SEQ ID NO: 350:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -25..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.5  
seq GLAMLHVTRGVXG/SR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Thr Val Glu Leu Trp Leu Arg Leu Arg Gly Lys Gly Leu Ala Met  
-25                  -20                  -15                  -10  
Leu His Val Thr Arg Gly Val Xaa Gly Ser Arg Val Arg Val Xaa Xaa  
                  -5                  1                  5  
Xaa Leu Pro Ala Leu Leu Gly Xaa Pro Arg Ala Leu Ser Ser Xaa Ala  
          10                  15                  20  
Ala Lys Met Gly Xaa Tyr Arg Xaa Met Trp  
          25                  30



## (2) INFORMATION FOR SEQ ID NO: 351:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4  
seq LLILLCSSPPDRV/SY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

```

Met Ser Ile Glu Asp Phe Val Asn Arg Ser Ile Leu Leu Ile Leu Leu
 -20 -15 -10
Cys Ser Ser Pro Pro Asp Arg Val Ser Tyr Arg Ala Lys Val Leu His
 -5 1 5
Ser Leu Leu Gln Leu Pro Ala Gln
 10 15

```

## (2) INFORMATION FOR SEQ ID NO: 352:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4  
seq FALLFLFLVPVPG/HG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

```

Met Arg Ile His Tyr Leu Leu Phe Ala Leu Leu Phe Leu Phe Leu Val
-20 -15 -10 -5
Pro Val Pro Gly His Gly Gly Ile Ile Asn Thr Leu Gln Lys Tyr Xaa

```

1 5 10  
 Leu Gln Ser Gln Arg Arg Pro Val Cys Cys Ala Gln Leu Pro Ser Lys  
 15 20 25  
 Gly Glu Arg  
 30

## (2) INFORMATION FOR SEQ ID NO: 353:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -13...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4  
seq MCLLTALVTQVIS/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

Met Cys Leu Leu Thr Ala Leu Val Thr Gln Val Ile Ser Leu Arg Lys  
 -10 -5 1  
 Asn Ala Glu Arg Thr Cys Leu Cys Lys Arg Arg Trp Pro Trp Xaa Pro  
 5 10 15  
 Ser Pro Arg Ile Tyr Cys Ser Ser Thr Pro Cys Asp Ser Lys Phe Pro  
 20 25 30 35  
 Thr Val Tyr Ser Ser  
 40

## (2) INFORMATION FOR SEQ ID NO: 354:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -18..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq GLALVAGTPPSRS/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Met Met Gly Asn Pro Gly Leu Ala Leu Val Ala Gly Thr Pro Pro Ser  
-15 -10 -5

Arg Ser Cys Pro Gln Ala Asn Ser Gln Thr Arg  
1 5

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney.

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -38..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq PCVSLLLWAPRXFA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

Met Asn His Leu Met Pro Leu Thr Val Leu His Ser Val Leu Glu Met  
-35 -30 -25

Leu Arg Thr Pro Arg Thr Pro Pro Trp Pro Cys Val Ser Leu Leu Trp  
-20 -15 -10

Ala Pro Arg Xaa Phe Ala Ser Ser Cys Ser Gln Ala Phe Thr Thr Leu  
-5 1 5 10

Xaa Xaa Asn Cys Leu Leu Thr Asn Pro Ser Pro Thr Leu Asp Cys Asp  
15 20 25

Leu Pro Glu Gly Ser Glu Ile Leu Asn Ser Ser Leu Tyr Pro His Cys  
30 35 40

Leu Leu Ser Ala Trp Asn Thr Arg His Ser Thr  
45 50

## (2) INFORMATION FOR SEQ ID NO: 356:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq SLLXLRASQLSEG/DT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

Met Gly His Val Val Phe Gly Asp Ile Lys Asn Ser Leu Leu Xaa Leu  
                    -20                    -15                    -10

Arg Ala Ser Gln Leu Ser Glu Gly Asp Thr Xaa Xaa Xaa Xaa Cys Pro  
                    -5                            1                            5

Xaa Met Xaa Arg Gly Lys His Ile Ser Tyr  
            10                            15

## (2) INFORMATION FOR SEQ ID NO: 357:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -81..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq FLSLLXSVSETPG/SL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Ala Gly Gly Arg Arg Asp Tyr Ser Gln Leu Phe Gly Arg Gly Pro  
-30                    -75                    -70

Gly Arg Leu Ser Arg Ala Arg Ala Ser Val Val Arg Trp Ser Pro Arg  
 -65 -60 -55 -50  
 Ala Thr Ala Cys Pro Ala Pro Pro Ser Leu Pro Asp Leu Lys Arg Gln  
 -45 -40 -35  
 Glu Leu Val Ser Arg Ile Glu Cys Gly Cys Arg Gly Pro Val Gly Ala  
 -30 -25 -20  
 Thr Ala Asp Phe Phe Leu Ser Leu Leu Xaa Ser Val Ser Glu Thr Pro  
 -15 -10 -5  
 Gly Ser Leu Arg Xaa Asn Asp Leu Phe Phe Val Ser Gln Leu Ile Trp  
 1 5 10 15  
 Gly Arg

## (2) INFORMATION FOR SEQ ID NO: 358:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1  
seq LWCFFHSFISFSLSS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

Met Phe Trp Xaa Gly Ser Leu Trp Cys Phe His Ser Phe Ile Ser Phe  
 -15 -10 -5  
 Ser Leu Ser Ser Ser Arg  
 1

## (2) INFORMATION FOR SEQ ID NO: 359:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq FLLTFFSYSLHA/SR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

Met Ala Trp Pro Asn Val Phe Gln Xaa Gly Ser Leu Leu Ser Gln Phe  
-35 -30 -25

Xaa Xaa His His Val Val Val Phe Leu Leu Thr Phe Phe Ser Tyr Ser  
-20 -15 -10 -5

Leu Leu His Ala Ser Arg Lys Thr Phe Xaa Asn Val Lys Val Ser Ile  
1 5 10

Ser Glu Gln Trp Thr Pro Ser Ala Phe Asn Thr Ser Val Glu Leu Pro  
15 20 25

Val Glu Ile Trp Ser Ser Xaa His Leu Phe Pro Ser Ala Glu  
30 35 40

## (2) INFORMATION FOR SEQ ID NO: 360:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq WILAVGLSLPSSS/XI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

Met Ile Leu Arg Asn Leu Trp Ile Leu Ala Val Gly Leu Ser Leu Pro  
-15 -10 -5

Ser Ser Ser Xaa Ile Lys Phe His Phe Ser Leu Tyr Ser  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 361:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq LCGLLHLWLKVFS/LK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

```
Met Leu Thr Val Asn Asp Val Arg Phe Tyr Arg Asn Val Arg Ser Asn
-35 -30 -25 -20

His Phe Pro Phe Val Arg Leu Cys Gly Leu Leu His Leu Trp Leu Lys
 -15 -10 -5

Val Phe Ser Leu Lys Gln Leu Lys Lys
 1 5
```

## (2) INFORMATION FOR SEQ ID NO: 362:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq LFLNLCILAXPFS/KQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

```

Met Asn Leu Lys Pro Gly Leu Pro Cys Asn Leu Phe Leu Asn Leu Cys
 -20 -15 -10

Ile Leu Ala Xaa Pro Phe Ser Lys Gln Ile Ile Glu Leu Leu Glu Tyr
 -5 1 5

Val Ser Tyr His Pro Cys Val Leu Val Tyr Ser Glu Tyr Xaa Asn Ile
 10 15 20 25

Ser Ile Val Tyr Thr Leu
 30

```

## (2) INFORMATION FOR SEQ ID NO: 363:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq VVLAWGLLNVSMA/GM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

```

Met Met Gln Gly Glu Ala His Pro Ser Ala Ser Leu Ile Asp Arg Thr
-40 -35 -30 -25

Ile Lys Met Arg Lys Glu Thr Glu Ala Arg Lys Val Val Leu Ala Trp
 -20 -15 -10

Gly Leu Leu Asn Val Ser Met Ala Gly Met Ile Tyr Thr Glu Met Thr
 -5 1 5

Gly Lys Leu Ile Ser Ser Tyr Tyr Asn Val Thr Tyr Trp Pro Leu Trp
 10 15 20

Tyr Xaa Glu Leu Ala Leu Ala Ser Leu Phe Ser Leu Asn Ala Leu Phe
 25 30 35 40

Asp Phe Trp Arg Tyr Phe Lys Tyr Thr Val Ala Pro Thr Ser Leu Val
 45 50 55

Val Ser Pro Gly Arg
 60

```



## (2) INFORMATION FOR SEQ ID NO: 364:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq PXXLLILAHITQS/CP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

Met Met Asn Gln Thr His Pro Xaa Xaa Leu Leu Ile Leu Ala His Ile  
                  -15                  -10                  -5

Thr Gln Ser Cys Pro Trp Ala His Val Gly Ala Ala Pro Ser Ala Leu  
                  1                  5                  10

Leu Ile His Arg Trp Glu Leu Arg Gly Cys Ser Tyr Leu Lys Leu Phe  
          15                  20                  25

Leu Val Met Val Leu Ile Phe Glu Met Leu  
          30                  35

## (2) INFORMATION FOR SEQ ID NO: 365:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8  
seq GLVLLLSLAELF/KI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

```

Met Gly Leu Pro Glu Arg Arg Gly Leu Val Leu Leu Ser Leu Ala
-20 -15 -10 -5

Glu Ile Leu Phe Lys Ile Met Ile Leu Glu Gly Gly Gly Val Met Asn
 1 5 10

Leu Asn Pro Gly Asn Asn Leu Leu His Gln Pro Pro Ala Trp Thr Asp
 15 20 25

Ser Tyr Ser Thr Cys Asn Val Ser Ser Gly Phe Phe Gly Gly Gln Trp
 30 35 40

His Glu Ile His Pro Gln Tyr Trp Thr Lys Tyr Gln Val Trp Glu Trp
 45 50 55 60

Leu Gln His Leu Leu Asp Thr Asn Gln Leu Asp Ala Asn Cys Ile Pro
 65 70 75

Phe Gln Glu Phe Asp Ile Asn Gly Glu Xaa Arg
 80 85

```

## (2) INFORMATION FOR SEQ ID NO: 366:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8  
seq LCWALLYNCFSSS/CV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

```

Met Trp Gly Leu Glu Glu Asp Arg Ser Tyr Gln Gly Leu Arg Pro Leu
 -25 -20 -15

Cys Trp Ala Leu Leu Tyr Asn Cys Phe Ser Ser Ser Cys Val Pro Val
 -10 -5 1

Ala Leu Val
 5

```

## (2) INFORMATION FOR SEQ ID NO: 367:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -85..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq ALLASLGIAFSRS/RA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

Met Leu Cys Arg Asp Gly Ser Ala Cys Val Pro Arg Ser Arg Arg Leu  
-85 -80 -75 -70  
Pro Leu Pro Ala Ala Val Arg Ala His Gly Pro Met Ala Asp Xaa Xaa  
-65 -60 -55  
Asp Ser Ala Arg Gly Cys Val Val Phe Glu Asp Val Phe Val Tyr Phe  
-50 -45 -40  
Ser Arg Glu Glu Trp Glu Leu Leu Asp Asp Ala Gln Arg Leu Leu Tyr  
-35 -30 -25  
His Asp Val Met Leu Glu Asn Phe Ala Leu Leu Ala Ser Leu Gly Ile  
-20 -15 -10  
Ala Phe Ser Arg Ser Arg Ala Val Met Lys Leu  
-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 368:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -56..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.7  
seq FLCFLNLTSLSG/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

```

Met Leu Ile Thr Arg Leu Gln Ser Gly Ile Asp Phe Ala Ile Gln Leu
 -55 -50 -45

Asp Glu Ser Thr Asp Ile Gly Ser Cys Thr Thr Leu Leu Val Tyr Val
-40 -35 -30 -25

Arg Tyr Ala Trp Gln Asp Asp Phe Leu Glu Asp Phe Leu Cys Phe Leu
 -20 -15 -10

Asn Leu Thr Ser His Leu Ser Gly Leu Asp Ile Phe Thr Glu Leu Glu
 -5 1 5

Arg Arg Gly
 10

```

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 64 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

```
(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -38..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.7
 seq LAFLSCLAFLVLVD/TQ
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

```
Met Glu Ser Pro Gln Leu His Cys Ile Leu Asn Ser Asn Ser Val Ala
 -35 -30 -25

Cys Ser Phe Ala Val Gly Ala Gly Phe Leu Ala Phe Leu Ser Cys Leu
 -20 -15 -10

Ala Phe Leu Val Leu Asp Thr Gln Glu Thr Arg Ile Ala Gly Thr Arg
 -5 1 5 10

Phe Lys Thr Ala Phe Gln Leu Leu Asp Xaa Ile Leu Ala Val Leu Trp
 15 20 25
```

## (2) INFORMATION FOR SEQ ID NO: 370:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq DHLFLLFPRSCSS/LV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

Met Ser Asn Lys Tyr Ile Lys Pro Ser Met Ser Pro Gly Asn Thr Asp  
-25 -20 -15  
His Leu Phe Leu Leu Phe Pro Arg Ser Cys Ser Ser Leu Val  
-10 -5 1

## (2) INFORMATION FOR SEQ ID NO: 371:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq FFFFLFLLPPXP/TG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Val Glu Leu Lys Gln Leu Gly Pro Arg Ser Phe Phe Phe Phe Leu  
-20 -15 -10  
Phe Leu Leu Pro Pro Xaa Pro Pro Thr Gly  
-5 1

## (2) INFORMATION FOR SEQ ID NO: 372:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq LILPALFFFPLHC/TF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Met Pro Tyr Val Thr Ile Pro Tyr Ile Ile Val Tyr Ser Leu Ile Leu  
-25 -20 -15

Pro Ala Leu Phe Phe Phe Pro Leu His Cys Thr Phe His Gly Leu Thr  
-10 -5 1 5

Tyr Tyr Ile Ser Cys Val Cys Ser Leu Ser Leu Pro Thr  
10 15

## (2) INFORMATION FOR SEQ ID NO: 373:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq LLLCMDLPHSVLS/NW

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

Met Pro Pro Leu Ala Ala Val Met Gly Ser Leu Pro Leu Leu Leu Cys

-25                      -20                      -15                      -10  
Met Asp Leu Pro His Ser Val Leu Ser Asn Trp  
                         -5                                      1

## (2) INFORMATION FOR SEQ ID NO: 374:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: AMINO ACID
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo Sapiens
  - (D) DEVELOPMENTAL STAGE: Fetal
  - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: -21..-1
  - (C) IDENTIFICATION METHOD: Von Heijne matrix
  - (D) OTHER INFORMATION: score 5.5  
seq EFLFLGFPSNSWP/HR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met Leu Gln Ile Pro Glu Arg Arg Glu Phe Leu Phe Leu Gly Phe Pro  
-20                      -15                                      -10  
Ser Asn Ser Trp Pro His Arg  
-5                                      1

## (2) INFORMATION FOR SEQ ID NO: 375:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 amino acids
  - (B) TYPE: AMINO ACID
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo Sapiens
  - (F) TISSUE TYPE: Muscle
- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: -18..-1
  - (C) IDENTIFICATION METHOD: Von Heijne matrix
  - (D) OTHER INFORMATION: score 5.5  
seq FLITLFCCCVVVG/FF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

Met Phe Phe Val His Phe Leu Ile Thr Leu Phe Cys Cys Cys Val Val  
                   -15                                  -10                                  -5

Val Gly Phe Phe Gly His Asp His Ser Phe Ile Ser Gln Phe Ile Leu  
                   1                                          5                                          10

Val Thr Trp Ala Arg Ala Gly  
                   15                                          20

## (2) INFORMATION FOR SEQ ID NO: 376:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq CLLHLRCLQLYWA/AR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

Met Ala Cys Phe Gly Glu Lys Arg His Ala Lys Ser Cys Leu Leu His  
   -25                                  -20                                  -15                                  -10

Leu Arg Cys Leu Gln Leu Tyr Trp Ala Ala Arg  
                                   -5                                          1

## (2) INFORMATION FOR SEQ ID NO: 377:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix



(D) OTHER INFORMATION: score 5.4  
seq PLSLALQSSCCLC/LT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

Met Val Asp Arg Asp Glu Asn Ile Leu Leu Lys Gln Ile Tyr Ser Pro  
-25 -20 -15  
Leu Ser Leu Ala Leu Gln Ser Ser Cys Cys Leu Cys Leu Thr Ser Cys  
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq VSVSLCVCDCVRG/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

Met Lys Val Lys Pro Pro Phe Val Ser Val Ser Leu Cys Val Cys Asp  
-20 -15 -10 -5  
Cys Val Arg Gly Ser Thr Leu Thr Trp Asn Arg Leu Leu Arg Val Gly  
1 5 10  
Gly

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq ILLTSCFYTLVSS/TF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

```

Met Ile Ser Ser Cys Gly Val Lys Tyr Leu Phe Ser His Ala Ser Leu
 -35 -30 -25

Phe Phe Met Val Gly Ser Thr Gly Ser Leu Ile Leu Leu Thr Ser Cys
 -20 -15 -10

Phe Tyr Thr Leu Val Ser Ser Thr Phe Leu Gln Lys Leu Ser Ser Leu
 -5 1 5

Leu Leu Ile Leu Phe Thr Glu Thr Ser Val Leu Met Leu Lys Thr Phe
 10 15 20 25

Val Ala Asn Ser Cys Cys Xaa Leu Trp Ser His Asn Cys Ile Asn Phe
 30 35 40

Phe Lys Lys Val Xaa Pro Ser Tyr Cys Xaa Ser Ser Leu Leu Phe Leu
 45 50 55

Ala Val Pro Arg
 60

```

## (2) INFORMATION FOR SEQ ID NO: 380:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq SFLCNFLVSLSL/FL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

```

Met Gly Gly Gly Ile Ala Glu Ser Phe Leu Cys Asn Phe Leu Val Ser
-20 -15 -10 -5

Leu Ser Leu Ser Phe Leu His Gly Arg

```

1

5

## (2) INFORMATION FOR SEQ ID NO: 381:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq LAYFLCCQGVIFG/SL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

Met Asp Ala Leu Glu Arg Gly Ser Leu Arg Asn Glu Gln Ala Leu Val  
          -30                          -25                          -20  
  
Ile Tyr Ala Gly Leu Ala Tyr Phe Leu Cys Cys Gln Gly Val Ile Phe  
          -15                          -10                          -5  
  
Gly Ser Leu Pro Ser Asn Ala Gly Ala Gly Pro Leu Gly Trp Ser Ser  
      1                              5                              10                              15

## (2) INFORMATION FOR SEQ ID NO: 382:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq SLWFLPLPTHVYT/HT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

Met Glu Tyr Leu Phe Gln Gln Pro Gly His Ser Arg Gly Glu Ala Arg  
                   -35                  -30                  -25

Ala Ala Ala Ala Ser Leu Glu Thr Leu Ser Ser Leu Trp Phe Leu Pro  
                   -20                  -15                  -10

Leu Pro Thr His Val Tyr Thr His Thr His Ala Asn  
                   -5                  1                  5

## (2) INFORMATION FOR SEQ ID NO: 383:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq SSMLITILSFIFA/LG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

Met Val Ser Ser Met Leu Ile Thr Ile Leu Ser Phe Ile Phe Ala Leu  
   -15                  -10                  -5                  1

Gly Tyr His Thr Ala Ser Tyr Pro Val Ser Leu His Pro Leu Ser Phe  
                   5                  10                  15

Phe Leu His  
                   20

## (2) INFORMATION FOR SEQ ID NO: 384:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -18..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.3  
 seq MNLVVSALASSAXG/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

Met Pro Leu Phe Thr Met Asn Leu Val Ser Ala Leu Ala Ser Ser Ala  
                   -15                  -10                  -5  
 Xaa Gly Gln Arg Gly Ala Gly Pro Ala Leu Trp His Leu Cys  
                   1                          5                          10

(2) INFORMATION FOR SEQ ID NO: 385:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -39..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.2  
 seq LILLHCSIRVFF/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

Met Ile Cys Lys His Tyr Cys Ile Lys Lys Asn Asn Leu Asp Tyr Leu  
                   -35                  -30                  -25  
 Asn Arg Met Val Tyr Ser Ala Gln Leu Lys Leu Ile Leu Leu Leu His  
                   -20                  -15                  -10  
 Cys Ser Ile Arg Val Phe Phe Phe Phe  
                   -5                          1

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -53..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq SFLLLQLIHEDKA/IQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

```

Met Lys Ile Pro Val Trp His Lys Thr Cys Phe Leu Lys Ser Glu Ser
 -50 -45 -40

Phe Ser Pro Asp Asn Leu Ser Val Ser Leu Pro Cys Arg Pro Ser Gln
 -35 -30 -25

Val Pro Ser Gln Gly Gln Gly Lys Ser Phe Leu Leu Leu Gln Leu Ile
 -20 -15 -10

His Glu Asp Lys Ala Ile Gln Asn Glu Ala Ile Phe Gln Pro Ser Leu
 -5 1 5 10

Gln Leu

```

## (2) INFORMATION FOR SEQ ID NO: 387:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq FGCTFVAFXPAFA/LS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

```

Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Xaa Pro
 -15 -10 -5

Ala Phe Ala Leu Ser Leu Ile Thr Val Ala Gly Asp Arg Gly
 1 5 10

```

## (2) INFORMATION FOR SEQ ID NO: 388:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq LWSSCWLA PLADG/ML

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

```

Met Val Gly Gly Leu Asp Pro Pro Gly Arg Arg Arg Phe Gln Lys Gly
 -30 -25 -20

Phe Asp Trp Arg Asn Leu Trp Ser Ser Cys Trp Leu Ala Pro Leu Ala
 -15 -10 -5

Asp Gly Met Leu Arg Tyr Met Gly Gln Xaa Gln Arg Xaa Ala Ser Asn
 1 5 10

Pro Glu Gly Ser Thr Leu Glu Ala Arg Pro Pro Ala Pro Xaa Ala Ser
 15 20 25 30

Val Ser Pro Ser Val Xaa Xaa Pro His Arg Pro Trp Ala Ala Lys Met
 35 40 45

Glu Thr Val Ser Pro Ala Thr Ser Xaa Ile Ala Gly Gly
 50 55

```

## (2) INFORMATION FOR SEQ ID NO: 389:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.1  
seq SLLVVSCFYQISG/RW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

Met Ser Lys Met Pro Val Phe Ala Ser Leu Leu Val Val Ser Cys Phe  
-20 -15 -10  
Tyr Gln Ile Ser Gly Arg Trp  
-5 1

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR  
(ii) MOLECULE TYPE: PROTEIN  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney  
(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -15..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.1  
seq VTQLLPFSSPDSA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Met Xaa Val Thr Gln Leu Leu Pro Phe Ser Ser Pro Asp Ser Ala Gly  
-15 -10 -5 1  
Pro Phe Leu Ser Pro Phe Ser  
5

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR  
(ii) MOLECULE TYPE: PROTEIN  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle



## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq SFHFLPWALGAMA/SS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

```

Met Gly Lys Ala Trp Gln Glu Met Arg Val Glu Trp Gly Ala Asp Lys
 -30 -25 -20

Gly Asn Val Arg Ser Ser Phe His Phe Leu Pro Trp Ala Leu Gly Ala
 -15 -10 -5

Met Ala Ser Ser Glu Gln Gly Lys Glu Arg Ser Asn Leu Cys Phe Arg
 1 5 10

Lys Thr Pro Leu Ala Ile Thr Gly Arg Gly Ile Ala Arg Arg Pro Gly
 15 20 25 30

Gly Gly Trp Met Gly Met Trp Val
 35

```

## (2) INFORMATION FOR SEQ ID NO: 392:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1  
seq VIRLSQFLLKCWP/RT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

```

Met Lys Val Met Met Arg Lys Arg Lys Lys Lys Asp Gln Cys Leu Pro
 -45 -40 -35

Gly Ile Cys Arg Ser Leu Lys Arg Arg Lys Ser Pro Arg Ser Pro Gly
 -30 -25 -20

Met Lys Val Ile Arg Leu Ser Gln Phe Leu Leu Lys Cys Trp Pro Arg
 -15 -10 -5 1

Thr Ser Leu Thr Ala Ala Thr

```

5

## (2) INFORMATION FOR SEQ ID NO: 393:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5  
seq SFSIXTLLWGLNC/KR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

```

Met Thr Phe Ser Phe Phe Cys Phe Phe Pro Gly Phe Lys Pro Leu Leu
-35 -30 -25

Phe His Tyr Phe Leu Phe Xaa Ser Phe Ser Ile Xaa Thr Leu Leu Trp
-20 -15 -10 -5

Gly Leu Asn Cys Lys Arg Ser Trp Asn Ile Asn Leu Arg Ile Val Xaa
 1 5 10

Ser Tyr Ser Ser Gly Tyr
 15

```

## (2) INFORMATION FOR SEQ ID NO: 394:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5

seq RLLILSGCLVYG/TA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

Met Ala Gly Gly Met Lys Val Ala Val Ser Pro Ala Val Gly Pro Gly  
 -40 -35 -30

Pro Trp Gly Ser Gly Val Gly Gly Gly Gly Thr Val Arg Leu Leu Leu  
 -25 -20 -15 -10

Ile Leu Ser Gly Cys Leu Val Tyr Gly Thr Ala Glu Thr Asp Val Asn  
 -5 1 5

Val Val Met Leu Gln Glu Ser Gln Val Cys Glu Lys Arg Ala Ser Leu  
 10 15 20

Gly

(2) INFORMATION FOR SEQ ID NO: 395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5  
seq PLLSCSCP?PLLG/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

Met Val Glu Met Thr Gly Val Trp Gln Cys Gln Ala Glu Ala Val Lys  
 -30 -25 -20

Gly Leu Pro Pro Leu Leu Ser Cys Ser Cys Pro Pro Pro Leu Leu Gly  
 -15 -10 -5

Glu Gly His Ala Gln Ala Ser Pro Leu Ala Gln Glu Glu Asp Lys Lys  
 1 5 10 15

His Thr Glu Gln Thr Gln Ala Thr Ser Pro Thr Gln Pro  
 20 25

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -21..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5  
 seq AGLLPPLLGNAPG/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Met Gln Ile Thr Pro Gly Ser Ala Ala Gly Leu Leu Pro Leu Leu Leu  
 -20 -15 -10  
 Gly Asn Ala Pro Gly Glu Ser Val Gly Gly Arg Cys Xaa Pro Gly Cys  
 -5 1 5 10  
 Trp

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -17..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5  
 seq TWLLLTQLQNSVFT/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Met Ile Leu Ser Thr Trp Leu Leu Leu Thr Leu Gln Asn Ser Val Phe  
 -15 -10 -5  
 Thr Ser Phe Arg Ile Ser Pro Asn Arg Ile Gln Ser Met Leu Pro Pro  
 1 5 10 15  
 Met

## (2) INFORMATION FOR SEQ ID NO: 398:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5  
seq VCIVLALCHTSRP/MS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Met Ala Phe His Ser Tyr Trp Gly Lys Ser Leu Gln Ser Phe Lys Thr  
-30 -25 -20

Phe Met Arg Val Cys Ile Val Leu Ala Leu Cys His Thr Ser Arg Pro  
-15 -10 -5

Met Ser Tyr His Val Pro Leu Ala Ala Gly Ser Pro Leu Met His Trp  
1 5 10 15

Ser Pro Cys Ser Pro Val Pro Phe Ile Gly  
20 25

## (2) INFORMATION FOR SEQ ID NO: 399:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
seq RFTLLPLVLHSQS/SC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Lys Leu Arg Phe Thr Leu Leu Pro Leu Val Leu His Ser Gln Ser  
 -15 -10 -5  
 Ser Cys Val Phe Trp Lys Ala Gly  
 1 5

## (2) INFORMATION FOR SEQ ID NO: 400:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -30..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
seq FIPFLVIYSFVLS/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met Met Ile Ile Leu Gly Phe Ala Phe Cys Pro Gly His Phe Arg Phe  
 -30 -25 -20 -15  
 Asn Phe Ile Pro Phe Leu Val Ile Tyr Ser Phe Val Leu Ser Ser Pro  
 -10 -5 1  
 His Thr His Arg Glu Pro Tyr Ser Pro Val Ala Asp Phe Asn Glu Cys  
 5 10 15  
 Asn Arg Ser  
 20

## (2) INFORMATION FOR SEQ ID NO: 401:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -27..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.9  
 seq CLLSYIALGAIHA/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile Cys Leu  
 -25 -20 -15  
 Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys Arg Arg  
 -10 -5 1 5  
 Ala Phe Gln Glu Glu Gly Arg Ala Xaa Ala Lys Thr Gly Val  
 10 15

(2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -15..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.8  
 seq LFLNLPLVIGTIP/LH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

Met Asp Leu Phe Leu Asn Leu Pro Leu Val Ile Gly Thr Ile Pro Leu  
 -15 -10 -5 1  
 His Pro Phe Gly Ser Arg Thr Ser Ser Val Ser Ser Gln Cys Ser Met  
 5 10 15  
 Asn Met Asn Trp Leu Ser Leu Ser Leu Pro Glu  
 20 25

(2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -73..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8  
seq VIRSTLVLSQCCLC/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

```
Met Xaa Lys Asn His Arg Asn Lys Lys Ser Ile His Phe Pro Leu Cys
 -70 -65 -60
Thr Ile Pro Ser Xaa Met Xaa Lys Ser Cys Thr Leu Pro Leu Gln Arg
 -55 -50 -45
Thr Trp Asp Xaa Xaa Pro Ser Phe Val His Trp Xaa Gln Ala Arg Leu
 -40 -35 -30
Gln Ser Pro Pro Xaa Ser His Leu Val Xaa Leu Ser Val Ile Arg Ser
 -25 -20 -15 -10
Thr Leu Val Leu Ser Gln Cys Leu Cys Ser Arg Xaa Pro Tyr Phe Ser
 -5 1 5
Ala Met Met Thr Pro Lys Cys Lys Ser Ile Xaa Ala Gly Asn Ser Gly
 10 15 20
Met Pro Lys Arg Asn Cys Lys Val Leu Pro Ser Ser Glu Lys Met Xaa
 25 30 35
Val His
 40
```

(2) INFORMATION FOR SEQ ID NO: 404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1



(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.8  
seq SFIALVYSSLSFQ/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

Met Ser Phe Ile Ala Leu Val Tyr Ser Ser Leu Ser Phe Gln Lys Val  
-10 -5 1  
Pro Gly

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR  
(ii) MOLECULE TYPE: PROTEIN  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney  
(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -22..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.7  
seq IVLFLNSXFPIIC/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

Met Val Phe Asp Thr Leu Lys Ser Arg Ile Val Leu Phe Leu Asn Ser  
-20 -15 -10  
Xaa Phe Pro Ile Ile Cys Ser Arg  
-5 1

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 69 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR  
(ii) MOLECULE TYPE: PROTEIN  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney  
(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -59..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq IFLFSILLMSLRT/FH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

```

Met Leu Glu Met Glu Met Thr Trp Leu Arg Leu Cys Asp Glu Cys Ser
 -55 -50 -45

Arg Trp Gly Met Ala Ser Ala Trp Gly Arg Gly Gly Lys Leu Leu Gly
 -40 -35 -30

Ala Gln Val Ala Leu His Pro Arg Asn Cys Ser Lys Ala Lys Ile Phe
 -25 -20 -15

Leu Phe Ser Ile Leu Leu Met Ser Leu Arg Thr Phe His Cys Asn Tyr
 -10 -5 1 5

Phe Arg Gly Asn Gly
 10

```

(2) INFORMATION FOR SEQ ID NO: 407:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 99 amino acids
  - (B) TYPE: AMINO ACID
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo Sapiens
  - (D) DEVELOPMENTAL STAGE: Fetal
  - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: -17..-1
  - (C) IDENTIFICATION METHOD: Von Heijne matrix
  - (D) OTHER INFORMATION: score 4.7  
seq MLFFLGALCRESG/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

```

Met Asp Asp Leu Met Leu Phe Phe Leu Gly Ala Leu Cys Arg Glu Ser
 -15 -10 -5

Gly Val Pro Ser Leu Gly Lys Gln Glu Arg Met Arg Ala Tyr Ala Ala
 1 5 10 15

Glu Met Pro Pro Leu Leu Pro Ser Pro Cys Pro Pro Pro Ser His Leu
 20 25 30

Pro Lys Pro Ala Ser Pro Cys Pro Tyr Pro Leu Xaa Leu Leu Thr Phe
 35 40 45

```

Pro Val Gly Val Pro His Leu Pro Gly Thr Arg Leu Gln Cys Gln Gly  
           50                          55                          60  
 Leu Gly His Ser Leu Xaa Arg Ala Glu Arg Gly Val Gly Gly Gly Val  
           65                          70                          75  
 Ser Pro Gly  
           80

## (2) INFORMATION FOR SEQ ID NO: 408:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq LPTLLLLPVGAPG/KK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

Met Val Leu Gly Ala Leu Asn Leu Pro Ser Gln Glu Leu Pro Thr Leu  
 -25                          -20                          -15                          -10  
 Leu Leu Leu Pro Val Gly Ala Pro Gly Lys Lys Lys Gly Met Glu Gly  
                           -5                          1                          5  
 Lys Thr Pro Leu Asp Leu Phe Ala His Phe Gly Pro Glu Pro Gly Asp  
           10                          15                          20  
 His Ser Asp Pro Leu Pro Pro Ser Ala Pro Ser Pro Thr Arg Glu Gly  
           25                          30                          35  
 Ala Leu Thr Pro Pro Pro Gly  
           40                          45

## (2) INFORMATION FOR SEQ ID NO: 409:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq QTFVSFLSIPVLG/LV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

```

Met Leu Val Ser Lys Ile Gln Thr Phe Val Ser Phe Leu Ser Ile Pro
 -15 -10 -5
Val Leu Gly Leu Val Pro Asp His Ile Leu Gln Leu Ile Thr Glu Lys
 1 5 10
Glu Thr
 15

```

## (2) INFORMATION FOR SEQ ID NO: 410:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq LLSTGLNILGTQA/FR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

```

Met Cys Asn Pro Val Ala His Thr Phe Arg Gly Val His Glu His His
 -30 -25 -20
Ala Met Leu Leu Ser Thr Gly Leu Asn Ile Leu Gly Thr Gln Ala Phe
 -15 -10 -5 1
Arg Tyr Glu Asp Gly Gln Leu
 5

```

## (2) INFORMATION FOR SEQ ID NO: 411:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq ILLWEACTGRCQA/SL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Gln Cys Trp Ile Leu Leu Trp Glu Ala Cys Thr Gly Arg Cys Gln  
-15 -10 -5  
Ala Ser Leu Leu Ser Pro Trp Pro Arg Gly Gly Arg Gly Lys Leu Val  
1 5 10 15  
Ala Val Val Ala Ala Lys Trp Leu Ala Ala Ile Cys Gly Ile Trp Ala  
20 25 30  
Ile Lys Glu Met Pro Ser His Gly His Ser Leu Gln Ala Gly Ala Gly  
35 40 45  
Glu Gly Ala Leu Val Thr Trp Ser Leu Gln Thr Ser Phe Gly Val Lys  
50 55 60  
Gln Tyr Lys Trp Gly Val Val Trp His Glu Ala Asn Leu Leu Leu  
65 70 75

## (2) INFORMATION FOR SEQ ID NO: 412:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

- (B) LOCATION: -25...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: . score 4.6  
seq VLCILGCHGNLCC/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

Met Thr Gly Tyr Pro Trp Ala Asn Ser Ile Thr Thr Val Leu Cys Ile  
-25                      -20                      -15                      -10  
Leu Gly Cys His Gly Asn Leu Cys Cys Glu Pro Ala Val Arg Ala Leu  
                    -5                      1                      5  
Gly

(2) INFORMATION FOR SEQ ID NO: 413:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 amino acids
  - (B) TYPE: AMINO ACID
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo Sapiens
  - (D) DEVELOPMENTAL STAGE: Fetal
  - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: -24...-1
  - (C) IDENTIFICATION METHOD: Von Heijne matrix
  - (D) OTHER INFORMATION: score 4.6  
seq IFTALFLXLHSA/IN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

Met Val Ser Cys Asp Val Xaa Ser Tyr Val Ile Ile Phe Thr Ala Leu  
                    -20                      -15                      -10  
Phe Leu Xaa Leu His Ser Val Ala Ile Asn Glu Glu Phe  
                    -5                      1                      5

(2) INFORMATION FOR SEQ ID NO: 414:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 amino acids
  - (B) TYPE: AMINO ACID
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -20..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.6  
 seq LFAIFLMCLKSIG/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Met Lys Ser Phe Asp Lys Lys Leu Phe Ala Ile Phe Leu Met Cys Leu  
 -20 -15 -10 -5

Lys Ser Ile Gly Ser Val Val Met Pro Gln Pro  
 1 5

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -33..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.5  
 seq LASLFGLDQXAXG/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

Met Phe Gly Ala Gly Asp Glu Asp Asp Thr Asp Phe Leu Ser Pro Ser  
 -30 -25 -20

Gly Gly Ala Arg Leu Ala Ser Leu Phe Gly Leu Asp Gln Xaa Ala Xaa  
 -15 -10 -5

Gly His Gly Asn Glu Phe Phe Gln Tyr Thr Ala Pro Lys Gln Pro Lys  
 1 5 10 15

Lys Gly Gln Gly Thr Ala Ala Thr Gly Asn Gln Ala Xaa Pro Lys Thr  
 20 25 30

Ala Pro Ala Xaa Met Ser Thr Pro Thr Ile Leu Val Ala Thr Ala Val  
 35 40 45

His Ala Tyr Arg Tyr Thr Xaa Gly Xaa Tyr Val Lys Gln Xaa Asn Leu  
 50 55 60

Val Leu Gln Phe Trp  
65

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq RFLSLSAADGXDX/SX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

Met Val Leu Thr Leu Gly Glu Ser Trp Pro Val Leu Val Gly Arg Arg  
-25 -20 -15  
Phe Leu Ser Leu Ser Ala Ala Asp Gly Xaa Asp Xaa Ser Xaa Asp Ser  
-10 -5 1  
Trp Asp Val Glu Arg Val Ala Glu Trp Pro Trp Leu Ser Gly Thr Ile  
5 10 15 20  
Arg Ala Val Ser His Thr Asp Val Thr Lys Lys Asp Leu Lys  
25 30

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1



(C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.4  
 seq LTSVFQAMIWSQG/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

Met Val Ile Glu Leu Thr Ser Val Phe Gln Ala Met Ile Trp Ser Gln  
           -15                          -10                          -5  
 Gly Val Ser Asp Ser Ser Lys  
           1                                  5

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -50..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.4  
 seq ILFLFYFPAAYYA/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

Met Glu Ser Thr Leu Gly Ala Gly Ile Val Ile Ala Glu Ala Leu Gln  
   -50                          -45                          -40                          -35  
 Asn Gln Leu Ala Trp Leu Glu Asn Val Trp Leu Trp Xaa Xaa Leu Xaa  
                           -30                          -25                          -20  
 Xaa Xaa Ile Pro Xaa Ile Leu Phe Leu Phe Tyr Phe Pro Ala Ala Tyr  
                           -15                          -10                          -5  
 Tyr Ala Ser Arg Arg Val Gly Ile Ala Val Leu Trp Ile Ser Leu Ile  
           1                                  5                                  10  
 Thr Glu Trp Leu  
   15

(2) INFORMATION FOR SEQ ID NO: 419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids  
 (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN .

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -25..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.4  
seq VLVGVFLSTFLYC/EC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

Met Ile Ile Val Ser Glu Leu Gly Thr Pro Thr Gly Val Leu Val Gly  
-25 -20 -15 -10

Val Phe Leu Ser Thr Phe Leu Tyr Cys Glu Cys Val Lys Gly Pro  
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN .

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -22..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.4  
seq GFLLCPLVCGLRR/WT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

Met Asn Trp Asn Val Arg Gly Thr Arg Gly Phe Leu Leu Cys Pro Leu  
-20 -15 -10

Val Cys Gly Leu Arg Arg Trp Thr Ser Pro Asp Cys Cys Leu Ile Glu  
-5 1 5 10

Lys Thr His Arg Gly  
15

## (2) INFORMATION FOR SEQ ID NO: 421:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq RGLLLGLAVAAAA/VR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

Met Leu Arg Cys Gly Gly Arg Gly Leu Leu Leu Gly Leu Ala Val Ala  
                  -15                  -10                  -5  
Ala Ala Ala Val Arg  
                  1

## (2) INFORMATION FOR SEQ ID NO: 422:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq ILLMIVFSIFLLL/CN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

Met Ile Leu Leu Met Ile Val Phe Ser Ile Phe Leu Leu Leu Cys Asn  
                  -10                  -5                  1  
Leu Thr Asp Phe Tyr Leu Phe Arg Ser Asp Gly  
                  5                  10

## (2) INFORMATION FOR SEQ ID NO: 423:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4  
seq SLLFIFRSILISC/FS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

Met Ser Leu Leu Phe Ile Phe Arg Ser Ile Leu Ile Ser Cys Phe Ser  
                  -10                  -5                          1

Gly Asp Phe Phe Phe Phe  
                  5

## (2) INFORMATION FOR SEQ ID NO: 424:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
seq SKVLIQLSQAFWA/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

Met Pro Leu Ile Ser Lys Val Leu Ile Gln Leu Ser Gln Ala Phe Trp  
          -15                  -10                          -5

Ala Ser Pro Glu Gly Arg Asn Ser Ser Gly Ser Lys Arg Lys Gln Leu  
 1 5 10 15  
 Val Ala Ala Val Glu Met Arg Tyr Cys Lys Arg Gln Gln Gly  
 20 25

## (2) INFORMATION FOR SEQ ID NO: 425:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
seq VLLGSTAMATSLT/NV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

Met Asp Thr Ser Ser Val Gly Gly Leu Glu Leu Thr Asp Gln Thr Pro  
 -25 -20 -15  
 Val Leu Leu Gly Ser Thr Ala Met Ala Thr Ser Leu Thr Asn Val Gly  
 -10 -5 1  
 Asn Ser Phe Ser Gly Pro Ala Asn Pro Leu Val Ser Arg Ser Asn Lys  
 5 10 15  
 Phe Gln Asn Ser Ser Val Glu Asp Asp Asp Val Val Phe Ile Glu  
 20 25 30 35  
 Pro Val Gln Pro Pro Pro Pro Ser Val Pro Val Val Ala Asp Gln Arg  
 40 45 50  
 Thr Ile Thr Phe Thr Ser Ser Lys Asn Xaa Glu Leu Gln Gly Asn Asp  
 55 60 65  
 Ser Lys Ile Thr Pro Ser Ser Lys Glu Leu Ala Ser  
 70 75

## (2) INFORMATION FOR SEQ ID NO: 426:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -31..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.3  
seq ILLLTHVPPWILE/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

```
Met Asp Thr Gly Glu Ser Phe Ser Pro His Thr Ser Cys Arg Gly His
-30 -25 -20

Trp Arg Ile Leu Leu Leu Thr His Val Pro Pro Trp Ile Leu Glu Asn
-15 -10 -5 1

Pro Ser Cys His Thr Arg Pro Ala Val Asp Thr Gly Glu Ser Phe Ser
 5 10 15

Pro Gln Arg
 20
```

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -31..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.3  
seq LVLLSVLKEPVSR/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

```
Met Pro Tyr Leu Asp Pro Tyr Ile Thr Gln Pro Ile Ile Gln Ile Glu
-30 -25 -20

Arg Lys Leu Val Leu Leu Ser Val Leu Lys Glu Pro Val Ser Arg Ser
-15 -10 -5 1
```

Ile Phe Asp Tyr Ala Leu Arg Ser Lys Asp Ile Thr Ser Leu Phe Arg  
                   5                  10                  15  
 His Leu His Met Arg Gln Lys Lys Arg Asn Gly Ser Leu Pro Asp Cys  
           20                  25                  30  
 Pro Pro Pro Glu Asp Pro Ala Ile Ala Gln Leu Leu Lys Lys Leu Leu  
       35                  40                  45  
 Ser Gln Gly Met Thr Glu Glu Glu Asp Lys Leu Leu Ala Leu Lys  
   50                  55                  60                  65  
 Asp Phe Met Met

## (2) INFORMATION FOR SEQ ID NO: 428:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
seq VLLGSTAMATSLT/NV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

Met Asp Thr Ser Ser Val Gly Gly Leu Glu Leu Thr Asp Gln Thr Pro  
                   -25                  -20                  -15  
 Val Leu Leu Gly Ser Thr Ala Met Ala Thr Ser Leu Thr Asn Val Gly  
           -10                  -5                  1  
 Asn Ser Phe Ser Gly Pro Ala Asn Pro Leu Val Ser  
       5                  10                  15

## (2) INFORMATION FOR SEQ ID NO: 429:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq FGLLDFVQCCDS/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

Met His Val Leu Phe Asn Ile Val Thr Thr Asn Xaa Xaa Asn His Phe  
-25 -20 -15  
Gly Leu Leu Asp Phe Val Val Gln Cys Cys Asp Ser Leu Arg Asn His  
-10 -5 1  
Xaa Xaa Ser Phe Gln Ser Ser Tyr Leu Arg Leu Asn His Ser Xaa His  
5 10 15 20  
Thr Cys

## (2) INFORMATION FOR SEQ ID NO: 430:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq TAYWLSFMSWAQS/SS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

Met Pro Pro Gln Ser Cys Cys Ser Lys Thr Ala Tyr Trp Leu Ser Phe  
-20 -15 -10  
Met Ser Trp Ala Gln Ser Ser Ser Phe Gly Ser Arg Xaa Glu Ser Thr  
-5 1 5 10  
Ser Pro Cys Thr Asp His Cys Ser Gly Pro Arg Glu Glu Gln Leu Cys  
15 20 25  
Ser Ser Arg Val Phe His Cys Ile Thr His Pro Asn Gly Arg Ile His





Met Ser Ile Ser Leu Ser Ser Leu Ile Leu Leu Pro Ile Trp Ile Asn  
 -20 -15 -10 -5

Met Ala Gln Ile Gln Gln Gly Gly Pro Asp Glu Lys Glu Lys Thr Thr  
 1 5 10

Ala Leu Lys Asp Leu Leu Ser Arg Ile Asp Leu Asp Glu Leu Met Lys  
 15 20 25

Lys Asp Glu Pro Pro Gly  
 30

## (2) INFORMATION FOR SEQ ID NO: 433:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2  
seq SFCNAVVLSPVFQ/EE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

Met Thr Ala Leu Asn Leu Val Ala Pro Phe Ser Asp Gly Asp Ser Gly  
 -30 -25 -20

Ser Val Ser Leu Ala Ser Phe Cys Asn Ala Val Val Leu Ser Pro Val  
 -15 -10 -5

Phe Gln Glu Glu Glu His Leu Leu Phe Gln Lys Arg Lys Thr Lys Thr  
 1 5 10

Trp Pro Pro Arg  
 15

## (2) INFORMATION FOR SEQ ID NO: 434:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -17..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.2  
seq PVQVLGLLATCQH/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

Met Trp Ser Arg Pro Val Gln Val Leu Gly Leu Leu Ala Thr Cys Gln  
-15 -10 -5  
His Ala Pro Ser Pro Ser Phe Lys Gly Glu Thr Cys Thr Glu Ile Glu  
1 5 10 15  
Ser Val Tyr Leu Ala Pro Met  
20

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -24..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.2  
seq SLNQILLFLLISC/RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

Met Arg Tyr Arg Leu Arg Ile Gln Ile Thr Thr Ser Leu Asn Gln Ile  
-20 -15 -10  
Leu Leu Phe Leu Leu Ile Ser Cys Arg Thr Leu Ser  
-5 1

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -25..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.2  
seq VLLFFCCSPLYSP/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

```
Met Pro Phe Phe Ser Asn Gln Pro Thr Gln Val Ser Val Leu Leu Phe
-25 -20 -15 -10

Phe Cys Cys Ser Pro Leu Tyr Ser Pro Leu Phe Leu Leu Xaa Leu Ile
 -5 1 5

Pro His Gln
 10
```

(2) INFORMATION FOR SEQ ID NO: 437:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -44..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.1  
seq IAVGLTCQHVSHA/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

```
Met Arg Val Lys Asp Pro Thr Lys Ala Leu Pro Glu Lys Ala Lys Arg
 -40 -35 -30

Ser Lys Arg Pro Thr Val Pro His Asp Glu Asp Ser Ser Asp Asp Ile
 -25 -20 -15

Ala Val Gly Leu Thr Cys Gln His Val Ser His Ala Ile Ser Val Asn
 -10 -5 1
```

```

His Val Lys Arg Ala Ile Ala Glu Asn Leu Trp Ser Val Cys Ser Glu
 5 10 15 20
Cys Leu Lys Glu Arg Arg Phe Tyr Asp Gly Gln Leu Val Leu Thr Ser
 25 30 35
Asp Ile Trp Leu Cys Leu Lys Cys Gly Phe Gln Gly Cys Gly Lys Asn
 40 45 50
Ser Glu Ser Gln His Ser Leu Lys His Phe Lys Ser Ser Arg Thr Glu
 55 60 65
Pro Leu Arg
 70

```

## (2) INFORMATION FOR SEQ ID NO: 438:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq GTYLTSSSPICQL/QP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

```

Met Val Ser Leu Gly Tyr Tyr Leu Ile Phe Val Leu Tyr Leu Trp Leu
 -40 -35 -30
Cys Phe Met Gln Ile Ser Glu Glu Lys Leu Ile Glu Glu His Thr Gly
 -25 -20 -15
Thr Tyr Leu Thr Ser Ser Ser Pro Leu Cys Gln Leu Gln Pro Pro Gly
 -10 -5 1

```

## (2) INFORMATION FOR SEQ ID NO: 439:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (D) DEVELOPMENTAL STAGE: Fetal  
    (F) TISSUE TYPE: kidney
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -35..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 4.1  
                            seq VLCCLLIATPTFF/LL
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

```
Met Ser Leu Thr Ser Arg Xaa Xaa Ile Met Xaa Thr Ile Lys Ile Gln
-35 -30 -25 -20

Asn Ile Ser Ile Thr Lys Val Leu Cys Cys Leu Leu Ile Ala Thr Pro
 -15 -10 -5

Thr Phe Phe Leu Leu Leu Pro Ser Ser Ile Pro Arg
 1 5
```

(2) INFORMATION FOR SEQ ID NO: 440:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 27 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (D) DEVELOPMENTAL STAGE: Fetal  
    (F) TISSUE TYPE: kidney
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -18..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 4.1  
                            seq AGVVSTSVAAAVA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

```
Met Xaa Ala Glu Ala Ala Gly Val Val Ser Thr Ser Val Ala Ala Ala
 -15 -10 -5

Val Ala Ala Val Ala Ala Pro Ala Gly Ala Gly
 1 5
```

(2) INFORMATION FOR SEQ ID NO: 441:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq IMSSCLALTYTNS/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

```
Met Trp Ile Met Ser Ser Cys Leu Ala Leu Thr Tyr Thr Asn Ser Ile
-15 -10 -5 1
Ser His Ser Leu Cys Leu Glu Arg Ala Tyr Ser Leu Phe Lys Val Asp
 5 10 15
```

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq SNALVLVTRGSSS/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

```
Met Pro Arg Gly Val Tyr Asn Ser Asn Ala Leu Val Leu Val Thr Arg
-20 -15 -10 -5
Gly Ser Ser Ser Leu Pro Leu Gly Leu Tyr Gly Ile Asn Cys Val Gln
 1 5 10
Val Ile Lys Leu Phe Tyr Arg Gly His Leu His Trp Glu Thr Leu Leu
 15 20 25
```

Pro Ser  
30

(2) INFORMATION FOR SEQ ID NO: 443:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 amino acids
  - (B) TYPE: AMINO ACID
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo Sapiens
  - (D) DEVELOPMENTAL STAGE: Fetal
  - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: -44..-1
  - (C) IDENTIFICATION METHOD: Von Heijne matrix
  - (D) OTHER INFORMATION: score 4  
seq FLLPCVHPFSVIA/VY
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

Met Ile Glu Pro Cys Glu Lys Met Lys His Tyr Asp Met Asn Trp Phe  
                    -40                    -35                    -30

Leu Cys Met Tyr Glu Cys Phe Phe Phe His Leu Leu Glu Thr Glu Phe  
                    -25                    -20                    -15

Leu Leu Pro Cys Val His Pro Phe Ser Val Ile Ala Val Tyr Val Phe  
                    -10                    -5                    1

(2) INFORMATION FOR SEQ ID NO: 444:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 58 amino acids
  - (B) TYPE: AMINO ACID
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo Sapiens
  - (F) TISSUE TYPE: Muscle
- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: -55..-1
  - (C) IDENTIFICATION METHOD: Von Heijne matrix
  - (D) OTHER INFORMATION: score 4  
seq AALCGISLSQXFP/EP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:



```

Met Ala Met Trp Asn Arg Pro Cys Gln Xaa Leu Pro Gln Gln Pro Leu
-55 -50 -45 -40

Val Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu Pro Thr Gly Arg
 -35 -30 -25

Glu Leu Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala Leu Cys Gly Ile
 -20 -15 -10

Ser Leu Ser Gln Xaa Phe Pro Glu Pro Gly
 -5 1

```

## (2) INFORMATION FOR SEQ ID NO: 445:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq CLLVSYAVDSAAG/RF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

```

Met Glu Gln Val Cys Leu Leu Val Ser Tyr Ala Val Asp Ser Ala Ala
-15 -10 -5

Gly Arg Phe Gly
1

```

## (2) INFORMATION FOR SEQ ID NO: 446:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq ATLRCWASTPVSG/RL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

```

Met Arg Lys Ile Ser His Cys Leu His Cys Trp Pro Glu Ser Gly Ala
 -25 -20 -15

Thr Leu Arg Cys Trp Ala Ser Thr Pro Val Ser Gly Arg Leu Ser Ser
 -10 -5 1

Met Ala Val Xaa Xaa Xaa Gly Glu Xaa Pro Pro Gln Asp Ala Phe Thr
 5 10 15 20

Thr Gln Trp Leu Val Arg Asp Leu Arg Gly Lys Thr Glu Lys Glu Phe
 25 30 35

Lys Ala Tyr Val Ser Leu Phe Met Arg His Leu Cys Glu Pro Gly Ala
 40 45 50

Asp Gly Ser Glu Thr Phe Ala Asp Gly Val Pro Arg Glu Gly Leu Ser
 55 60 65

Arg Gln Gln Val Leu Thr Arg Ile Gly Val Met Ser Leu Val Lys Lys
 70 75 80

Lys Gly Gln
 85

```

## (2) INFORMATION FOR SEQ ID NO: 447:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq LLHPCGSITLTSS/ST

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

```

Met Cys Ile Asn Asp His Ile Ile Lys Leu Leu His Pro Cys Gly Ser

```

-20

-15

-10

Ile Thr Leu Thr Ser Ser Ser Thr Thr Arg  
 -5 1

## (2) INFORMATION FOR SEQ ID NO: 448:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq VALQCGLTIPALX/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

Met Arg Cys Arg Val Ala Leu Gln Cys Gly Leu Thr Ile Pro Ala Leu  
 -15 -10 -5

Xaa Leu Pro Gln Gly Asp Glu Ala Gly Asp Ala Gln Asp Leu Arg Gly  
 1 5 10 15

Pro Ala Gln Ala Glu Tyr Leu Tyr Ile Ile Ser Pro Ser  
 20 25

## (2) INFORMATION FOR SEQ ID NO: 449:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -93..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9

seq LTSAFLWLPRLHI/SV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

Met Thr Val Arg Tyr Gly Lys Phe Leu Ser Leu Leu Lys Asp Gly Ala  
                   -90                  -35                  -80

Glu Asn Asp Leu Thr Trp Val Leu Lys His Cys Glu Arg Phe Leu Lys  
                   -75                  -70                  -65

Gln Gln Gln Thr Ser Ile Lys Ser Ser Leu Leu Cys Leu Gln Gly Asn  
                   -60                  -55                  -50

Tyr Ala Gly His Asp Trp Phe Val Ser Ser Leu Phe Met Ile Met Leu  
                   -45                  -40                  -35                  -30

Gly Asp Lys Glu Lys Thr Phe Gln Phe Leu His Gln Phe Ser Arg Leu  
                   -25                  -20                  -15

Leu Thr Ser Ala Phe Leu Trp Leu Pro Arg Leu His Ile Ser Val Arg  
                   -10                  -5                  1

Leu Gln Ser Val Phe Lys Gly Gly Phe Xaa Ile Leu Arg Thr Leu Tyr  
                   5                  10                  15

Leu His Ser Xaa Gly Arg  
                   20                  25

## (2) INFORMATION FOR SEQ ID NO: 450:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq FFWVLFSGCKV/IT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

Met Ala Phe Asp Val Ser Cys Phe Phe Trp Val Val Leu Phe Ser Ala  
                   -20                  -15                  -10                  -5

Gly Cys Lys Val Ile Thr Ser Trp Asp Gln Met Cys Ile Glu Lys Glu  
                   1                  5                  10

Ala Thr

## (2) INFORMATION FOR SEQ ID NO: 451:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq HLSSTTSPPWTHA/AI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

Met Leu Thr Arg Leu Val Leu Ser Ala His Leu Ser Ser Thr Thr Ser  
-20 -15 -10

Pro Pro Trp Thr His Ala Ala Ile Ser Trp Glu Leu Asp Asn Val Leu  
-5 1 5 10

Met Pro Ser Pro Arg Ile Trp Pro Leu  
15

## (2) INFORMATION FOR SEQ ID NO: 452:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq CVNLLLGFEFVIS/RS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

Met Arg Tyr Phe Gln Gly Pro Ser Pro Tyr Ser Glu Ile Glu Ile Glu  
 -40 -35 -30 -25  
 Leu Cys Asp His Val Tyr Ser Phe Gln Gly Leu Cys Val Asn Leu Leu  
 -20 -15 -10  
 Leu Gly Phe Glu Pro Val Ile Ser Arg Ser Arg Xaa Ser Ser Leu Ala  
 -5 1 5  
 Val Glu Ser  
 10

## (2) INFORMATION FOR SEQ ID NO: 453:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq LASLECYVPSTNQ/WQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

Met Xaa Xaa Lys Arg Thr His Xaa Xaa Xaa Ser Val Phe Asn Gly Leu  
 -40 -35 -30  
 Val Tyr Ala Ala Gly Gly Arg Asn Ala Glu Gly Ser Leu Ala Ser Leu  
 -25 -20 -15 -10  
 Glu Cys Tyr Val Pro Ser Thr Asn Gln Trp Gln Pro Lys Xaa Xaa Leu  
 -5 1 5  
 Glu Val Ala Arg Cys Cys His Ala Ser Ala Val Ala Asp Gly Arg Val  
 10 15 20  
 Leu Val Thr Gly Gly Leu  
 25

## (2) INFORMATION FOR SEQ ID NO: 454:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids

(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -38..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.9  
seq LLFFHLLLNDFFT/FY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

Met Phe Leu Lys Val Gln Ser Gln Ser Phe Tyr Xaa Pro Tyr Arg Asp  
-35 -30 -25  
Cys Leu Asn Phe His Lys Ser Thr Tyr Leu Leu Phe Phe His Leu Leu  
-20 -15 -10  
Leu Asn Asp Phe Phe Thr Phe Tyr Xaa Ala Lys  
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -27..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.9  
seq WIILLIYTFQCNS/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

Met Gln Pro Leu Lys Ile Ile Phe Tyr Leu Ser Val Ser Ile Trp Ile  
-25 -20 -15  
Ile Leu Ile Ile Tyr Thr Phe Gln Cys Asn Ser Ser Leu Ser Ile Leu  
-10 -5 1 5  
Leu Leu Glu Leu

## (2) INFORMATION FOR SEQ ID NO: 456:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq RVAACTAAAPLQA/HG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

Met Met Arg Thr Thr Ala Arg Val Ala Ala Cys Thr Ala Ala Ala Pro  
                    -15                    -10                    -5

Leu Gln Ala His Gly Ala Xaa Ile Gln Gln Xaa Pro Asp Xaa Leu Xaa  
                    1                    5                    10

Ser Xaa Arg Leu Ser Arg Xaa Gly Leu Ser Ala Gly Arg Leu His Gln  
          15                    20                    25

Ser Glu Thr Glu Ala Glu Leu Glu Ala Pro Gly Arg Ala  
  30                    35                    40

## (2) INFORMATION FOR SEQ ID NO: 457:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq RWASSCLHPSARS/SN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:



Met Glu Ala Ala Thr Thr Leu His Pro Gly Pro Arg Pro Ala Leu Pro  
-30 -25 -20

Leu Gly Ala Arg Ala Arg Trp Ala Ser Ser Cys Leu His Pro Ser Ala  
-15 -10 -5

Arg Ser Ser Asn Pro Ala Gly Lys Ser Ser Arg Thr Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -29..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.8  
seq LCPVIFFPSNCWK/EY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

Met Gln Gly Val Arg Gly Pro Val Ser Phe Ser Trp Ser Thr Thr Met  
-25 -20 -15

Leu Cys Pro Val Ile Phe Phe Pro Ser Asn Cys Trp Lys Glu Tyr Asn  
-10 -5 1

Arg Thr Gln  
5

## (2) INFORMATION FOR SEQ ID NO: 459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq FXLLFXXFXFFRQ/XG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

Met Xaa Xaa Phe Ser Phe Xaa Leu Leu Phe Xaa Xaa Phe Xaa Phe Phe  
-15 -10 -5

Arg Gln Xaa Gly  
1

## (2) INFORMATION FOR SEQ ID NO: 460:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq SVRLLFRFSVIMA/SE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

Met Leu Leu Leu Ser Glu Ala Leu Ser Glu Ser Val Arg Leu Leu Phe  
-20 -15 -10

Arg Phe Ser Val Ile Met Ala Ser Glu Lys Gln Ser Phe Gln Ile  
-5 1 5

## (2) INFORMATION FOR SEQ ID NO: 461:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -17..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.8  
seq SLPCTTAFPLLSS/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

Met Ala Leu Ile Ser Leu Pro Cys Thr Thr Ala Phe Pro Leu Leu Ser  
-15 -10 -5

Ser Lys Val Ser Gln Leu Leu Leu Pro Leu Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 462:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -37..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.8  
seq RVVALPLVRATCT/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

Met Ser Glu Glu Glu Ala Ala Gln Ile Pro Arg Ser Ser Val Trp Glu  
-35 -30 -25

Gln Asp Gln Gln Asn Val Val Gln Arg Val Val Ala Leu Pro Leu Val  
-20 -15 -10

Arg Ala Thr Cys Thr Ala Val Cys Asp Val Tyr Ser Ala Ala Lys Asp  
-5 1 5 10

Arg His Pro Leu Leu Gly Ser Ala Trp  
15 20

(2) INFORMATION FOR SEQ ID NO: 463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -72..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8  
seq LAELTVDPQGALA/IR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

```
Met Ala Ala Ala Ala Ala Gly Ala Ala Ser Gly Leu Pro Gly Pro
 -70 -65 -60

Val Ala Gln Gly Leu Lys Glu Ala Leu Val Asp Thr Leu Thr Gly Ile
 -55 -50 -45

Leu Ser Pro Val Gln Glu Val Arg Ala Ala Ala Glu Glu Gln Ile Lys
 -40 -35 -30 -25

Val Leu Glu Val Thr Glu Glu Phe Gly Val His Leu Ala Glu Leu Thr
 -20 -15 -10

Val Asp Pro Gln Gly Ala Leu Ala Ile Arg Gln Leu Ala Ser Val Ile
 -5 1 5

Leu Lys Gln Tyr Val Glu Thr His Trp Cys Ala Gln Ser Glu Lys Phe
 10 15 20

Arg
 25
```

(2) INFORMATION FOR SEQ ID NO: 464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -117..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.8  
 seq XXXYLNFCPVCYC/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

```

Met Asn Ser Gly Gly Gly Phe Gly Leu Gly Leu Gly Phe Gly Leu Thr
-115 -110 -105

Pro Thr Ser Val Ile Gln Val Thr Asn Leu Ser Ser Ala Val Thr Ser
-100 -95 -90

Glu Gln Met Arg Thr Leu Phe Ser Phe Leu Gly Glu Ile Glu Glu Leu
-85 -80 -75 -70

Arg Leu Tyr Pro Pro Asp Asn Ala Pro Leu Ala Phe Ser Ser Xaa Val
-65 -60 -55

Cys Tyr Val Lys Phe Arg Asp Pro Ser Ser Val Gly Val Ala Gln His
-50 -45 -40

Leu Thr Asn Thr Val Phe Ile Asp Arg Xaa Leu Xaa Ser Cys Ser Leu
-35 -30 -25

Cys Arg Arg Leu Val Ser Arg Phe Xaa Xaa Xaa Tyr Leu Asn Phe Cys
-20 -15 -10

Pro Val Cys Tyr Cys Phe Ser Phe Pro Arg Asp Trp Gln Val Asp Ser
-5 1 5 10

Thr Leu

```

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -13...-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.7  
 seq MIEMLIPLDCVLS/SK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

```

Met Ile Glu Met Leu Ile Phe Leu Asp Cys Val Leu Ser Ser Lys Asp
-10 -5 1

```

Thr Ile Thr Met Phe Val Lys Phe Ile Pro Ile Phe Pro Phe Pro Leu  
           5                          10                          15  
 Gln Phe Tyr Leu Pro Ser Phe Leu Leu Leu Glu  
       20                          25                          30

## (2) INFORMATION FOR SEQ ID NO: 466:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -79..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7  
seq VIGSLLVLTMLTC/RR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

Met His Pro Phe Leu Ala Ala His Gly Pro Ala Phe His Lys Gly Tyr  
                           -75                          -70                          -65  
 Lys His Ser Thr Ile Asn Ile Val Asp Ile Tyr Pro Met Met Cys His  
                           -60                          -55                          -50  
 Ile Leu Gly Leu Lys Pro His Pro Asn Asn Gly Thr Phe Gly His Thr  
                           -45                          -40                          -35  
 Lys Cys Leu Leu Val Asp Gln Trp Cys Ile Asn Leu Pro Glu Ala Ile  
                           -30                          -25                          -20  
 Ala Ile Val Ile Gly Ser Leu Leu Val Leu Thr Met Leu Thr Cys Arg  
                           -15                          -10                          -5                          1  
 Arg

## (2) INFORMATION FOR SEQ ID NO: 467:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Kidney

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -14..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq IWPMSASVATLWS/FT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

```
Met Ile Trp Pro Met Ser Ala Ser Val Ala Thr Leu Trp Ser Phe Thr
 -10 -5 1
Ser Tyr Ile Ser Tyr Pro Ser Arg Phe Tyr Tyr Asp Ala Trp
 5 10 15
```

(2) INFORMATION FOR SEQ ID NO: 468:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -31..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.6  
seq LFIYLVFVECLLC/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

```
Met Gly Ile Asp Ile Phe Tyr Pro Ser His Ile Pro Asp Phe His Pro
-30 -25 -20
Ile His Leu Phe Ile Tyr Leu Val Phe Val Glu Cys Leu Leu Cys Thr
-15 -10 -5 1
Arg Asn Xaa Xaa Xaa Leu Ser Xaa Phe Asn Cys Asp Asn Ala Gln Ile
 5 10 15
Ile Phe Thr Thr Gly Ser Ser Ser Ser Gly Gly Asn Lys Pro Phe Lys
 20 25 30
Ser Ser Leu Cys Thr Val His Arg Gly Gln Glu Arg Glu Arg Ile Glu
 35 40 45
Cys Gln Gly Asn Gly
```

50

## (2) INFORMATION FOR SEQ ID NO: 469:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -87..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq LILQASLKGELEA/SQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

```

Met Lys Glu Leu Asn Gln Lys Leu Thr Asn Lys Asn Asn Lys Ile Glu
 -85 -80 -75

Asp Leu Glu Gln Glu Ile Lys Ile Gln Lys Gln Lys Gln Glu Thr Leu
 -70 -65 -60

Gln Glu Glu Ile Thr Ser Leu Gln Ser Ser Val Gln Glu Tyr Glu Glu
 -55 -50 -45 -40

Lys Asn Xaa Lys Ile Lys Gln Leu Leu Val Lys Thr Lys Lys Glu Leu
 -35 -30 -25

Ala Asp Ser Lys Gln Ala Glu Thr Asp His Leu Ile Leu Gln Ala Ser
 -20 -15 -10

Leu Lys Gly Glu Leu Glu Ala Ser Gln Gln Gln Val Glu Val Tyr Lys
 -5 1 5

Val Arg Val Leu Leu Phe Lys Ile Lys Lys Met Phe Phe His Val Glu
 10 15 20 25

Val Arg Asn Gly

```

## (2) INFORMATION FOR SEQ ID NO: 470:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN



## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -113..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.6  
 seq RLLLCILIIVCYI/LF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

```

Met Gly Asn Thr Leu Lys Glu Met Gln Asp Val Gln Gly Ala Leu Gln
 -110 -105 -100

Cys Tyr Thr Arg Ala Ile Gln Ile Asn Pro Ala Phe Ala Asp Ala His
 -95 -90 -85

Ser Asn Leu Ala Ser Ile His Lys Asp Ser Gly Asn Ile Pro Glu Ala
 -80 -75 -70

Ile Ala Ser Tyr Arg Thr Ala Leu Lys Leu Lys Pro Asp Phe Pro Asp
 -65 -60 -55 -50

Ala Tyr Cys Asn Leu Ala His Cys Leu Gln Ile Val Cys Asp Trp Thr
 -45 -40 -35

Asp Tyr Asp Glu Arg Met Lys Lys Leu Val Ser Ile Val Ala Asp Gln
 -30 -25 -20

Leu Glu Lys Asn Arg Leu Leu Leu Cys Ile Leu Ile Ile Val Cys Tyr
 -15 -10 -5

Ile Leu Phe Leu Met
 1

```

## (2) INFORMATION FOR SEQ ID NO: 471:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -39..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.6  
 seq VAYAIPSIPSLFC/QR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

Met Leu Ile Leu Ala Asp Thr Arg Arg Val Gln Gly Gly Thr Leu Gly  
                           -35                          -30                          -25

Leu Ile Pro Ala Val Leu Asn Arg Val His Val Ala Tyr Ala Ile Pro  
                           -20                          -15                          -10

Ser Ile Pro Ser Leu Phe Cys Gln Arg Trp  
                           -5                          1

## (2) INFORMATION FOR SEQ ID NO: 472:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq CVFLFPLISNTSS/YK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

Met Leu Val Gly Ile Tyr Phe Cys Val Phe Leu Phe Pro Leu Ile Ser  
                           -20                          -15                          -10                          -5

Asn Thr Ser Ser Tyr Lys Asn Cys His Lys Thr Leu Gln His Thr Ile  
                           1                          5                          10

Pro Pro His Gly  
                           15

## (2) INFORMATION FOR SEQ ID NO: 473:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -42..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq LLLQGACPLIFL/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

Met Phe Leu Ala Pro Ser Leu Leu Ile Thr Lys Leu Leu Thr Gly Ser  
-40 -35 -30  
Glu Ser Pro Asp Gly Asn Pro Pro Ala Leu Gly Arg Pro Leu Leu Leu  
-25 -20 -15  
Gln Gly Ala Cys Pro Cys Leu Ile Phe Leu Arg Pro Asp Glu Asn Lys  
-10 -5 1 5  
Lys Glu Gly Xaa Glu Glu Lys Lys Asn His Lys Leu Pro Leu Lys Thr  
10 15 20  
Ser Leu Gly  
25

(2) INFORMATION FOR SEQ ID NO: 474:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -18..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq SKSCLFYLLQKVSG/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

Met Asp Pro Ser Ala Ser Lys Ser Cys Leu Phe Tyr Leu Gln Lys Val  
-15 -10 -5  
Ser Gly Ile Pro Gly Leu Leu Thr  
1 5

## (2) INFORMATION FOR SEQ ID NO: 475:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -46..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq RWLCLQAYLASFS/LE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

```
Met Ser Leu Thr Ala Ser Gly Pro Arg Ala Ala Trp Glu Glu Arg Val
-45 -40 -35

Gly Gly Leu His Thr Trp Gly Ala Asn Ile Pro Thr Ala Pro Asp Ser
-30 -25 -20 -15

Gln Arg Trp Leu Cys Leu Gln Ala Tyr Leu Ala Ser Phe Ser Leu Glu
-10 -5 1

Ser Pro His Arg Ile Tyr Leu Glu Ser Pro Pro Thr Leu Leu Phe Pro
5 10 15

Pro Pro
20
```

## (2) INFORMATION FOR SEQ ID NO: 476:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq AQLASPLLPGATP/VA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

```

Met Lys Tyr Gln Met Val Ser Gly Ser Ala Gln Leu Ala Ser Pro Leu
-20 -15 -10

Leu Pro Gly Ala Thr Pro Val Ala Gly Thr Ile Leu Lys Ser Leu Leu
-5 1 5 10

Leu Arg Thr Val Lys Met Met Arg Val Met
15 20

```

## (2) INFORMATION FOR SEQ ID NO: 477:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq CFWGLMYXWLLLG/SX

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

```

Met Asn Gly Thr Phe Pro Gly Thr Tyr Val Tyr Leu Val Ala Tyr Gly
-35 -30 -25 -20

Asp Leu Arg Ile Phe Gly Cys Phe Trp Gly Leu Met Tyr Xaa Trp Leu
-15 -10 -5

Leu Leu Gly Ser Xaa Gly
1

```

## (2) INFORMATION FOR SEQ ID NO: 478:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12.7  
seq ILFLLSWSGPLQG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser  
-20 -15 -10

Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg  
-5 1 5 10

Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser  
15 20 25

Ser Arg His Ala Ala Glu Leu Arg Asn Phe Lys Asn Lys Met Leu Pro  
30 35 40

Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala Leu Arg Thr Glu Ala  
45 50 55

Xaa Thr Ile Ser Xaa Gly Val Asp Arg Leu Glu Arg Glu Val Asp Tyr  
60 65 70 75

Leu

(2). INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5  
seq LMLLVSSLSPVQG/VL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

Met Lys Phe Ile Ser Thr Ser Leu Leu Met Leu Leu Val Ser Ser  
-20 -15 -10

Leu Ser Pro Val Gln Gly Val Leu Glu Val Tyr Tyr Thr Ser Leu Arg  
     -5                    1                    5                    10  
 Cys Arg Cys Val Gln Glu Ser Ser Val Phe Ile Pro Arg Arg Phe Ile  
           15                    20                    25  
 Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn Gly Cys Pro Arg Lys Glu  
           30                    35                    40  
 Ile Ile Val Trp Lys Lys Asn Lys Ser Ile Val Cys Val Asp Leu Lys  
       45                    50                    55  
 His Arg  
       60

## (2) INFORMATION FOR SEQ ID NO: 480:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8  
seq VLELLAAVCLVRG/GH

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

Met Asn Tyr Gln Tyr Gly Phe Asn Met Val Met Ser His Pro His Ala  
     -45                    -40                    -35  
 Val Asn Glu Ile Ala Leu Ser Leu Asn Asn Lys Asn Pro Arg Thr Lys  
     -30                    -25                    -20  
 Ala Leu Val Leu Glu Leu Leu Ala Ala Val Cys Leu Val Arg Gly Gly  
     -15                    -10                    -5                    1  
 His Glu Ile Ile Leu Ser Ala Phe Asp Asn Phe Lys Glu Val Cys Gly  
       5                    10                    15  
 Glu Lys Gln Arg Phe Glu Lys Leu Met Glu His Phe Arg Asn Glu Asp  
       20                    25                    30  
 Asn Asn Ile Asp Phe Met Val Ala Ser Met Gln Phe Ile Asn Ile Val  
       35                    40                    45  
 Val His Ser Val Glu Asp Met Asn Phe Arg Val His Leu Gln Tyr Glu  
       50                    55                    60                    65

Phe Thr Lys Leu Gly Leu Xaa Glu Tyr Leu Xaa Lys Leu Lys His Thr  
70 75 80  
Glu Ser Asp Lys Leu Gln Val Gln Ile  
85 90

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -28..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.7  
seq LVMCFLSYFGTFA/VE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

```

Met Ala Gln Ser Ile His Met Tyr Ala Ala Arg Val Gln Trp Gly Leu
 -25 -20 -15

Val Met Cys Phe Leu Ser Tyr Phe Gly Thr Phe Ala Val Glu Phe Arg
 -10 -5 1

His Tyr Arg Tyr Glu Ile Val Cys Ser Glu Tyr Gln Glu Asn Phe Leu
 5 10 15 20

Ser Phe Ser Glu Ser Leu Ser Glu Ala Ser Glu Tyr Gln
 25 30

```

(2) INFORMATION FOR SEQ ID NO: 482:

## (2) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney





Asn Gln Gln Leu Asn Phe Thr Glu Xaa Xaa Gly Gly Xaa Xaa Ala Ala  
35 40 45  
Gly Thr Lys Phe Gly  
50

## (2) INFORMATION FOR SEQ ID NO: 484:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq MTCLSVLFGYATS/HP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala Met Leu  
-30 -25 -20  
Ala Leu Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly Tyr Ala Thr  
-15 -10 -5  
Ser His Pro Gln Gly Leu Tyr Ile  
1 5

## (2) INFORMATION FOR SEQ ID NO: 485:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.3  
seq RQLLLPLPPFSFP/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

```

Met Pro Gln Gln Pro Val Glu Gln Gly Ser Pro Leu Leu Arg Gln Leu
-25 -20 -15

Leu Leu Pro Leu Pro Pro Phe Ser Phe Pro Ala Pro Ser Pro Cys Pro
-10 -5 1 5

Ser Trp Pro Val Ala Leu Gly Ser His Gly Val Ala Tyr Trp Gly Ser
10 15 20

Cys Ser Leu Gly His
25

```

(2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -80..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.2  
seq RASLLPMLGSWA/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

```

Met Pro Ser Arg Ser Pro Phe Thr Trp Ser His Leu Cys Trp Arg Ala
-80 -75 -70 -65

Gly Arg Cys Pro Arg Trp Arg Ala Cys Leu Ser Ser Ser Ser Val Arg
-60 -55 -50

Met Cys Ser Pro Ala Ala Pro Ser Arg Phe Gly Ala Leu Gly Xaa Ser
-45 -40 -35

Ala Arg Arg Trp Pro Arg Arg Asp Ala Asp Thr Trp Cys Ala Pro Gln
-30 -25 -20

Gly Val Met Arg Ala Ser Leu Leu Pro Met Leu Leu Gly Ser Trp Ala
-15 -10 -5

Phe Leu Pro Pro Ser Cys Ser Pro Arg Ala
1 5 10

```

## (2) INFORMATION FOR SEQ ID NO: 437:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6  
seq LTYGIILTHGASG/DM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

Met Ser His Thr Glu Val Lys Leu Lys Ile Pro Phe Gly Asn Lys Leu  
-40                      -35                      -30                      -25

Leu Asp Ala Val Cys Leu Val Pro Asn Lys Ser Leu Thr Tyr Gly Ile  
                    -20                      -15                      -10

Ile Leu Thr His Gly Ala Ser Gly Asp Met Asn Leu Pro His Leu Met  
                    -5                      1                      5

Ser Leu Ala Ser His Leu Ala Ser His Gly Phe Phe Cys Leu Arg Phe  
10                      15                      20

Thr Cys Lys Gly Leu Asn Ile Val His Arg Ile Lys Ala Tyr Lys Ser  
25                      30                      35                      40

Val Leu Asn Tyr Leu Lys Thr Ser Gly Xaa Tyr Lys Leu Ala Gly  
                    45                      50                      55

## (2) INFORMATION FOR SEQ ID NO: 488:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -40..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6  
 seq LCXEFXSVASCD/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

```

Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg Glu Ala Ala Glu Glu
-40 -35 -30 -25

Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu Leu Cys Xaa Glu Phe
 -20 -15 -10

Xaa Ser Val Ala Ser Cys Asp Ala Ala Val Ala Gln Cys Phe Leu Ala
 -5 1 5

Xaa Asn Asp Trp Glu Met Glu Arg Ala Leu Asn Ser Tyr Phe Glu Pro
 10 15 20

Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro Xaa
 25 30 35

```

(2) INFORMATION FOR SEQ ID NO: 489:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -36..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.8  
 seq AFVSGLLIGQCSS/QK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

```

Met Gly Arg Thr Tyr Ile Val Glu Glu Thr Val Gly Gln Tyr Leu Ser
-35 -30 -25

Asn Ile Asn Leu Gln Gly Lys Ala Phe Val Ser Gly Leu Leu Ile Gly
-20 -15 -10 -5

Gln Cys Ser Ser Gln Lys Asp Tyr Val Ile Leu Ala Thr Arg Thr Pro
 1 5 10

Pro Lys Glu Glu Gln Ser Glu Asn Leu
 15 20

```

## (2) INFORMATION FOR SEQ ID NO: 490:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq CLSCLLIPLALWS/II

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

```

Met Gly Ser Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu Leu Ile Pro
-20 -15 -10

Leu Ala Leu Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr Phe Pro Asn
-5 1 5 10

Gly Gln Thr Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn Tyr Val Trp
15 20 25

Tyr Phe Glu Gly Ile Cys Phe Ser Gly Ile Met Met Leu Ile Val Thr
30 35 40

Thr Val Leu Leu Val Leu Glu Asn Asn Asn Asn Tyr Lys Cys Cys Gln
45 50 55

Ser Glu Asn Cys Ser Lys Lys Tyr Val Thr Leu Leu Ser Ile Ile Phe
60 65 70 75

Ser Ser Leu Gly Ile Ala Phe Ser Gly Tyr Cys Leu Val Ile Ser Ala
80 85 90

Leu Gly Leu Val Gln Gly Pro Tyr Cys Arg
95 100

```

## (2) INFORMATION FOR SEQ ID NO: 491:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq CLSCLLIPLALWS/II

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

```

Met Gly Ser Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu Leu Ile Pro
-20 -15 -10
Leu Ala Leu Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr Phe Pro Asn
-5 1 5 10
Gly Gln Thr Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn Tyr Val Trp
15 20 25
Tyr Phe Glu Gly Ile Cys Phe Ser Gly Ile Met Met Leu Ile Val Thr
30 35 40
Thr Val Leu Leu Val Leu Glu Asn Asn Asn Asn Tyr Lys Cys Cys Gln
45 50 55
Ser Glu Asn Cys Ser Lys Lys Tyr Val Thr Leu Leu Ser Ile Ile Phe
60 65 70 75
Ser Ser Leu Gly Ile Ala Phe Ser Gly Tyr Cys Leu Val Ile Ser Ala
80 85 90
Leu Gly Leu Val Gln Gly Pro Tyr Cys Arg Thr Leu Asp Gly Trp Glu
95 100 105
Tyr Ala Phe Glu Gly Thr Xaa Gly Arg Phe Leu Thr Asp Ser Ser Ile
110 115 120
Trp Ile Gln Cys Leu Glu
125

```

## (2) INFORMATION FOR SEQ ID NO: 492:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq SFLPSALVIWTS/AF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

```

Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
-20 -15 -10

Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr
-5 1 5 10

Leu His His Ile
 15

```

## (2) INFORMATION FOR SEQ ID NO: 493:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq PLIFSLWCSGVLL/HI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

```

Met Phe Asn Ala Ser Thr Phe Thr Asp Trp Ser Ser Ser Ile Phe Phe
-40 -35 -30

Val Phe Thr Phe Lys Ser Lys Lys Ser Ala Gly Leu Pro Leu Ile Phe
-25 -20 -15 -10

Ser Leu Trp Cys Ser Gly Val Leu Leu His Ile His Gln Lys Ala Gly
-5 1 5

Gly Pro Arg Leu Trp Arg Ile His Gly Glu Gln
10 15

```

## (2) INFORMATION FOR SEQ ID NO: 494:



- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 37 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (D) DEVELOPMENTAL STAGE: Fetal  
    (F) TISSUE TYPE: kidney
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -29..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 13.4  
                            seq SLLLVQLLTPCSA/QF
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

Met Lys Met Ala Ser Ser Leu Ala Phe Leu Leu Leu Asn Phe His Val  
                    -25                    -20                    -15

Ser Leu Leu Leu Val Gln Leu Leu Thr Pro Cys Ser Ala Gln Phe Ser  
                    -10                    -5                    1

Val Leu Gly Pro Leu  
                    5

(2) INFORMATION FOR SEQ ID NO: 495:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 47 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (D) DEVELOPMENTAL STAGE: Fetal  
    (F) TISSUE TYPE: kidney
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -42..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 5.2  
                            seq LLFDLVCHEFCQS/DD
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

Met His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala  
                    -40                    -35                    -30

Ile Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe  
 -25 -20 -15  
 Asp Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Ala Arg  
 -10 -5 1 5

## (2) INFORMATION FOR SEQ ID NO: 496:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2  
seq PMQLLQVLSDVLA/EI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

Met Ser Asp Gln Ile Lys Phe Ile Met Asp Ser Leu Asn Lys Glu Pro  
 -40 -35 -30  
 Phe Arg Lys Asn Tyr Asn Leu Ile Thr Phe Xaa Ser Leu Glu Pro Met  
 -25 -20 -15  
 Gln Leu Leu Gln Val Leu Ser Asp Val Leu Ala Glu Ile Asp Pro Lys  
 -10 -5 1 5  
 Gln Leu Val Asp Ile Arg Glu Glu Met Pro Glu Gln Thr Ala Lys Arg  
 10 15 20  
 Met Leu Ser Leu Leu Gly Ile Leu Lys Tyr Lys Pro Ser Gly Asn Ala  
 25 30 35  
 Thr Asp Met Ser Thr Phe Arg Gln Gly Leu Val Ile Gly Ser Lys Pro  
 40 45 50  
 Val Ile Tyr Pro Val Leu  
 55

## (2) INFORMATION FOR SEQ ID NO: 497:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -79..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.6  
seq IIHAXGLVRECLA/XT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

```
Met Ala Thr Ser Ser Gln Xaa Arg Gln Leu Leu Ser Asp Tyr Gly Pro
 -75 -70 -65

Pro Ser Leu Gly Tyr Thr Gln Gly Thr Gly Asn Ser Gln Xaa Pro Gln
 -60 -55 -50

Ser Lys Tyr Ala Glu Leu Leu Ala Ile Ile Xaa Glu Leu Gly Lys Glu
 -45 -40 -35

Ile Arg Pro Met Tyr Ala Gly Ser Lys Ser Ala Met Glu Arg Leu Lys
 -30 -25 -20

Arg Gly Ile Ile His Ala Xaa Gly Leu Val Arg Glu Cys Leu Ala Xaa
-15 -10 -5 1

Thr Glu Arg Met Pro Asp Pro Ser Cys Leu Val Gly Phe
 5 10
```

(2) INFORMATION FOR SEQ ID NO: 498:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -15..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.5  
seq LLGAAVAALGRG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

Met Arg Leu Leu Gly Ala Ala Ala Val Ala Ala Leu Gly Arg Gly Arg  
 -15                      -10                      -5                      1

Ala Pro Ala Ser Leu Gly Trp Gln Arg Lys Gln Val Asn Trp Lys Ala  
                     5                      10                      15

Cys Arg Trp Ser Ser Ser Gly Val Ile Pro Asn Glu Lys Ile Arg Asn  
                     20                      25                      30

Ile Gly Ile Ser Ala His Ile Asp Ser Gly Lys  
                     35                      40

## (2) INFORMATION FOR SEQ ID NO: 499:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq RLLRRFLASVIS/RK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

Met Ala Gln Arg Leu Leu Leu Arg Arg Phe Leu Ala Ser Val Ile Ser  
 -15                      -10                      -5

Arg Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser Arg Ala Leu  
   1                      5                      10                      15

Gln Thr Pro Gln Cys Ser Pro Gly Gly Leu Thr Val Thr Pro Asn Pro  
                     20                      25                      30

Ala Pro Gly  
                     35

## (2) INFORMATION FOR SEQ ID NO: 500:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -16..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.4  
 seq LNSLSALAEAVG/SR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

```

Met Phe Arg Leu Asn Ser Leu Ser Ala Leu Ala Glu Leu Ala Val Gly
-15 -10 -5

Ser Arg Trp Tyr His Gly Gly Ser Gln Pro Ile Gln Ile Arg Leu Ala
 1 5 10 15

```

## (2) INFORMATION FOR SEQ ID NO: 501:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -61..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
 seq YTAHSVLAGPRWA/DP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

```

Met Ser Gly Ser Asn Gly Ser Lys Glu Asn Ser His Asn Lys Ala Arg
-60 -55 -50

Thr Ser Pro Tyr Pro Gly Ser Lys Val Glu Arg Ser Gln Val Pro Asn
-45 -40 -35 -30

Glu Lys Val Gly Trp Leu Val Glu Trp Gln Asp Tyr Lys Pro Val Glu
-25 -20 -15

Tyr Thr Ala Val Ser Val Leu Ala Gly Pro Arg Trp Ala Asp Pro Gln
-10 -5 1

Ile Ser Glu Ser Asn Phe Ser Pro Lys Phe Asn Glu Lys Asp Gly His
 5 10 15

```

Val Glu Arg Lys Ser Lys Asn Gly Leu Tyr  
20 25

(2) INFORMATION FOR SEQ ID NO: 502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq TLMFSLTAQWXTS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Met Arg Thr Thr Leu Met Phe Ser Leu Thr Ala Gln Trp Xaa Thr Ser  
-15 -10 -5

Arg Ser Ser Phe Gln  
1 5

(2) INFORMATION FOR SEQ ID NO: 503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 14.1  
seq LTLLLLLTLLAFA/GY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

Met Ser Asp Leu Leu Leu Leu Gly Leu Ile Gly Gly Leu Thr Leu Leu  
 -25 -20 -15 -10  
 Leu Leu Leu Thr Leu Leu Ala Phe Ala Gly Tyr Ser Gly Leu Leu Ala  
 -5 1 5  
 Gly Val Glu Val Ser Ala Gly Ser Pro Pro Ile Arg Asn Val Thr Val  
 10 15 20  
 Ala Tyr Lys Phe His Met Gly Leu Tyr Gly Glu Thr Gly Arg Leu Phe  
 25 30 35  
 Thr Glu Ser Cys Ser Ile Ser Pro Lys Leu Arg Ser Ile Ala Val Tyr  
 40 45 50 55  
 Tyr Asp Asn Pro His Met Val Pro Pro Asp Lys Cys Arg Cys Ala Val  
 60 65 70  
 Gly Ser Ile Leu Ser Glu Gly Glu  
 75

## (2) INFORMATION FOR SEQ ID NO: 504:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.4  
seq LWSLALWLPLALS/VS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

Met Glu Gly Thr Glu Met Gly Ala Arg Pro Gly Gly His Pro Xaa Lys  
 -30 -25 -20  
 Trp Ser Phe Leu Trp Ser Leu Ala Leu Trp Leu Pro Leu Ala Leu Ser  
 -15 -10 -5  
 Val Ser Leu Phe Leu Gly Leu Ser Leu Ser Pro Pro Gln Pro Gly Leu  
 1 5 10 15  
 Ser Leu Trp Cys Thr Leu Ser Tyr Cys Cys Glu Gln Trp Lys Phe Lys  
 20 25 30  
 Gly Thr Pro Ser Pro Ala Leu Leu Asn Leu Gly Thr Arg Gly  
 35 40 45

## (2) INFORMATION FOR SEQ ID NO: 505:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2  
seq LLFALGSLGLIFA/LI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

Met Xaa Phe Leu Arg Lys Val Xaa Ser Ile Leu Ser Leu Gln Val Leu  
-55 -50 -45 -40  
Leu Thr Thr Val Thr Ser Thr Val Phe Leu Tyr Phe Glu Ser Val Arg  
-35 -30 -25  
Thr Phe Val Xaa Glu Ser Pro Ala Leu Ile Leu Leu Phe Ala Leu Gly  
-20 -15 -10  
Ser Leu Gly Leu Ile Phe Ala Leu Ile Leu Asn Xaa His Lys Tyr Pro  
-5 1 5  
Leu Asn Leu Tyr Leu Leu Phe Gly Phe Thr Leu Leu Xaa Ala Leu Thr  
10 15 20 25  
Val Ala Val Val Val Thr  
30

## (2) INFORMATION FOR SEQ ID NO: 506:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide



(B) LOCATION: -38..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 10.8  
 seq MLLLLLLLGSQG/PQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

Met Ala Ala Thr Leu Gly Pro Leu Gly Ser Trp Gln Gln Trp Arg Arg  
                   -35                  -30                  -25  
 Cys Leu Ser Ala Arg Asp Gly Ser Arg Met Leu Leu Leu Leu Leu  
                   -20                  -15                  -10  
 Leu Gly Ser Gly Gln Gly Pro Gln Gln Val Gly Ala Gly  
                   -5                  1                  5

(2) INFORMATION FOR SEQ ID NO: 507:

(i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 53 amino acids  
     (B) TYPE: AMINO ACID  
     (D) TOPOLOGY: LINEAR  
 (ii) MOLECULE TYPE: PROTEIN  
 (vi) ORIGINAL SOURCE:  
     (A) ORGANISM: Homo Sapiens  
     (D) DEVELOPMENTAL STAGE: Fetal  
     (F) TISSUE TYPE: kidney  
 (ix) FEATURE:  
     (A) NAME/KEY: sig\_peptide  
     (B) LOCATION: -41..-1  
     (C) IDENTIFICATION METHOD: Von Heijne matrix  
     (D) OTHER INFORMATION: score 9.9  
                                   seq ILPFLFFFPVNA/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

Met Ser Ser Trp Met Tyr Leu Gly Tyr Pro Ile Val Thr Ser Asn Thr  
                   -40                  -35                  -30  
 Thr Cys Leu Lys Leu Ile Ser Ser Ser Phe Pro Gln Ile Leu Pro Phe  
                   -25                  -20                  -15                  -10  
 Leu Leu Phe Pro Phe Pro Val Asn Ala Arg Ser His Xaa Val Ala Gln  
                   -5                  1                  3  
 Thr Lys Ser Pro Arg  
                   10

(2) INFORMATION FOR SEQ ID NO: 508:

(i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 38 amino acids

- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.7  
seq QLCLLLLPSCLS/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

Met Ala Pro Gly Val Ile Ile Ile Gln Leu Cys Leu Leu Leu Leu Pro  
-20 -15 -10  
Ser Cys Ser Leu Ser Val Ser Gly Cys Ser Cys Pro Ser Ala Cys Phe  
-5 1 5 10  
Ser Thr Thr Ser Arg Glu  
15

(2) INFORMATION FOR SEQ ID NO: 509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -93..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.6  
seq LSLSLGASAPVQC/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

Met Arg His Gly Phe Ile Gln Gln Gln Phe Ser Leu Thr Ala Phe Ser  
-90 -85 -80  
Xaa Xaa Xaa Xaa Ile Phe Thr Leu Xaa Xaa Leu Ser Gln Leu Leu Ser  
-75 -70 -65  
Ser Ala Ala Pro Lys His Thr Ala Ala Pro Thr Ala Leu Pro Cys Leu

-60                      -55                      -50  
 Gln Gly Gln Gln Leu Asn Ser Leu Ser Leu Gly Thr Ser Glu Leu Ser  
 -45                      -40                      -35                      -30  
 Cys Val Leu Ala Ser Ser Cys Leu Ser Thr Lys Thr Asp Pro Ser Gly  
                          -25                      -20                      -15  
 Leu Ser Leu Ser Leu Gly Ala Ser Ala Pro Val Gln Cys Gln Gln Asp  
                          -10                      -5                      1  
 Asn Tyr Thr Phe Cys Xaa Gln Tyr Trp Leu Arg Ala Arg His  
       5                      10                      15

## (2) INFORMATION FOR SEQ ID NO: 510:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5  
seq LIIFLSFLPFINS/SE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

Met Phe Gln Asn Ile Gln Lys Cys Leu Asn Val Pro Phe Val Arg Gly  
 -40                      -35                      -30  
 Tyr His Val Phe Tyr Ile Asn Leu Asn Ala Val Ile Leu Ile Ile Phe  
 -25                      -20                      -15                      -10  
 Leu Ser Phe Leu Pro Phe Ile Asn Ser Ser Phe Val Tyr Lys Thr Asn  
                          -5                      1                      5  
 Pro Leu Tyr Asp Ala Ile Ser Asn Tyr Val Phe Ser Phe Arg Tyr Pro  
       10                      15                      20  
 Asn Leu Xaa Xaa Phe Ala Leu Asp Val Arg Leu Val Phe  
       25                      30                      35

## (2) INFORMATION FOR SEQ ID NO: 511:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids

(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -20..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 9.2  
seq FPVLALFLSGSLA/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

Met Ser Leu Ser Gln Arg Gly Phe Pro Val Leu Ala Leu Phe Leu Ser  
-20 -15 -10 -5

Gly Ser Leu Ala Leu Phe His His Thr Ser Gly  
1 5

(2) INFORMATION FOR SEQ ID NO: 512:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -29..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.9  
seq ALLIVCDVPSASA/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val  
-25 -20 -15

Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln Arg Lys  
-10 -5 1

Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met Glu Trp Thr  
5 10 15

Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys Phe Arg Arg Leu  
20 25 30 35

Val Lys Xaa Pro Pro Arg  
40

(2) INFORMATION FOR SEQ ID NO: 513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8  
seq VPMLLLIVGGSFG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu  
-30 -25 -20  
Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly  
-15 -10 -5  
Leu Arg Glu Phe Ser Xaa Ile Arg Tyr Asp Ala Val Lys Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5

seq LLVLLLYAPVGFC/LL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

```

Met Glu Leu Pro Ser Gly Pro Gly Pro Glu Arg Leu Phe Asp Ser His
 -35 -30 -25

Arg Leu Pro Gly Asp Cys Phe Leu Leu Leu Val Leu Leu Leu Tyr Ala
 -20 -15 -10

Pro Val Gly Phe Cys Leu Leu Val Leu Xaa Leu Phe Leu Gly Ile His
 -5 1 5 10

Val Phe Leu Val Ser Cys Ala Leu Pro Asp Ser Val Leu Arg Arg Phe
 15 20 25

Val Val Arg Thr Met Cys Ala Val Leu Gly Leu Val Ala Arg Gln Glu
 30 35 40

Asp Ser Gly Leu Arg Asp His Ser Val Arg Val Leu Ile Ser Asn His
 45 50 55

Val Thr Pro Phe Asp His Gln
 60 65

```

## (2) INFORMATION FOR SEQ ID NO: 515:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -90..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.4  
seq SLVLLTVTPSXRQ/QE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

```

Met Ala Gln Ser Gln Gly Trp Val Xaa Arg Tyr Xaa Lys Ala Phe Cys
 -90 -85 -80 -75

Lys Gly Phe Phe Val Ala Val Pro Val Ala Val Thr Phe Leu Asp Arg
 -70 -65 -60

Val Ala Cys Val Ala Arg Val Glu Gly Ala Ser Met Gln Pro Ser Leu
 -55 -50 -45

```

Asn Pro Gly Gly Ser Xaa Ser Ser Asp Val Val Xaa Xaa Asn His Trp  
-40 -35 -30

Lys Val Arg Asn Phe Glu Val His Arg Gly Asp Ile Val Ser Leu Val  
-25 -20 -15

Leu Leu Thr Val Thr Pro Ser Xaa Arg Gln Gln Glu  
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -23..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.1  
seq WLLVLSFVFGCNV/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

```
Met Ser Ser Ala Ala Ala Asp His Trp Ala Trp Leu Leu Val Leu Ser
-20 -15 -10
```

Phe Val Phe Gly Cys Asn Val Leu Arg Ile Leu Xaa Pro Xaa Xaa Xaa  
-5 1 5

Ile Xaa Xaa Val Gln Gly Ala Ala Glu Gly Arg Gly Xaa Glu Ser Gln  
10 15 20 25

Met Arg Ala Glu Ile Gln Asp Met Lys Gln Glu Leu Ser Thr Val Asn  
30 35 40

Met Met Asp Glu Phe Ala Arg Tyr Ala Arg Leu Xaa Arg Lys Ile Asn  
45 50 55

Lys Met Thr Asp Lys  
60

(2) INFORMATION FOR SEQ ID NO: 517:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -20..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8  
seq HVFFLLLLLAHIIA/LE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

Met Asn Leu Phe Lys Thr Asn His Val Phe Phe Leu Leu Leu Leu Ala  
-20 -15 -10 -5

His Ile Ile Ala Leu Glu Ser Ile Ala Trp Phe Thr Val Phe Tyr Phe  
1 5 10

Gly Asn

(2) INFORMATION FOR SEQ ID NO: 518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -24..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

Met Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg  
-20 -15 -10

Val Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro  
-5 1 5

Ala Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly  
10 15



## (2) INFORMATION FOR SEQ ID NO: 519:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -66..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

Met Ile Gly Ser Gly Leu Ala Gly Ser Gly Gly Ala Gly Gly Pro Ser  
-65 -60 -55

Ser Thr Val Thr Trp Cys Ala Leu Phe Ser Asn His Val Ala Ala Thr  
-50 -45 -40 -35

Gln Ala Ser Leu Leu Leu Ser Phe Val Trp Met Pro Ala Leu Leu Pro  
-30 -25 -20

Val Ala Ser Arg Leu Leu Leu Leu Pro Arg Val Leu Leu Thr Met Ala  
-15 -10 -5

Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro Ala Ser Asp Ser Gly Ser  
1 5 10

Gly Tyr Val Pro Gly Ser Val Ser Ala Ala Phe Val Thr Cys Pro Arg  
15 20 25 30

## (2) INFORMATION FOR SEQ ID NO: 520:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

- (B) LOCATION: -24...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

```

Met Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg
 -20 -15 -10
Val Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro
 -5 1 5
Ala Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly Ser Val Ser Ala Ala
 10 15 20
Phe Val Thr Cys Pro Asn Glu Lys Val Ala Lys Glu Ile Ala Arg Ala
 25 30 35 40
Val Val Glu Lys Arg Leu Ala Ala Cys Val Asn Leu Ile Pro Gln Ile
 45 50 55
Thr Ser Ile Tyr Glu Trp Lys Gly Xaa Ile Glu Glu Asp Ser Glu Val
 60 65 70
Leu Met Met Ile Lys Thr Gln Ala
 75 80

```

(2) INFORMATION FOR SEQ ID NO: 521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -92...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq FLLLTVALLASYS/VH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

```

Met Glu Ala Ser Trp Gly Ser Phe Asn Ala Glu Arg Gly Trp Tyr Val
 -90 -85 -80
Ser Val Gln Gln Pro Glu Glu Ala Glu Ala Glu Glu Leu Ser Pro Leu
 -75 -70 -65

```

Leu Ser Asn Glu Leu His Arg Gln Arg Ser Pro Gly Val Ser Phe Gly  
 -60 -55 -50 -45  
 Leu Ser Val Phe Asn Leu Met Asn Ala Ile Met Gly Ser Gly Ile Leu  
 -40 -35 -30  
 Gly Leu Ala Tyr Val Met Ala Asn Thr Gly Val Phe Gly Phe Ser Phe  
 -25 -20 -15  
 Leu Leu Leu Thr Val Ala Leu Leu Ala Ser Tyr Ser Val His Leu Leu  
 -10 -5 1  
 Leu Ser Met Cys Ile Gln Thr Ala Val Thr Ser Tyr Glu Asp Leu Gly  
 5 10 15 20  
 Leu Phe Ala Phe Gly Leu Pro Gly Leu  
 25

## (2) INFORMATION FOR SEQ ID NO: 522:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq FFLLLRFFLRIDG/VP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

Met Pro Ser Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp  
 -15 -10 -5  
 Gly Val Pro  
 1

## (2) INFORMATION FOR SEQ ID NO: 523:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.6  
seq FIVGIYFLSSCRA/EE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

```
Met Lys Arg Thr His Leu Phe Ile Val Gly Ile Tyr Phe Leu Ser Ser
 -15 -10 -5

Cys Arg Ala Glu Glu Gly Leu Asn Phe Pro Thr Tyr Asp Gly Lys Asp
 1 5 10

Arg Val Val Ser Leu Ser Glu Lys Asn Phe Lys Gln Val Leu
 15 20 25
```

## (2) INFORMATION FOR SEQ ID NO: 524:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -23..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.4  
seq VLLLAALPPVLLP/GA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

```
Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
 -20 -15 -10

Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
 -5 1 5

Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
 10 15 20 25

Tyr Gln Pro Met Pro Leu Xaa Ala Ser Leu Glu Ile Glu
 30 35
```

## (2) INFORMATION FOR SEQ ID NO: 525:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3  
seq LLSACLVTWGLG/EP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His  
-35 -30 -25  
Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr  
-20 -15 -10  
Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val  
-5 1 5 10  
Leu Xaa Leu Ala Ser Leu Gln Leu Gly  
15 20

## (2) INFORMATION FOR SEQ ID NO: 526:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3  
seq HLLLLLLPAPTLK/GL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

Met Gly Ala Trp Gly Arg Gly Trp Pro Trp Glu Glu Arg Gln Gly His  
                   -25                  -20                  -15

His Leu Leu Leu Leu Leu Pro Ala Pro Thr Leu Lys Gly Leu Gly  
                   -10                  -5                  1

Ala Ala Gln Leu Pro Leu Cys Pro Ser Gly Gly Leu Ser Pro Leu Leu  
           5                  10                  15

Thr Leu Leu Gln Ser Gly  
   20                  25

## (2) INFORMATION FOR SEQ ID NO: 527:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -75..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq LLFIIGLIGCCAT/IR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

Met Gly Gln Cys Gly Ile Thr Ser Ser Lys Thr Val Leu Val Phe Leu  
 -75                  -70                  -65                  -60

Asn Leu Ile Phe Trp Gly Ala Ala Gly Ile Leu Cys Tyr Val Gly Ala  
                   -55                  -50                  -45

Tyr Val Phe Ile Thr Tyr Asp Asp Tyr Asp His Phe Phe Glu Asp Val  
                   -40                  -35                  -30

Tyr Thr Leu Ile Pro Ala Val Val Ile Ile Ala Val Arg Ala Leu Leu  
                   -25                  -20                  -15

Phe Ile Ile Gly Leu Ile Gly Cys Cys Ala Thr Ile Arg Glu Ser Arg  
                   -10                  -5                  1                  5

Cys Gly Leu Ala Thr Phe Val Ile Ile Leu Leu Leu Val Phe Val Thr  
                   10                  15                  20

Glu Val Val Val Val Val Leu Gly Tyr Val Tyr Arg Ala Lys Val Glu  
                   25                  30                  35

Asn Glu Val Asp Arg Ser Ile Gln Lys Val Tyr Lys  
                   40                  45

## (2) INFORMATION FOR SEQ ID NO: 528:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -65...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq IGHFLCLVLVYC/AE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

```

Met Pro Xaa Ala Phe Ser Val Ser Ser Phe Pro Val Ser Ile Pro Ala
-65 -60 -55 -50

Val Leu Thr Gln Thr Asp Trp Thr Glu Pro Trp Leu Met Gly Leu Ala
 -45 -40 -35

Thr Phe His Ala Leu Cys Val Leu Leu Thr Cys Leu Ser Ser Arg Ser
 -30 -25 -20

Tyr Arg Leu Gln Ile Gly His Phe Leu Cys Leu Val Ile Leu Val Tyr
-15 -10 -5

Cys Ala Glu Tyr Ile Asn Glu Ala Ala Ala Met Asn Trp Arg Leu Phe
 1 5 10 15

Ser Xaa Tyr Gln Tyr Phe Asp Ser Arg Gly Met Phe Ile Ser Ile Val
 20 25 30

Phe Ser Ala Pro Leu Leu Val Asn Ala Met Ile Ile Val Val Met Trp
 35 40 45

Val Trp Lys
 50

```

## (2) INFORMATION FOR SEQ ID NO: 529:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq LLLSLFFPLRISL/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

```

Met Leu Leu Leu Ser Leu Phe Phe Pro Leu Arg Ile Ser Leu Ser Pro
 -10 -5 1
Ser Asn His Leu Trp Ser Ala Ser Ser Gly
 5 10

```

## (2) INFORMATION FOR SEQ ID NO: 530:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6  
seq LILVLQLLLRIRR/NR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

```

Met Glu Thr Gly Glu Arg Ala Arg Leu Ile Leu Ile Leu Val Leu Gln
 -20 -15 -10
Leu Leu Leu Arg Ile Arg Arg Asn Arg Gln Gln Arg Cys Xaa Ala Ser
 -5 1 5
Ser Ala Thr Ala Pro Ser Ser His Gly Cys Asp Leu Arg Gly Gly Lys
 10 15 20 25
Leu Asn Phe Lys Thr Thr Pro Met Asp Ala Asp Ser Asp Val Ala Leu
 30 35 40
Asp Ile Leu Ile Thr Asn Val Val Cys Val Phe Arg Thr Arg Cys Arg

```



45

50

55

## (2) INFORMATION FOR SEQ ID NO: 531:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4  
seq ILGCSSVCQLCTG/RQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

Met Cys Gly Xaa Xaa Phe Ser Leu Pro Cys Leu Arg Leu Phe Leu Val  
-40 -35 -30

Val Thr Cys Tyr Xaa Leu Leu Leu Leu His Lys Glu Ile Leu Gly Cys  
-25 -20 -15 -10

Ser Ser Val Cys Gln Leu Cys Thr Gly Arg Gln Ile Asn Cys Arg Asn  
-5 1 5

Leu Gly Leu Ser Ser Ile Leu Arg Ile Phe Leu Lys Val Gln Phe Phe  
10 15 20

Cys Ile  
25

## (2) INFORMATION FOR SEQ ID NO: 532:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

(E) LOCATION: -73..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.4  
 seq ACCFLSAFSPTLT/KS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

```

Met Asn Pro Val Thr Glu Ser Pro Ser Cys Leu Phe Ser Pro Pro Ser
 -70 -65 -60

Glu Ser Ala Leu Ala Ser Gln Leu Ala Leu Ser Ala Ser Cys Asp Gln
 -55 -50 -45

Arg Ala Pro Phe Ser Leu Ala Gly Val Xaa Ser Xaa Xaa Pro Arg Leu
 -40 -35 -30

Ala Ser Arg Gln Val Ala Pro Pro Phe Gly Ser Arg Ala Cys Cys Phe
 -25 -20 -15 -10

Leu Ser Ala Phe Ser Pro Thr Leu Thr Lys Ser Ala Ala Ala Thr Ser
 -5 1 5

Thr Ala His Thr Phe Leu Ala Asn Gln Leu Ser Cys Leu Phe Thr Lys
 10 15 20

Cys Leu His Asn Asn Tyr Ser Ser Ser Leu Arg Leu Thr Lys Lys Gln
 25 30 35

Glu Lys Ser Thr Thr Pro Gln
 40 45

```

(2) INFORMATION FOR SEQ ID NO: 533:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -21..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.3  
 seq LGLSVLLTAATVA/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

```

Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu Thr
 -20 -15 -10

Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp

```

-5

1

5

## (2) INFORMATION FOR SEQ ID NO: 534:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3  
seq GVGLVTLLGLAVG/SY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

```
Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
-25 -20 -15

Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
-10 -5 1 5

Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Ser Glu Lys Tyr Leu
10 15 20

Leu Arg Leu Leu Asp Lys Thr Thr Pro Gly
25 30
```

## (2) INFORMATION FOR SEQ ID NO: 535:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -51..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2  
seq VLLSSAXLVXXS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

```

Met Tyr Pro Ser Tyr Leu Leu Ile Xaa Pro Pro Ile Pro Ser Gln Phe
-50 -45 -40

Leu Lys Gln Cys Xaa Pro Pro Thr Leu Ser Asp Pro Phe Leu Pro Leu
-35 -30 -25 -20

Ala Leu Arg Ser Leu Asp Val Leu Leu Leu Ser Ser Ala Xaa Leu Val
 -15 -10 -5

Xaa Xaa Ser Ser Pro Leu Glu Phe Ile Arg
 1 5

```

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2  
seq ILLXTFQWCLR/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

```

Met Glu Gln Lys His Arg Xaa Glu Leu Glu Gln Leu Lys Leu Xaa Thr
-30 -25 -20

Lys Glu Asn Lys Ile Leu Leu Leu Xaa Thr Phe Gln Thr Trp Cys Leu
-15 -10 -5

Arg Ile Ser His Leu Gly Tyr Gln Lys His Xaa Arg Xaa Gly Cys Leu
 1 5 10 15

Asp Xaa Arg Ser Ser Leu Cys Cys Pro Trp
 20 25

```

(2) INFORMATION FOR SEQ ID NO: 537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9  
seq TLKFLTLQKSNA/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

```
Met Met Thr Ala Pro Val Leu Ala Ala Gln Thr Leu Lys Phe Leu Thr
 -20 -15 -10

Leu Leu Gln Lys Ser Asn Ala Lys Arg Xaa Asn Leu Asp Arg Leu His
 -5 1 5

Asp Glu Leu Trp Tyr Asn Asp Pro Gly Gln Met Asn Asp Gly Pro Leu
 10 15 20 25

Cys Lys Cys Ser Ala Lys Ala Arg Arg Thr Gly Ile Arg His Ser Ile
 30 35 40

Tyr Pro Gly Glu Glu Ala Ile Lys Pro Cys Arg Pro Met Thr Asn Asn
 45 50 55

Ala Gly Arg Leu Phe His Tyr Arg Ile Thr Val Ser Pro Pro Thr Asn
 60 65 70

Phe Leu Thr Asp Arg Pro Thr Val Ile Glu Tyr Asp Asp His Glu Tyr
 75 80 85

Ile Phe Glu
 90
```

(2) INFORMATION FOR SEQ ID NO: 538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -27..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.9

seq ALALAXAPDLAQA/PL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

```

Met Asp Ser Ala Ala Cys Ala Ala Ala Thr Pro Val Pro Ala Leu
 -25 -20 -15

Ala Leu Ala Xaa Ala Pro Asp Leu Ala Gln Ala Pro Leu Ala Leu Pro
 -10 -5 1 5

Gly Leu Leu Ser Pro Ser Cys Leu Leu Ser Ser Gly Gln Glu Val Asn
 10 15 20

Gly Ser Glu Arg Gly Thr Cys Leu Trp Arg Pro Trp Leu Ser Ser Thr
 25 30 35

Asn Asp Ser Pro Arg Gln Met Arg Lys Leu Val Asp Leu Ala Ala Gly
 40 45 50

Gly Ala Thr Ala Ala Glu Val Thr Lys Ala Glu Ser Xaa Xaa His His
 55 60 65

Pro Val Arg Leu Phe Trp
 70 75

```

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -24..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.7

seq ILGLLGLLGTLVA/ML

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

```

Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu
 -20 -15 -10

Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr
 -5 1 5

Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys

```

```

 10 15 20
Gly Leu Trp Met Glu Cys Ala Thr Xaa Ser Thr Gly Ile Thr Gln Cys
 25 30 35 40
Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala Asp Ile Gln Ala Ala
 45 50 55
Gln Ala Met Met Val Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile
 60 65 70
Ile Ser Val Val Gly Met Arg Cys Thr Val Phe Cys Gln Glu Ser Arg
 75 80 85
Ala Arg
 90

```

## (2) INFORMATION FOR SEQ ID NO: 540:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (E) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7  
seq ILGLLGLLGTLVA/ML

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

```

Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu
 -20 -15 -10
Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr
 -5 1 5
Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys
 10 15 20
Gly Leu Trp Met Glu Cys Ala
 25 30

```

## (2) INFORMATION FOR SEQ ID NO: 541:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids

- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6  
seq LLCECLLLVAGYA/HD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

```
Met Leu Cys Ser Leu Leu Leu Cys Glu Cys Leu Leu Leu Val Ala Gly
 -15 -10 -5
Tyr Ala His Asp Asp Asp Trp Ile Asp Pro Thr Asp Met Leu Asn Tyr
 1 5 10
Asp Ala Ala Ser Gly Thr Met Arg Lys Ser
15 20
```

(2) INFORMATION FOR SEQ ID NO: 542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq LWYVCPCPSGAWM/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

```
Met Ala Ser Arg Leu Cys Gly Gly Ala Leu Trp Tyr Val Cys Pro Cys
 -20 -15 -10
Pro Ser Gly Ala Trp Met Val Pro Gly
 -5 1
```



## (2) INFORMATION FOR SEQ ID NO: 543:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5  
seq LGYLVLSEGAFLA/SS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

Met Thr Ser Ala Leu Thr Gln Gly Leu Glu Arg Ile Pro Asp Gln Leu  
-25 -20 -15

Gly Tyr Leu Val Leu Ser Glu Gly Ala Val Leu Ala Ser Ser Gly Asp  
-10 -5 1

Leu Glu Asn Asp Glu Gln Ala Xaa Ser Ala Ile Ser Glu Leu Val Ser  
5 10 15 20

Thr Ala Cys Gly Phe Arg Leu His Arg Gly Met Asn Val Pro Arg  
25 30 35

## (2) INFORMATION FOR SEQ ID NO: 544:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -42..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4  
seq ITGVILLAVGIWG/KV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

```

Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys
 -40 -35 -30

Phe Lys Ser Val Leu Leu Ile Xaa Thr Xaa Ile Xaa Trp Ile Thr Gly
 -25 -20 -15

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn
 -10 -5 1 5

Tyr Phe Xaa Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Xaa Leu
 10 15 20

Ile Ala Thr Gly Thr Val Xaa Ile Leu Leu Gly Tyr Arg
 25 30 35

```

## (2) INFORMATION FOR SEQ ID NO: 545:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3  
seq VLLGSGLTILSQP/IM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

```

Met Ala Asp Ala Ala Ser Gln Val Leu Leu Gly Ser Gly Leu Thr Ile
-20 -15 -10 -5

Leu Ser Gln Pro Leu Met Tyr Val Lys Val Leu Ile Gln Val Gly Tyr
 1 5 10

Glu Pro Leu Pro Pro Thr Ile Gly Arg Asn Ile Phe Gly Arg Gln Val
 15 20 25

Xaa Xaa Leu Pro Xaa Leu Phe Ser Tyr Ala Gln His Gly
 30 35 40

```

## (2) INFORMATION FOR SEQ ID NO: 546:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids

(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -20..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.3  
seq ALIFGGFISLIGA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

Met Ser Arg Asn Leu Arg Thr Ala Leu Ile Phe Gly Gly Phe Ile Ser  
-20 -15 -10 -5

Leu Ile Gly Ala Ala Phe Tyr Pro Ile Tyr Phe Arg Pro His Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 547:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -17..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 5.1  
seq LWCFHLVVLSLYS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

Met Pro His Gly Leu Trp Cys Phe His Leu Val Val Leu Ser Leu Tyr  
-15 -10 -5

Ser Ser Val Ala Thr Ala Arg  
1 5

(2) INFORMATION FOR SEQ ID NO: 548:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 35 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (D) DEVELOPMENTAL STAGE: Fetal  
    (F) TISSUE TYPE: kidney
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -14..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 5  
                            seq SLVAVFLSCGLIS/KN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

Met Ser Leu Val Ala Val Phe Leu Ser Cys Gly Leu Ile Ser Lys Asn  
                    -10                    -5                    1

His Met Leu Leu Asn Leu Pro Gly Ile Leu Ile Pro His Asn Ala Asn  
            5                    10                    15

His Leu Leu  
            20

(2) INFORMATION FOR SEQ ID NO: 549:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 42 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Kidney
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -24..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 5  
                            seq GALAVGAVPVVLS/AM
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

Met Met Lys Arg Ala Ala Ala Ala Val Gly Gly Ala Leu Ala Val  
                    -20                    -15                    -10

Gly Ala Val Pro Val Val Leu Ser Ala Met Gly Phe Thr Gly Ala Gly  
            -5                    1                    5

Ile Ala Ala Ser Ser Ile Ala Ala His Gly  
 10 15

(2) INFORMATION FOR SEQ ID NO: 550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -81..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9  
 seq LISFSWFANYIRA/GT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

Met Ala Val Ile Val Asp Lys Pro Trp Phe Tyr Asp Met Lys Lys Val  
 -30 -75 -70

Trp Glu Gly Tyr Pro Ile Gln Ser Thr Ile Pro Ser Gln Tyr Trp Tyr  
 -65 -60 -55 -50

Tyr Met Ile Glu Leu Ser Phe Tyr Trp Ser Leu Leu Phe Ser Ile Ala  
 -45 -40 -35

Ser Asp Val Lys Arg Lys Asp Phe Lys Glu Gln Ile Ile His His Val  
 -30 -25 -20

Ala Thr Ile Ile Leu Ile Ser Phe Ser Trp Phe Ala Asn Tyr Ile Arg  
 -15 -10 -5

Ala Gly Thr Leu Ile Met Ala Leu His Asp Ser Ser Asp Tyr Leu Leu  
 1 5 10 15

Glu Ser Ala Lys Met Phe Asn Tyr Ala Gly Trp Lys Asn Thr Cys Asn  
 20 25 30

Asn Ile Phe Thr Val Phe Ala Ile Val Phe Ile Ile Thr Arg Leu Val  
 35 40 45

Ile Leu Pro Phe Trp Ile Leu His Cys  
 50 55

(2) INFORMATION FOR SEQ ID NO: 551:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 78 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (D) DEVELOPMENTAL STAGE: Fetal  
    (F) TISSUE TYPE: kidney
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -16..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 4.8  
                            seq SLFIYIFLTCSNT/SP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser Asn Thr  
-15                                 -10                                 -5

Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala  
1                                 5                                 10                                 15

Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe  
20                                 25                                 30

Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His Leu Ile  
35                                 40                                 45

Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Gly Thr  
50                                 55                                 60

- (2) INFORMATION FOR SEQ ID NO: 552:
- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 86 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (D) DEVELOPMENTAL STAGE: Fetal  
    (F) TISSUE TYPE: kidney
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -32..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 4.7  
                            seq LQMLLG FVGRSKS/GL
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

```

Met Ala Ala Glu Leu Val Glu Ala Lys Asn Met Val Met Ser Phe Arg
 -30 -25 -20

Val Ser Asp Leu Gln Met Leu Leu Gly Phe Val Gly Arg Ser Lys Ser
 -15 -10 -5

Gly Leu Lys His Glu Leu Val Thr Arg Ala Leu Gln Leu Val Gln Phe
 1 5 10 15

Asp Cys Ser Pro Glu Leu Phe Lys Lys Ile Lys Glu Leu Tyr Glu Thr
 20 25 30

Arg Tyr Ala Lys Lys Asn Ser Glu Pro Ala Pro Gln Pro His Arg Pro
 35 40 45

Leu Asp Pro Leu Thr Gly
 50

```

## (2) INFORMATION FOR SEQ ID NO: 553:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7  
seq VHALCPLSPLVTT/GC

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

```

Met Thr Gly Leu Ser Met Xaa Gly Gly Gly Ser Xaa Xaa Gly Asp Val
-60 -55 -50 -45

Xaa Pro Xaa Tyr Tyr Gly Lys Xaa Gly Pro Leu Arg Xaa Leu Pro Glu
 -40 -35 -30

Pro Ser Gly Pro Leu Pro Pro Ser Ser Gly Leu Ser Gln Pro Gln Val
 -25 -20 -15

His Ala Leu Cys Pro Leu Ser Pro Leu Val Thr Thr Gly Cys Cys Gly
 -10 -5 1

Gln Ala Ala
 5

```

## (2) INFORMATION FOR SEQ ID NO: 554:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6  
seq GLLGXGLXXXSLT/AG

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Xaa Glu Trp Leu Thr Ile  
-30 -25 -20

Gln Gly Gly Leu Leu Gly Xaa Gly Leu Xaa Xaa Xaa Ser Leu Thr Ala  
-15 -10 -5 1

Gly

## (2) INFORMATION FOR SEQ ID NO: 555:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -54..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
seq LIVWLLVKSFSES/GI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg Arg Ser Arg Arg Glu



-50                      -45                      -40  
 Leu Glu Val Arg Ser Pro Arg Gln Asn Lys Tyr Ser Val Leu Leu Pro  
                          -35                      -30                      -25  
 Thr Tyr Asn Glu Arg Glu Asn Leu Pro Leu Ile Val Trp Leu Leu Val  
                          -20                      -15                      -10  
 Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu Ile Ile Ile Ile Asp  
                          -5                      1                      5                      10  
 Asp Gly Ser Pro Asp Gly Thr Arg Asp Val Ala Glu Gln Leu Glu Lys  
                          15                      20                      25  
 Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro Arg Glu Lys Lys Leu  
                          30                      35                      40  
 Gly Leu Gly Thr Ala Tyr Ile Xaa Xaa Met Lys His Ala Gln Glu Thr  
                          45                      50                      55  
 Thr Ser Leu Leu Trp Xaa Leu Ile Ser His  
                          60                      65

## (2) INFORMATION FOR SEQ ID NO: 556:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3  
seq LLDSSLMASGTAS/RS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

Met Asp Lys Asp Ser Gln Gly Leu Leu Asp Ser Ser Leu Met Ala Ser  
 -20                      -15                      -10                      -5  
 Gly Thr Ala Ser Arg Ser Glu Asp Glu Glu Ser Leu Ala Gly Gln Lys  
                          1                      5                      10  
 Arg Ala Ser Ser Gln Ala Leu Gly Thr Gly  
                          15                      20

## (2) INFORMATION FOR SEQ ID NO: 557:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 83 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (D) DEVELOPMENTAL STAGE: Fetal  
    (F) TISSUE TYPE: kidney
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -36..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 4.2  
                            seq CLAVSWEAAGCHG/AG
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

Met Gly Leu Leu Thr Phe Gly Tyr Ile Glu Xaa Xaa Xaa Lys Thr Glu  
-35 -30 -25

His Asn Pro Asp His His Ser Cys Leu Ala Val Ser Trp Glu Ala Ala  
-20 -15 -10 -5

Gly Cys His Gly Ala Gly Thr Gln Gln Ser Pro Leu Gly Val Ala Gly  
1 5 10

Pro Trp Arg Pro Arg Pro Pro Cys Val Gly Ser Leu Leu Ala Ala Arg  
15 20 25

Ser Leu His Lys Gln Val Ile Leu Phe Gly Leu Leu Gly Phe Ala Tyr  
30 35 40

Asp His Trp  
45

(2) INFORMATION FOR SEQ ID NO: 558:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 65 amino acids  
    (B) TYPE: AMINO ACID  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (F) TISSUE TYPE: Dystrophic muscle
- (ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: -16..-1  
    (C) IDENTIFICATION METHOD: Von Heijne matrix  
    (D) OTHER INFORMATION: score 4.1  
                            seq YAAVAGVLAGVES/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

Met Gly Leu Tyr Ala Ala Val Ala Gly Val Leu Ala Gly Val Glu Ser  
-15 -10 -5

Arg Gln Gly Ser Asn Gln Gly Ala Gly Val Leu Gln Gln Leu Pro Glu  
1 5 10 15

Arg Glu Xaa Ala Val Arg Ala Gly Val Arg Xaa Ala Ala Leu Leu Arg  
20 25 30

Arg Ala Gly Xaa Arg Asp Leu Gln Arg Arg Pro Pro Gln Cys Glu Glu  
35 40 45

Ala

(2) INFORMATION FOR SEQ ID NO: 559:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -62..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.1  
seq LDAVIASAGLLRA/EK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

Met Gly Leu Tyr Ala Ala Ala Ala Gly Val Leu Ala Gly Val Glu Ser  
-60 -55 -50

Arg Gln Gly Ser Ile Lys Gly Leu Val Tyr Ser Ser Asn Phe Gln Asn  
-45 -40 -35

Val Lys Gln Leu Tyr Ala Leu Val Cys Glu Thr Gln Arg Tyr Ser Ala  
-30 -25 -20 -15

Val Leu Asp Ala Val Ile Ala Ser Ala Gly Leu Leu Arg Ala Glu Lys  
-10 -5 1

Lys Leu Arg Pro His Leu Ala Lys Val Leu Val Tyr Glu Leu Leu Leu  
5 10 15

Gly Lys Gly Phe Arg Gly Gly Gly Gly Arg Trp Lys Ala Arg  
20 25 30

## (2) INFORMATION FOR SEQ ID NO: 560:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -64..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1  
seq WLLRLAYLADIFT/KL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

```

Met Gly Ala Gln His Thr Ala Leu Leu Leu Asn Thr Glu Val Arg Trp
 -60 -55 -50

Leu Ser Arg Gly Lys Val Leu Val Arg Leu Phe Glu Leu Arg Arg Glu
 -45 -40 -35

Leu Leu Val Phe Met Asp Ser Ala Phe Arg Leu Ser Asp Cys Leu Thr
 -30 -25 -20

Asn Ser Ser Trp Leu Leu Arg Leu Ala Tyr Leu Ala Asp Ile Phe Thr
 -15 -10 -5

Lys Leu Asn Glu Val Asn Leu Ser Met Gln Gly Lys Asn Val Thr Val
 1 5 10 15

Phe Thr Val Phe Asp Lys Met Ser Ser Leu Leu Arg Lys Leu Glu Phe
 20 25 30

Trp Ala Ser Ser Val Glu Glu Glu Asn Phe Asp Cys Phe Pro Thr Leu
 35 40 45

Ser Asp Phe Leu Thr Glu Ile Asn Ser Thr Val Asp Lys Asp Ile Cys
 50 55 60

Ser Ala Ile Val Gln His Leu Arg Gly Leu Arg Ala Thr Leu Leu Lys
 65 70 75 80

Tyr Phe Pro Val Thr Asn Asp
 85

```

## (2) INFORMATION FOR SEQ ID NO: 561:

## (i) SEQUENCE CHARACTERISTICS;

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4  
seq LVVMVPLVGLIHL/GW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

```
Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Val Met
-25 -20 -15 -10

Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser
 -5 1 5

Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asn Met
 10 15
```

(2) INFORMATION FOR SEQ ID NO: 562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -51..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq GKLLQLVLGCAIS/CE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

```
Met Val Leu Arg Ser Leu Val Glu Tyr Ser Gln Asp Val Leu Ala His
-50 -45 -40

Pro Val Ser Glu Glu His Leu Pro Asp Val Ser Leu Ile Gly Glu Phe
-35 -30 -25 -20

Ser Asp Pro Ala Glu Leu Gly Lys Leu Leu Gln Leu Val Leu Gly Cys
```

-15                  -10                  -5  
Ala Ile Ser Cys Glu Lys Lys Gln Asp His Ile Gln Arg Ile Met Thr  
                  1                  5                  10  
Leu Glu Glu Ser Val Gln His Val Val Met Glu Ala Ile Gln Glu Leu  
          15                  20                  25  
Met Thr Lys Asp Thr Pro Asp Ser Leu Ser Pro Glu Thr Tyr Gly Asn  
          30                  35                  40                  45  
Phe Asp Ser Gln Ser Arg Ser Thr Gly  
                  50

## (2) INFORMATION FOR SEQ ID NO: 563:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9  
seq MIHGFCLAPTSA/KN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

Met Ile His Gly Phe Cys Leu Ala Pro Thr Thr Ser Ala Lys Asn Ala  
          -10                  -5                  1

## (2) INFORMATION FOR SEQ ID NO: 564:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide

(B) LOCATION: -17..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: . score 3.7  
 seq RTWCLACVEASPG/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

Met Xaa Cys Pro Arg Thr Trp Cys Leu Ala Cys Val Glu Ala Ser Pro  
           -15                    -10                    -5  
 Gly Gln Pro Phe Leu Pro Pro Arg Pro Gly  
       1                                    5

(2) INFORMATION FOR SEQ ID NO: 565:

(i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 67 amino acids  
     (B) TYPE: AMINO ACID  
     (D) TOPOLOGY: LINEAR  
 (ii) MOLECULE TYPE: PROTEIN  
 (vi) ORIGINAL SOURCE:  
     (A) ORGANISM: Homo Sapiens  
     (F) TISSUE TYPE: Dystrophic muscle  
 (ix) FEATURE:  
     (A) NAME/KEY: sig\_peptide  
     (B) LOCATION: -21..-1  
     (C) IDENTIFICATION METHOD: Von Heijne matrix  
     (D) OTHER INFORMATION: . score 3.7  
                                     seq ETCALASHSGSSG/SK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His  
       -20                    -15                    -10  
 Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu  
       -5                                    1                    5                    10  
 Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp  
           15                                    20                    25  
 Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Xaa Arg Cys  
       30                                    35                    40  
 Gln Ala Gly  
       45

(2) INFORMATION FOR SEQ ID NO: 566:

(i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 28 amino acids  
     (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN .

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -26..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.7  
seq IIMFLLIIVCGSP/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

Met Phe Lys Val Ala Ala Pro Pro Met Leu Ile Xaa Xaa Ile Ile Met  
-25 -20 -15

Phe Leu Leu Ile Ile Val Cys Gly Ser Pro Arg Pro  
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -21..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.6  
seq FXMCLWSLRNLFS/RC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

Met Asp Phe Trp Asp Pro Ala Val Phe Xaa Met Cys Leu Trp Ser Leu  
-20 -15 -10

Arg Asn Leu Phe Ser Arg Cys Ser Pro Cys Leu Thr Glu Ile Ser Leu  
-5 1 5 10

His Leu Val His Leu Thr Ala Glu Lys Lys Gln His Gly Ser Asn Asn  
15 20 25

Gly Ser Ala  
30



## (2) INFORMATION FOR SEQ ID NO: 568:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6  
seq SVPLLSLSHSIGI/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

Met Ser Pro Ala Gly Lys His Asn Ser Glu Ser Lys Phe Thr Phe Phe  
                  -30                  -25                  -20  
Val Ala Leu Asp Gly Ser Val Pro Leu Leu Ser Leu Ser His Ser Ile  
                  -15                  -10                  -5  
Gly Ile Ser Pro Thr Arg  
                  1

## (2) INFORMATION FOR SEQ ID NO: 569:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq LVCVGLHTEGPWG/RP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

Met His Trp Ala Leu Val Cys Val Gly Leu His Thr Glu Gly Pro Trp  
           -15                          -10                          -5

Gly Arg Pro Ser Gly Leu Ala Ser Ala Ser Gly Met Asp Arg Ala Arg  
       1                              5                              10                              15

Gln Ala Ser Glu Leu Pro Pro Pro Gly Ala Ser Gln Thr Pro Gln  
                           20                                  25                                  30

## (2) INFORMATION FOR SEQ ID NO: 570:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -72..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5  
seq WFYIGSSLNGTRG/KR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

Met Phe Gly Ala Ala Ala Arg Ser Ala Asp Leu Val Leu Leu Glu Lys  
           -70                          -65                          -60

Asn Leu Gln Ala Ala His Gly Tyr Ala Gln Glu Asp Arg Glu Arg Met  
       -55                              -50                              -45

His Arg Xaa Ile Val Ser Leu Xaa Gln Asn Leu Leu Asn Phe Met Ile  
       -40                              -35                              -30                              -25

Gly Ser Ile Leu Asp Leu Trp Gln Cys Phe Leu Trp Phe Tyr Ile Gly  
                           -20                                  -15                                  -10

Ser Ser Leu Asn Gly Thr Arg Gly Lys Arg Val Pro Ala His Phe  
           -5                                  1                                  5

## (2) INFORMATION FOR SEQ ID NO: 571:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Heart .

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -27..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq VVALLIVCDVPSA/SA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

```
Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val
 -25 -20 -15

Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Arg
 -10 -5 1
```

## (2) INFORMATION FOR SEQ ID NO: 572:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -16..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq LLLQPSMIQEVWT/XY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

```
Met Val Val Leu Leu Leu Gln Pro Ser Met Ile Gln Glu Val Trp Thr
 -15 -10 -5

Xaa Tyr Ala Asn Leu Phe His Ser Phe Phe Val Asp Asn Pro Phe Gln
 1 5 10 15

Lys Glu Cys Phe His Gln Lys Asn Trp Tyr His Ile Thr Leu Met Gln
 20 25 30

Arg Thr Val Gly Thr Trp Arg Ile Leu Pro Asn Phe Leu Lys His Asp
 35 40 45
```

## (2) INFORMATION FOR SEQ ID NO: 573:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5  
seq LAVLLSLAPSASS/DI

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

Met Leu His Leu His Xaa Ser Cys Leu Cys Phe Arg Ser Trp Leu Pro  
-30 -25 -20

Ala Met Leu Ala Val Leu Leu Ser Leu Ala Pro Ser Ala Ser Ser Asp  
-15 -10 -5 1

Ile Ser Ala Ser Arg Pro Asn Ile Leu Leu Leu Met Ala Asp Asp Leu  
5 10 15

Gly Ile Gly Asp Ile Gly Cys Tyr Gly Asn Asn Thr Met Arg Thr Pro  
20 25 30

Xaa Ile Asp Arg Leu Ala Glu Asp Gly Val Lys Leu Thr Gln His Ile  
35 40 45

Ser Ala Ala Ser Leu Cys  
50 55